Fr m:

Chan, Christina

Sent:

To: Subject: Tuesday, January 07, 2003 10:25 AM
Duffy, Patricia; STIC-Biotech/ChemLib
RE: PLEASE RUSH SEQUENCE SEARCH--- Amendment due this Biweek

importance:

High

## Please rush Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message----

From: Duffy, Patricia

Sent: Monday, January 06, 2003 10:43 AM Chan, Christina

Subject:

PLEASE RUSH SEQUENCE SEARCH--- Amendment due this Biweek

Importance: High

In re: 09/438,185

Please search SEQ ID NO:1047.

Please search na residues 1200675-1199590 of SEQ ID NO:1.

Please include an interference search.

Please print out top 50 hits in each category.

Thank you.



AU 1645

703-305-7555

POINT OF CONTACT: PAUL SCHULWITZ TECHNICAL INFO. SPECIALIST CM1 6B06 TEL. (703) 305-1954

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| TYPE OF SEARCH: |
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| Structures:     |
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| Patent Family:  |
| Other:          |

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CURRENT APPLICATION NUMBER: US/09/205,658
CURRENT FILING DATE: 1998-12-03
EARLIER APPLICATION NUMBER: 08/857,076
EARLIER FILING DATE: 1997-05-15
EARLIER PLICATION NUMBER: 08/88,534
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EARLIER FILING DATE: 1997-07-07
EARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1642
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APPLICANT: RUYKUN, GARY
APPLICANT: OBG, SCOCT
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPARRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
                          Sequence 312, Application US/09205658
Patent No. US20010029617A1
GENERAL INFORMATION:
09-205-658-312/c
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Length 1642;
4.3%; Score 46.6; DB 10; Length 1
45.5%; Pred. No. 0.017;
ative 0; Mismatches 289; Indels
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Patent No. US/2010029617A1

GENERAL INFORMATION:
APPLICANT: RUNKUN, GARY

APPLICANT: OGG, SCOCT

TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FILE REFERENCE: 007086/351004

CURRENT APPLICATION NUMBER: US/09/205,658

CURRENT FILING DATE: 1998-12-03
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                          Similarity
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-09-205-658-314/c
  Query Match
                          Best Loca
Matches
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400 AAAGAAGTAGAGTTGCTAGCTTCTTCAAA-----TCTTCCTCTGATGCTCCAAGA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413 AAGAGTCTTCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473 IGCCCTAAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTT 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAACGTATTGAGTGCAGAAGAAGACACGATATGCAAGAACGTGCCAAGAAATCACGAGCT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459 ccarriterritacregas-aarcescascarcascascascaacaaarrcaaresa 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        579 TCAACAACACGATCCGGATCAAAACGAATAATGGTTGCACTACCCTCAACGGCATGTTGC 520
                                                                                                                                                                                                                                                                                                                                                                                      113 TCATCAAAATGTCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                              639 ICTICABABITICIAGIATAGAATACGCTGACTGGAAAGTAGTAATGAGACATTCTTGC 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACSULUA 3
SEQUENCE 1 APDIICATION US/0979098B
SEQUENCE 1 APDIICATION US/0979098B
SEQUENCE 1 APDIICATION
SECONDO 127687A1
SEQUENCE 1 STREAM SERVICE
SEQUENCE 1 STREAM SERVICE
SEQUENCE 1 SARAHIEN
SEQUENCE 1 SARAHIEN
SAPLICANT: SARAHIEN
SARAHIEN
SAPLICANT: SARAHIEN
SARAHIEN SARAHIEN
SAPLICANT: SARAHIEN
SARAHIEN SARAHIEN
SEDIER SERRENCE: 081356/0159
CURRENT APPLICATION UNMER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
SPRIOR APPLICATION NUMBER: JP2000-107160
SPRIOR FILING DATE: 2000-04-07
SOFTWARE PRODO 10 NOS: 7
SOFTWARE PATCHING UNCS: 7
SOFTWARE PATCHING UNCS: 7
SOFTWARE PATCHING UNCS: 7
SOFTWARE PATCHING UNCS: 7
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                  Score 41.4; DB 10; Length 817;
Pred. No. 0.28;
0; Mismatches 281; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593 GCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGA 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 08/857,076
EARLIER FILING DATE: 1997-05-15
EARLIER PLILING DATE: 1997-07-07
EARLIER APPLICATION NUMBER: 08/888,534
EARLIER APPLICATION NUMBER: 089/10080
EARLIER APPLICATION NUMBER: 089/10080
EARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SEQ_ID NO 314
                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-205-658-314
                                                                                                                                                                                                                                                                                                         3.8%;
Best Local Similarity 45.2%;
Matches 239; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228
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Xu, Tian XX, Tian TIIILE OF INVENTION: A NO. US20020127621A1el Family of Metalloproteases NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DD 190422 GTAGATGTTTTTTAAATGTTTTAAATTGTAATGTGAATCGTAGTAAAGTGAAGTGTATT 190481
                                                                                                                                                                                                                                                         Db 190182 ATAGTGCCTAAAAAAATATTAAAAATAATTTTTTCTCAATTATAGCCTGTATTCCTTGG 190241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD 190302 ACTAATTTAGTACAAAAAAAAAATCATAGAAGAAATAATCATATGGATACGCAT 190361
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 190242 AATCGAAACATCGTAACAACGTGTAATAGATCTTTTTAATTTTTAAATATACAACAT 190301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 TGTATGCGTTGTTTTTTACTAGGAAGAGCTTGTACTTTTTCTATGACTTTAGTGAAGAGT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 CTTCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACGTGCCCT 478
                                                                                                                                                                                                                                                                                                                                                                                                           299 CCGCTTTCAACAGTAAACCAAAAGCGGTACAATAGCGATCAGATTGCTTTGTAGGGTT 358
                                                                                                                                                                                                                                                                                                           179 ATCTGATCCAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCC 238
                                                                                                                                                                                                        119 AAATGTCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATA 178
                                                                                                                                                            0; Gaps
                                                                                                        Query Match 3.7%; Score 40.6; DB 10; Length 640681; Best Local Similarity 43.4%; Pred. No. 7.3; Matches 187; Conservative 0; Mismatches 244; Indels 0; C
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,388
FILING DATE: 31-May-2001
CLASSIFICATION: CUNKnown>
PRIOR APPLICATION: CUNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/937,931
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09871388 Patent No. US20020127621A1 GENERAL INFORMATION: GENERAL RUbin, Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA ZIP: 94104 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan, Duojia
Rooke, Jenny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yavari, Reza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      539 ACAGAGGCAAT 549
                    ; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
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LENGIH: 640681
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APPLICANT: Harper, Jeff
APPLICANT: Areps, Joel
APPLICANT: Areps, Joel
APPLICANT: Harper, Jeff
APPLICANT: Areps, Joel
APPLICANT: Hang, Xuol
APPLICANT: Mang, Xuol
TITLE OF INVEWTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVEWTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/224,647
PRIOR PLIAG DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR PLIAG DATE: 2001-06-2
NUMBER OF SEQ ID NOS: 5379
LENGTH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 TATGCGTTGTTTTTTACTAGGAAGAGCTTGTACTTTTTCTATGACTTTTAGTGAAGAGTCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 TATGCGTTGTTTTTTACTAGGAAGACTTGTACTTTTTCTATGACTTTTAGTGAAGAGTCT 420
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APPLICANT: Change, H.
APPLICANT: Change, H.
APPLICANT: Ann, B.
APPLICANT: Wang, Y.
APPLICANT: Wang, Y.
APPLICANT: Wang, Y.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1360.0010S1.
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,846
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR PLICATION NUMBER: US 60/214,087
PRIOR PLICATION NUMBER: US 60/258,692
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR PLICH GAME: 2000-06-23
PRIOR PLICH GAME: 2000-06-23
PRIOR PLICH GAME: 2000-06-23
PRIOR PLICH GAME: 2000-06-23
PRIOR SED ID NOS: 872
NUMBER OF SED ID NOS: 872
SOFTWARE: FESTSEQ for Windows Version 4.0
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3.4%; Score 36.4; DB 10; Length 2004;
Best Local Similarity 59.8%; Pred. No. 7.8;
Matches 61; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
3.4%; Score 36.4; DB 9; Length 2000;
Best Local Similarity 59.8%; Pred. No. 7.4%
Matches 61; Conservative 0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 TCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 256, Application US/09887576; Patent No. US20020144047A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Arabidopsis thaliana US-09-938-842A-3348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Arabidopsis thaliana US-09-887-576-256
   Patent No. US20020160378A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Budworth, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-09-887-576-256
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LENGTH: 2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            816 AGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fincher, Karen
APPLICANT: Fincher, Karen
APPLICANT: Fincher, Karen
APPLICANT: Fincher, Stanislaw
APPLICANT: Fincher, Jack
TITLE OF INVENTION: No. US20020144304Alel Plant Expression Constructs
FILE REFERENCE: 38-21(51499)B
CURRENT APPLICATION NUMBER: US/09/737,626A
CURRENT APPLICATION WUMBER: US/03/737,626
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
EEG ID NO 25
LENGTH: 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: promoter
LOCATION: (1)..(1241)
COTHER INFORMATION: n= a or g or c or t/u
COTHER INFORMATION: Act7 promoter polynucleotide sequence and intron US-09-737-626A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.4%; Score 36.6; DB 10; Length 2098; Best Local Similarity 65.1%; Pred. No. 7; Matches 54; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 3.4%; Score 36.4; DB 10; Length 1241; Best Local Similarity 59.8%; Pred. No. 6.3; Matches 61; Conservative 0; Mismatches 41; Indels 0;
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               NAME: OSNAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B97-081
TELECHONE: (415) 343-4341
TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2098 base pairs
                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-09-871-388-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-938-842A-3348
; Sequence 3348, Application US/09938842A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 25, Application US/09737626A
; Patent No. US20020144304A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       876 AAAATTCTAAAATAGAAATGCAT 898
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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US-09-737-626A-25
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CRAREAL INFORMATION:
APPLICANT: Li, Zuomei
APPLICANT: Li, Zuomei
APPLICANT: Bonfils, Claire
APPLICANT: Bosterman, Jeffrey
APPLICANT: Bosterman, Jeffrey
TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
FILE REFERENCE: 106101.145
CURRENT APPLICATION WHMER: US/09/817,913
CURRENT FILING DATE: 2000-03-26
PRIOR APPLICATION WHERE: US 60/192,157
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 33
SOGTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              799 AACAGCCATATCAGIGGAGCAACCTTCCCTTIGATTGTAATGACAGAAGAIGAAC 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 ATCAGCCACATTCTTCGACCTCCTTCTCCTTCATCCTCAGAATCTGAGAATTCTTCATC 442
                        859 AAAGAGTAAGTTTTTGAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTAAAGCTTG 918
                                                                                                                 799 AACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAAC 858
                                                                                                                                                                                                                                                                                                                                        US-LU-U33-228-111
; Sequence 111, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
APPLICANT: KING, GORGON E.
APPLICANT: KA, Jiangehun
APPLICANT: AX, Jiangehun
APPLICANT: Secrist, Headher
TITLE OF INVENTION: OWPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 2.012.1.54701
; CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.3%; Score 36.2; DB 12; Length 580; Best Local Similarity 53.1%; Pred. No. 5.2; Matches 77; Conservative 0; Mismatches 68; Indels 0
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US-09-817-913-4/c
; Sequence 4, Application US/09817913
; Patent No. US20020061860A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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ORGANISM: Human
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LENGTH: 1985
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TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE FOR INVENTION:
TITLE FOR INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
THEREFRAME:
CURRENT APPLICATION NUMBER:
US/09/731,231A
CURRENT FILING DATE:
CURRENT FILING DATE:
SOFTWARE:
STATE OF SEQ ID NOS:
GENERAL FILING DATE:
TOWNSER OF SEQ ID NOS:
TOWNSER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      815 GAGCAACCTTCCCTTTGATTCTTTGATAACAGAAGATGAACAAAGACTATTTG 874
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1789 TAGGIGTIGAIGITIACAAGIGAATICIAGIGITITICTCTTIGAGAICTGIGAAGITIGA 1848
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Patent No. US20020136728A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: Meadher, Madeleine Joy
APPLICANT: Xu, Janaghun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REPERENCE: 210121.547
CURRENT APPLICANTON NUMBER: US/09/920,300A
                                                                             421 TCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAG 462
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 111
LENGTH: 580
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; Sequence 3, Application US/09731231A
; Patent No. US20020082189A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
) LOCATION: (1)...(326014)
OTHER INFORMATION: n = A,T,C or G
US-09-731-231A-3
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CRGANISM: Homo sapiens
US-09-920-300A-111
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ORGANISM: Human
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DD 18667 GCAGGGTTTATGACGGGCATAGAAGAGACTGACTTTTTATTAGACTTTTTGC 18726
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Db 18727 TTTTAACTAGAAAATTAAATTTTTAAAAATTACCAAAAAGCAATGTAATT 18779
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US-09-764-869-1955
US-09-764-869-1955
Sequence 1955, Application US/09764869
Fatent No. US20020061521A1
GENERAL INRORATION:
TITLE OF INVENTION:
FILE REFRENCE: PCOO7
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1955
LENGTH: 32191
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                                                                                                                                                                                                        Length 18998;
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APPLICANT: Disson, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tank, Judith W.
APPLICANT: Tank, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48; Indels
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Best Local Similarity 57.5%; Pred. No. 28;
Matches 65; Conservative 0; Mismatches
                                                                                             ; LOCATION: (1690)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-869-1952
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; Sequence 4614, Application US/09815242
Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
  LENGTH: 18998
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-764-869-1955
                                                                                        NAME/KEY: SITE
LOCATION: (1690
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APPLICANT: Li, Zuomei
APPLICANT: Li, Zuomei
APPLICANT: Li, Zuomei
APPLICANT: Bonfils, Claire
APPLICANT: Bonfils, Claire
TITLE OF INVENTION: Antlsense Oligonucleotide Inhibition of Specific Histone
TITLE OF INVENTION: Deacetylase Isoforms
TITLE OF INVENTION: Deacetylase Isoforms
TITLE NUMBRICATION NUMBER: US/09/817,538
CURRENT FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4.0
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                                             Length 1985;
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53.1%; Pred. No. 8.7;
tive 0; Mismatches 68; Indels
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; Patent No. US20020137162A1
; GENERAL INFORMATION:
                                             Query Match 3.39
Best Local Similarity 53.19
Matches 77; Conservative
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Matches 77; Conservative
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; ORGANISM: Human
US-09-817-538-4
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US-09-764-869-1952
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US-09-817-538-4/c
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US-09-817-913-4
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; NAME/KEX: CDS
; LOCATION: (1)...(1134)
US-09-815-242-8602
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US-10-044-090-455
LENGTH: 1134
TYPE: DNA
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APPLICANT: Haselbeck, Nobell
APPLICANT: Syskind, Judith W. -
APPLICANT: Zyskind, Judith W. -
APPLICANT: APPLICANT: Syskind, Judith W. -
APPLICANT: Grant J. Daniel
APPLICANT: Grant J. Daniel
APPLICANT: Carry Grant J. -
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.0114, 708
PRIOR APPLICATION NUMBER: 60/201, 078
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR PILING DATE: 2000-10-21
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR PILING DATE: 2000-10-21
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR PILING DATE: 2000-10-216
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 6602
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4614
           PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-27
PRIOR PRICH DATE: 3000-10-27
PRIOR PLILOR DATE: 3000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Staphylococcus aureus
US-09-815-242-4614
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Sequence 455, Application US/10044090
Sequence 455, Application US/10044090
Patent No. US/20020137081A1
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
TITLE OF INVENTION UNMABER: US/10/044,090
CURRENT APPLICATION NUMBER: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
SEQ ID NOS: 850
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                                                                                                                                                                                                                                                                                                                    95 GAAGIGAGIICTACCAGIICAICAAAAIGICIIAIIGAAAAIAAAGICICIIGIGGAGII 154
                                                                                                                                                                                                                                                                                                                                                35 ICTIGATIGIAAAGGGGAATTGATTCTAACAGACCTTGGTCGAGCATCCATTCTAATTT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 3.3%; Score 35.8; DB 12; Length 7311; Best Local Similarity 50.9%; Pred. No. 19; Matches 85; Conservative 0; Mismatches 82; Indels 0;
                                                                                                                           3.3%; Score 36; DB 10; Length 1134; S0.0%; Pred. No. 7.7; tive 0; Mismatches 90; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 18
US-09-764-877-2599/C
Sequence 2599, Application US/09764877
Sequence 2590. Application US/09764877
September InfoRMATION:
SEMPRAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID NO. US20020137081A1 347926.5
OTHER INFORMATION: Incyte ID NO. US20020137081A1 347926.5
NAME/KEY: USORITON: 5438, 5455, 5470, 5482, 5495, 5512, 5559
OTHER INFORMATION: a, t, c, q, or other
US-10-044-090-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            912 AAGCTTGCTTCTCTTTTTTCCTTTTGTAGAATGATTCGGTAGTAG 958
ORGANISM: Staphylococcus aureus
                                                                                                                                                             Best Local Similarity 50.0%
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (1)...(1134)
US-09-815-242-8628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            712 AAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAA 771
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                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 952;
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xanmanco, Modert T.
APPLICANT: Xanmanco, Modert T.
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA,011A
CURRENT PELLOATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/201,727
PRIOR PELLNG DATE: 2000-05-23
PRIOR PELLNG DATE: 2000-05-26
PRIOR PELLNG DATE: 2000-05-26
PRIOR PELLNG DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PELLNG DATE: 2000-10-23
PRIOR PELLNG DATE: 2000-11-27
PRIOR PELLNG DATE: 2000-11-27
PRIOR PELLNG DATE: 2000-11-27
PRIOR PELLNG DATE: 2000-12-22
PRIOR PELLNG DATE: 2000-12-216
PRIOR FILING DATE: 2000-12-216
PRIOR FILING DATE: 2000-12-216
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-17
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3.3%; Score 35.4; DB 10; Length 9
Best Local Similarity 47.9%; Pred. No. 10;
Matches 102; Conservative 0; Mismatches 111; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8628, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Yokkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawatck, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2599
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US-09-815-242-8628
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                                                                                                                                                                                                                                                                                   799 AACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTGATAATGACAGAAGATGAAC 858
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Query Match
Best Local Similarity 49.7%; Pred. No. 11;
Matches 90; Conservative 0; Mismatches 91; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 Match 3.2%; Score 35.2; DB 10; Length 271; Local Similarity 52.4%; Pred. No. 6.8; hes 76; Conservative 0; Mismatches 69; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MESOUL 777-564-1653/C
US-09-777-564-1653/C
Sequence 1653, Application US/09777564
Patent No. US2002002591A1
GENERAL INFORMATION:
APPLICAMY: Algate, Paul A.
APPLICAMY: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 21012.49 3
CURRENT APPLICATION UNDER: US/09/777,564
CURRENT FILING DATE: 2001-205
NUMBER OF SEC ID NOS: 1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Window Version 4.0 FROID NO 1653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09754853A
Publication No. US20030005491A1
GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(271)
; OTHER INFORMATION: n = A,T,C or G
US-09-777-564-1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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0; Gaps

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DD 199885 TTAACCTTTGCATTGCTCATCATGCTGGAAAAATCAACGACTAAAAGAACCGTATGC 199944
                                                                                                                                                                                                                                                                                                                Db 199945 ATTTTAGAATGTAAAAATTGGTGTGTCTATATCATTACTAACTTCAATTAAGGAAAAG 200004
                                                                                                                                                                                                                                                                                                                                                                                                                      Db 199825 AAACGACGATTGCTTTTGCTATAGGACAGTTGCCAATTGAAGATAACAAGGTTCTTGACC 199884
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                                                                                                                                                                                                                                                                                                                                                                       754 AAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGT 813
                                                                                                                                                    634 TAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGAGAAAGC 693
                                                 574 AGACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTC 633
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0; Mismatches 162; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT APPLICATION NUMBER: 2001-08-10
PRIOR PELING DATE: 2001-08-10
PRIOR PILING DATE: 2000-0-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PETCHT VOICE
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, F
         Conservative
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LOCATION: (1343)
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            Matches 132;
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Best Local S:
Matches 61,
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APPLICANT: Hauge, Brian M.
APPLICANT: Parrell, Laurence D.
APPLICANT: Parrell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR APPLICATION NUMBER: US 60/174,880
NUMBER OF SEO ID NOS: 1119
         APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILICATION UNBER: 2001-01-05
PRIOR APPLICATION UNBER: US 60/174,880
PRIOR PILLING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
; GCGATION: (45163)..(45314),(45450)..(45509),(46941)..(48763),(48975)..(49573)
; GTHER INFORMATION: Clone ID: 240017_region_G3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 200005 AGIGTACAGGTACAACAATTTTGAACTTTTCATTTATTATTAATTGGCATTTGTGTAT 200064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 199945 ATTTTAGAATGTAAAAATTGGTGTGTCTATATCATTACTAACTTCAATTAAGGAAAAG 200004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34.8; DB 9; Length 335913;
Pred. No. 1.6e+02;
0; Mismatches 162; Indels 0;
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44.9%; Pred. No. 1.6e+02;
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O'THER INVENTION: Clone ID: 240017_region_G3
US-09-754-833A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09754853A Publication No. US20030005491A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.2%;
Best Local Similarity 44.9%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Glycine max
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Glycine max
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US-09-754-853A-3
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                                                                                                                                                                                                                                                           SEQ ID NO 2
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Gaps 0;

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GENERAL INFORMATION:
APPLICANT: SOppet, Daniel
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
TITLE OF INVENTION: Sets
FILE REFERENCE: 6892290-75
                                                                                                                                                                                                                                                                                            1884 GAAAAGAACAAAGATTTCTATCATTTAGATTTGGGGTAAAAGTTTGTTGTGGGTTTTTTTG 1943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     934 CTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTTGGAGTGATTG 993
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                                                     DB 10; Length 10195;
                                                                                                                                                                                                                                                                                                                                                                994 GCTGTTCTGGAAGAACAGGGAAAGTGATTGTCTCAGCTTTAGAGCAATCTTC 1045
                                                                                                                                                                                                                                                                                                                                                                                                   2004 GCTGCGATCTCAGCTCACCTCTGCTTCCCGGGTTCAGGGATTCTC 2055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2928 CCCATITITIAATGAACIGAAGTAGCAAAATCATCTITITCATTCTTTAGGA 2978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR PPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR PPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER: OF SEQ ID NOS: 1694
SOFTWARE: PALENTIN VET: 2.0
SEQ ID NO 478
LENGTH: 4201
TYPE: DAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: n equals a,t,g, or c NAME/KEY: m.sc_feature LOCATION: (4186); LOCATION: (4186); OTHER INFORMATION: n equals a,t,g, or c US-09-925-301-478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (4077)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 478, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
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                                                  Query Match
Best Local Similarity 50.00
Matches 86; Conservative
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LOCATION: (4161)
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  US-09-764-864-1600
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US-09-925-301-478
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3027 ITTTTTAATTCAATAAACATGTAGATTTATTTTAAGTCAGTTTGGTACATGATACAGATT 2968
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Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICAMY: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
CURRENT FAPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOCYMARE: Patentin Ver. 2.0
SSOCYMARE: Patentin Ver. 2.0
SSOC ID NO 1600
LENGTH: 10195
                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PALO4
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT APPLICATION NUMBER: US/09/925,302
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1099-03-12
PRIOR FILING DATE: 1999-03-12
                                                  688 GAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCC 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KRI: misc feature
LOCATION: (28)
OTHER INFORMATION: n equals a,t,g, or c
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NAME/KEY: misc feature
LOCATION: (3089)
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                                                                                                                                                                                                                                 ; Sequence 310, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 310
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LOCATION: (3086)
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ORGANISM: Homo sapiens
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US-09-764-864-1600
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US-09-925-302-310
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Local Similarity
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nes 71; Conserv
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US-10-003-806-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Human
US-10-003-806-6
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               672 AATCAGAAAGGAGCCGAAAGCTTCTAAGTAATCAAGAAAAAATCTTGGACAATAGCTTT 731
                                                                                                                                                                                                                                                                                                                                                                                                                    612 GATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGA 671
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US-09-880-107-2225
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Sequence 2225, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:
APPLICAMT: Horne, Darci T.
APPLICAMT: Scherf, Uwe
APPLICAMT: Scherf, Uwe
APPLICAMT: Scherf, Uwe
APPLICAMT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REPRENCE: 4921-5028-WO
CURRENT APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

NUMBER OF SED ID NOS: 3950

NUMBER OF SED ID NOS: 3950
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                                                                                                                                                                                                                                                                                                                      Score 34; DB 10; Length 35641;
Pred. No. 1.1e+02;
0; Mismatches 65; Indels 0.
CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FLIKNS DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR FILING DATE: 2000-09-25
PRIOR PPLICATION NUMBER: US/60/234,924
PRIOR FILING DATE: 2000-09-25
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Best Local Similarity 52.9%;
Matches 73; Conservative C
                                                                                                                                           NUMBER OF SEQ ID NOS: 568
SOFTWARE: PatentIn version 3.0
SEQ ID NO 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1196 TTCGTGATGTTAACAGTG 1213
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens US-09-962-436-306
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                                                                                                                                                                                                                 35641
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                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.1%; Score 33.8; DB 12; Length 180557; 53.4%; Pred. No. 2.3e+02; tive 0; Mismatches 62; Indels 0;
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US-10-0013-806-9
Sequence 9, Application US/10003806
Patent No. US20020119929A1
GENERAL INFORMATION:
APPLICANT: Bishop, Colin E.
APPLICANT: Agoulnik, Alexander I.
APPLICANT: Ayoulnik, Alexander I.
FILE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY
FILE REPERENCE: P02066012/10024824
CURRENT APPLICATION NUMBER: US/10/003,806
                                                                                  APPLICANT: Bishop, Colin E.
APPLICANT: Bishop, Colin E.
APPLICANT: Bishop, Oichao
TITLE APPLICANT: Aboulnik, Alexander I.
APPLICANT: Aboulnik, Alexander I.
APPLICANT: Aboulnik, Alexander I.
APPLICANT: Sub, Oichao
TITLE De INVENTION: CAN I AND ITS ROLE IN MAMMALIAN INFERTILITY
CURRENT APPLICANTON NUMBER: US/10/003,806
GURRENT FILING DATE: 2001-11-02
PRIOR PLING DATE: 2001-11-03
PRIOR FILING DATE: 2001-11-03
NUMBER OF SEC ID NOS: 14
SOFTWARE: PARCHIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Indels
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PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 14
SOSTWARE: PATENTIN VERSION 3.1
SEQ ID NO 9
Sequence 6, Application US/10003806; Patent No. US20020119929A1; GENERAL INFORMATION:
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1526 CAAAGGATGACAGGAGCCCAGCACATATGCCTTTATGGAGTCTCCTTGTTTGCAGAGCC 1467
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                                                                                                                                                                                                                                                                                                                                                     180 TCTGATCCAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCT 239
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APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK: 207US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

3.1%; Score 33.4; DB 10; Length 2680;
Best Local Similarity 52.5%; Pred. No. 52;
Matches 73; Conservative 0; Mismatches 66; Indels 0;
                                                                                                                                       Query Match
3 1%; Score 33.4; DB 10; Length 2679;
Best Local Similarity 52.5%; Pred. No. 52;
Matches 73; Conservative 0; Mismatches 66; Indels 0;
                                                                        ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L47726
US-09-880-107-2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bahou, Wadie
APPLICANT: Bahou, Wadie
APPLICANT: Sandalon, Ziv
TTTLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STOWNE 0.4970
CURRENT APPLICATION NUMBER: US/09/782,378A
CURRENT FILING DATE: 2001-02-12
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 20, Application US/09782378A;
; Patent No. US20020102731A1
; GENERAL INFORMATION:
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US-10-109-551-1
Sequence 1, Application US/10109551
Publication No. US20020194635A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1466 CAAACTCCACAGTAAACCA 1448
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                    ORGANISM: Homo sapiens
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US-09-782-378A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 33
US-09-782-378A-20/c
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                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                          Sequence 3, Application US/09742312

Patent No. US20020045166A1

GREREL INFORMATION:
TITLE OF INVENTION: SIGNATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEROF
TITLE OF INVENTION: AND USES THEROF
TITLE OF INVENTION: AND USES THEROF
CURRENT APPLICATION NUMBER: US/09/742,312
CURRENT FILING DATE: 2000-12-22
NUMBER OF SED ID NOS: 4
SOFTWARE: EastEED for Windows Version 4.0
SED ID NO 3
SED ID NO 3
SED ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 35254 GAATCAACATTTCTATATAAATGATGAAAATTAAAATGAAGAAAAATTTGTAAATTT 35313
Db 26358 TACTTTCAAAAGTGTAGTATACATGGTTGTACTTATCTGCAGTGGAAAAAAGATTAAAAC 26417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 814 GGAGCAACCTTCCCTTTGATTCTTTGATAATGACAAGAGATGAACAAAGAGTAAGTTTT 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     694 TICTAAGTAATCAAGAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  754 AAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGT 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.1%; Score 33.6; DB 10; Length 147309; Best Local Similarity 48.0%; Pred. No. 2.46+02; Matches 96; Conservative 0; Mismatches 104; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 32
US-09-880-107-2219/c
; Sequence 2219, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: HORNE, Darci T.
; APPLICANT: Goneley, Joseph G.
APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION Gene Expression Profiles in Liver Cancer; TITLE OF INVENTION Gene Expression Profiles in Liver Cancer; FILE OF INVENTION HUMBER: US/09/880,107
; CURRENT FILICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
; PRIOR FILING DATE: 2000-06-14
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patentin Ver: 2.1
; SEQ ID NO 2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(147309)
; OTHER INFORMATION: n = A,T,C or G
US-09-742-312-3
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                                                                              861 AGAGTAAGTTTTT 873
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ORGANISM: Human
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889 AGAAATGCATTTGTGTCGAGCTAAAGCTTGCTTCTCTTTATTTTCCTTTTGTAGAATGAT 948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                924 CITITALTITCCTTTTGTAGAATGALTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTT 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1%; Score 33.2; DB 10; Length 568; 54.0%; Pred. No. 30; tive 0; Mismatches 58; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT APPLICATION NUMBER: US/09/764,864
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SEQ ID NO 1784
LENGTH: 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO AC009266.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN FEART, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN FEART, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN PLACEMTA, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN PLACEMTA, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN PLACEMTA, SIGNAL = 2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78;
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 9781
LENGHH: 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            949 TCGGTAGTAGGAATATGGGGTCGAGTATGCACGTTGGA 986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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US-09-764-864-1784/c
IS-09-06-1784, Application US/09764864
Partent No. US20020132753A1
GENERAL INFORMATION.
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80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Conservative
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CORGANISM: Homo sapiens
US-09-764-864-1784
                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 984 GGAGTG 989
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US-09-864-761-9781
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Matches E
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2001-00-04
PRIOR FILING DATE: 2001-00-07
PRIOR FILING DATE: 2001-01-07
                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                              3.1%; Score 33.4; DB 9; Length 78056; 57.0%; Pred. No. 2.1e+02; tive 0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 35096 GAATAAAATCAGAATTGAAAAAGGAGAAGGTACAACAGATATAACAG 35142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PRILING DATE: 2001-01-30
         CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
SOFFWARE: PARENTIN NOS: 12
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9781, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                           61; Conservative
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Bos taurus
US-10-109-551-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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US-09-864-761-9781
                                                                                                                                                                            SEQ ID NO 1
LENGTH: 78056
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                                 US-US-1918 B42A-4/41

Sequence 4741, Application US/09938842A
Patent No. US2002016037841

GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Harper, Joel
APPLICANT: Harper, Joel
APPLICANT: Wang, Xun
APPLICANT: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT FILLING DATE: 2001-08-24
PRIOR PILLING DATE: 2001-08-24
PRIOR PILLING DATE: 2001-01-16
PRIOR PILLING DATE: 2001-01-16
PRIOR FILLING DATE: 2001-06-22
NUMBER OF SED ID NOS: 5379
SED ID NO4141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 GCGATCAGATTGCTTTGTAGGGTTTGTATGCGTTGTTTTTTACTAGGAAGAGCTTGTACT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 CTTCCTTCATGGTTTTCAATAAGTCCGCTTTCAACAGTAAACCAAAAGCAGCGTACAATA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.1%; Score 33.2; DB 10; Length 198285; 48.4%; Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              395 ITITCTATGACTTTAGTGAAGAGTCTTCCCATGTTTATGAAAATTCAGAAAAT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEMTURE:
. OTHER INFORMATION: Genbank Accession No. US20020142981A1 x87344
US-09-880-107-3814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT HOLE, Joseph G.
APPLICANT HOLE, Joseph G.
APPLICANT Scheft, Uwe
APPLICANT Scheft, Uwe
APPLICANT Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REPRENCE: 4921-5028 WO.
CURRENT APPLICATION NUMBER: 0209,9880,107
CURRENT PILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/217,054
PRIOR PILING DATE: 2000-06-14
SPGO ID NOS: 3950
NUMBER OF SEQ ID NOS: 3950
SOCTHARRE: Petentin Ver: 2.1
SEQ ID NO 3814
LENGTH: 198285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
3.1%; Score 33.2; DB 9; Length 2000;
Best Local Similarity 49.4%; Pred. No. 51;
Matches 86; Conservative 0; Mismatches 88; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3814, Application US/09880107; Patent No. US20020142981A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4741
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ORGANISM: Homo sapiens
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Best Local Similarity
                     US-09-938-842A-4741
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APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)
CURRENT APPLICATION NUMBER: US/09/878,574
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 733
LENGTH: 328
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                                                                                                                                                                    DD 149825 AAATAATTAATAAAATGGTGGCTTCTAGCTAGAATAAAGAAGAAAAGAAGAAGG 149884
                                                                                                                                                                                                                                                                                                                                                                                                                       Db 149885 ATTCAAATAAACACAATTAGGAATGACAAAGGAGGTATTACCACTGACCCCACAGAAATA 149944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DD 149945 CAGACAACCATCAGAGAATATTATGAATACTTCTATGACATAAAGTAGAAAATCTAGAAG 150004
                                                                                                       698 AAGTAATCAAGAAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGG 757
                                                                                                                                                                                                                                                                                                                      758 AGTCGATACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAG 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               818 CAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAA 877
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98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           897 ATTIGIGICGAGCIAAAGCITGCITCTCTTTATTTTCCTT 936
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ORGANISM: Glycine max

OTHER INFORMATION: Clone ID: LIB3028-047-Q1-B1-A3

US-09-878-574-733
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 733, Application US/09878574; Patent No. US20020110548A1; GENERAL INFORMATION:
Conservative
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LENGTH: 406
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APPLICANT: Black, Michael
Burnham, Martin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 GTGGA 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 TITGAGATITGIGITCTITAGITCTIACTTGTTAGTTGTTACACATTTTGTAAGAACCTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 GIGAAGAGICTICCCAIGITIAIGAAAAITCAGAAAAIGAGGGAIGIAGAAGCCAAGGC 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 ACGIGCCCIAAAAGGICAIGGAIGAGAICAGGAGIIAAGGAGAAAITAICITIAICGAGA 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 ATCCTCACCGCCATGAGCAATGCACATGCAACGGAAGGTAAAAGGAATAATATGCAGT 215
                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                           517 ATCTTTATCGAGAGTTCGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGA 576
                                                                                                                                                                                                                                                                                 577 CAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTTTAA 636
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                    Ouery Match
Best Local Similarity 48.0%; Pred. No. 33;
Matches 94; Conservative 0; Mismatches 102; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 92; Indels
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APPLICANT: Grant Jr.
TILLE OF INVENTION: Expressed Sequences of Arabidopsis;
TITLE OF INVENTION: thaliana
FILE REPERENCE: 2011US
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/148,784
PRIOR RILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 396
LENOTH: 548
         ; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-006-Q1-B1-H7
US-09-878-574-3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.0%; Score 32.8; I
48.9%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 41
US-09-924-035A-396/c
US-09-924-035A-396/c
; Sequence 396, Application US/09924035A
; Patent No. US2002012319A1
; GENERAL INFORMATION:
; APPLICANT: GTAGOh, Jrn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)...(548)
; OTHER INFORMATION: n = A,T,C or G
US-09-924-035A-396
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les 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   697 TAAGTAATCAAGAAAA 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 AAACAAATCAAGAAGA 79
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                                  87 CTAATTTTGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAGTCTCTT 146
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Josh Score 32.8; DB 10; Length 8
Local Similarity 53.68; Pred. No. 44;
Conservative O; Mismatches 58; Indels
es 67; Conservative O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         UPERMILLO SISTEMS: DOS SOFFWARE: FESTSED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,980 FILING DATE: 27-Aug-2001 CLASSIFICATION CURRENTA: PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/936,165 FILING DATE: 4CURROWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38.891
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; POPOLGGY: Linear MOLECULE TYPE: Genomic DNA SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-939-980-6
                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 43
US-10-109-551-3/c
; Sequence 3, Application US/10109551
; Publication No. US20020194635A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 806 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Hodgson, John
Knowles, David
Lonetto, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                              ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                           CITY: King of Prussia
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 CATCCATTCTAATTTTGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAA 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 ATCAAAATAAAGTAGAATAAAAAGGCACACTCGAAAAATTTGAGCGCAGAAAGGACA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      822 CTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATT 881
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APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK: 2070S
CURRENT APPLICATION NUMBER: US,10/109,551
CURRENT APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
SOFFWARE: PAGENICATION VUMBER: 60/280,549
SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LOGGS, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henson, Darin R.
APPLICANT: Scrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.0%; Score 32.8; DB 9; Length 31412; Best Local Similarity 58.0%; Pred. No. 2.1e+02; Matches 58; Conservative 0; Mismatches 42; Indels 0;
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3.0%; Score 32.6; DB 9; Length 601;
Best Local Similarity 46.1%; Pred No. 44.
Matches 107; Conservative 0; Mismatches 125; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 25496 AGIGITITCAATCATITCAGTAGAAAACTGCATGCGCAAA 25457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 294, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(601)
; OTHER INFORMATION: n = A,T,C or G
US-09-854-133-294
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                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA; ORGANISM: Ovis aries US-10-109-551-3
                                                                                                                                                                                                                                                                                                                                        LENGTH: 31412
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US-09-854-133-294
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Sequence 3797, Application US/09938842A
Parent No. US20020160738A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPERENCE: SCRIPL300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   702 AATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTC 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   822 CTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGATAAGTTTTTGAAAAATT 881
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188 TITICAAGTGAAGGTITCTGTCAGTTGAAGTAGTTAGCAATGGCTTCTTTTC 239
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3.0%; Score 32.6; DB 10; Length 601;
Best Local Similarity 46.1%; Pred. NO. 44;
Matches 107; Conservative 0; Mismatches 125; Indels 0;
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APPLICANT: Algate, Paul A.
APPLICANT: Secrist, Heather
APPLICANT: Indirias, Carol Yoseph
APPLICANT: Ellot, Mark
APPLICANT: Manion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.4750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 210121.4/5cy
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FASESEO FOR Windows Version 3.0
                                                                                                                                                                                                                                                          ; Sequence 294, Application US/09738973; Patent No. US20020110563A1; GENERAL INFORMATION:
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; LOCATION: (1)...(601)
; OTHER INFORMATION: n = A,T,C or G
US-09-738-973-294
                                                                                                                                                                                                                                                                                                                                                                                             Reed, Steven G.
Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
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SOFTWARE: Fas
SEQ ID NO 294
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APPLICANT:
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678 AAAGGAGCCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                738 GAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTA 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 1658;
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Local Similarity 46.8%; Pred. No. 76;
less 102; Conservative 0; Mismatches 116; Indels
                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILLE OF INVENITION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR ELLING DATE: 2000-03-08
PRIOR PELLING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wagner, Ry
APPLICANT: Mathews, Helena
APPLICANT: Liu, Xing Liang
APPLICANT: Liu, Xing Liang
APPLICANT: Waggoner, Wency J.
TITLE OF INVENTION: TRAIT-ASSOCIATED GENE IDENTIFICATION
TITLE OF INVENTION: METHOD
FILE REFERENCE: 4257-0018.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: L23 sequence from plasmid rescue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     859 AAACAATTGTGTATTAAAAATAGGGATAATAAAGTG 822
                                                  157 TGTATTGAAGGGAAGACGAATAATCTGATCCAA 189
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CURRENT FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/124,232
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/09522334 Patent No. US20020157130A1 GENERAL INFORMATION:
                                                                                                                                                                                                Sequence 228, Application US/09925302; Patent No. US20020044941A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                           -09-925-302-228/c
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; ORGANISM: HOMC
US-09-925-302-228
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US-09-522-334-26
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LENGTH: 1658
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Patent No. US20020102532A1

GENERAL INFORMATION:
FAPLICANT: Augustus, Meena
APPLICANT: Augustus, Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION WIMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION WIMBER: US/60/237,425
PRIOR PILING DATE: 2000-10-03
PRIOR SEQ ID NOS: 658
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       762 TAAGCCATITATCATACAACAATATITITITITITATITAAGTAGCTGGTITCTICATG 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 AGAACTGATAAGAACGGCTCCATATGCTTTTCTTCCTTCATGGTTTTCAATAAGTCCGCT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                   124 TCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATAATCTG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                               Query Match 3.0%; Score 32.6; DB 9; Length 2000; Best Local Similarity 47.0%; Pred. No. 73; Matches 101; Conservative 0; Mismatches 114; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 TTCAACAGTAAACCAAAAGCAGCGTACAATAGCGA 338
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FLILING DAFE: 2000-08-24
PRIOR FLILING DATE: 2001-01-16
PRIOR PELICATION NUMBER: US 60/264,647
PRIOR PELICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEC ID NOS: 5379
SEC ID NO 3797
LENGTH: 2000
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US-09-969-708-291
                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3797
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US-09-969-708-291
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Gaps

us-09-438-185a-1\_1199590\_1200675.rnpb

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APPLICANT: Hauge, Brian M.
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Wang, Ming Li.
APPLICANTON WOLGER Cycle Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION WUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                       602 CCTGAAACGGGATAATAGGAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGA 661
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## ALTGNMENTS

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RESULT 1

US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE FOR INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLGY & LARGHOR
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
COUNTRY: USA
COUNTRY: USA
ZIP: 22231-0229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    592 AGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAAT 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652 GACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  712 AAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         772 ATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 832 ATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                        30472/114 IMMU
                                                                                                                                                                                                              EP 91 114 300.6
                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                                                                                                                                                                                                                       29,768
                                                                                                                                                                                                          APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, SCEPHON A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                   TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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US-08-232-463-14
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816 AGCAACCTTCCCTTTGATTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGA 875
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APPLICANT: Rocke, Jenny
APPLICANT: You's Trian
APPLICANT: AND APPLICANT TO GOORESPONDENCE ADDRESS: 10
CORRESPONDENCE ADDRESS: TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                             3.4%; Score 36.6; DB 2; Length 2098; 65.1%; Pred. No. 0.87; ative 0; Mismatches 29; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,502
                                                          ATTORNEY AGENT INFORMATION:
NAME: OSBAT, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B97-081
TELEPHONE: (415) 343-4341
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2098 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
APPLICATION NUMBER: US/08/937,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1076 AGGCTACTGAAATATTATTTAT 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5-09-285-502-5/c; Sequence 5, Application US/09285502; Patent No. 6190076; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        876 AAAATTCTAAAATAGAAATGCAT 898
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TELEPAN: (415) 343-4341
TELEPAX: (415) 343-4342
INFORMATION FOR SED ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2098 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36,627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RICHARD A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                        CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: 11:
; MOLECULE TYPE:
US-08-937-931-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94104
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: GAN, Meinlu et al
APPLICANT: GAN, Meinlu et al
TITLE OF INVENTION:
USES THEREOF ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFRENCE: CLO01173
CURRENT APPLICATION NUMBER: US/09/813,133A
CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRSELSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29872 TGCAAGCTATCCAGCCAACAGGGACTTAATAACCAGAATATAAAGGAACGCAAACAATT 29813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             582 ATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGA 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522 TATCGAGAGTTCGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGT 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08937931

Patent No. 5935792

GENERAL INFORMATION

APPLICANT: Rubin, Gerald M.
APPLICANT: Pan, Duojia
APPLICANT: Pan, Duojia
APPLICANT: Roke, Jenny
APPLICANT: Xu, Tian
TITLE OF INVENTION: KUZ: A No. 5935792e1 Family of Metalloproteases
NUMBER OF SEQUENCES: IN CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
     908 TAAAACTAACTGCTGTGTGTATGAAATGCTTTAAGGAGGCTTCCTTTTCTAAACGATTGG 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29812 CAAAAGGAAAAAAAAAATAAAATTTTAAAAATGAGAAAGGAATCTGAACAG 29758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                702 AATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.7%; Score 39.8; DB 4; Length 55827;
48.1%; Pred. No. 0.46;
Live 0; Mismatches 122; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5: SCIENCE & TECHNOLOGY LAW GROUP 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                             Sequence 3, Application US/09813133A Patent No. 6455294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 48.1
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                        1012 GGAAAG 1017
                                                                                                     848 GTGAGG 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA; ORGANISM: Human US-09-813-133A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94104
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US-08-937-931-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q ID NO 3
LENGTH: 55827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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1136 AGCCACAAAAGCTTTGAAGGTTTGATATTCAGAGAAGATGACCAAAGAGTTCTTTTATTT 1077
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                                                                                      876 AAAATTCTAAAATAGAAATGCAT 898
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Xu, Tian
FINVENTION: KUZ: A No. 6319704el Family of Metalloproteases
OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  816 AGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGA 875
                                                                                                                                                                                                                                          Query Match
3.4%; Score 36.6; DB 4; Length 2098;
Best Local Similarity 65.1%; Pred. No. 0.87;
Matches 54; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 3.4%; Score 36.6; DB 4; Length 2098; Similarity 65.1%; Pred. No. 0.87; 54; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTE: USA
COMPUTE: USA
COMPUTE: USA
COMPUTE: ELOPPY disk
MEDIUM TYPE: FLOPPY disk
COMPUTEI: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/709,126
FILING DATE: 08 No. 6319704-2000
CLASSIFICATION AND CURRENT OF APPLICATION AND CURRENT OF APPLICATION AND COMPANION AND CLASSIFICATION AND COMPANION AND COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: BAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION.

NAME: OSMAN, RICHARD A
REGISTRAFON NUMBER: 36,627

REFERENCE/DOCKET NUMBER: 697-081

TELECOMMUNICATION INFORMATION:

TELEPAN: (415) 343-4341

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-709-126-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1076 AGGCTACTGAAATATTATTTAT 1054
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                876 AAAATTCTAAAATAGAAATGCAT 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09709126; Patent No. 6319709; GENERAL INFORMATION: APPLICANT: Rubin, Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan, Duojia
Rooke, Jenny
Yavari, Reza
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Best Local Similarity 65.18
Watches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ropology: linear
TYPE: nucleic acid
STRANDEDNESS: double
                                                                            TOPOLOGY: linear

MOLECULE TYPE: CDNA
US-09-285-502-5
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US-09-709-126-5/c
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TITLE OF INVENTION: KUZ: A No. 6399350el Family of Metalloproteases
NUMBER OF SEQUENCES: 10
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3.4%; Score 36.6; DB 4; Length 2098;
Best Local Similarity 65.1%; Pred. No. 0.87;
Matches 54; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: PEE: Floppy disk
COMPUTER: PAGE: Floppy disk
COMPUTER: PAGE: Floppy disk
COMPUTER: PAGE: Floop
SOFTWARE: PAGE: DOS/MS-DOS
SOFTWARE: PAGE: DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,385A
FILING DATE: 31 May-2001
CLASSIFICATION NUMBER: US/09/709,126
FILING DATE: 08-NO. 6399350-2000
APPLICATION NUMBER: 09/285,502
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: 09/285,502
FILING DATE: CUNKNOWN>
NAME: OSMAN, RICHARD A
REFERENCE/COKEFT UNBER: 36,627
REFERENCE/COKEFT UNBER: 36,627
TELEPHONE: (415) 343-4341
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CLARATERISTICS:
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA SEQUENCE DESCRIPTION: SEQ ID NO: 5: 05-09-871-385A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-737-698B-25 ; Sequence 25, Application US/09737698B
Sequence 5, Application US/09871385A; Patent No. 6399350; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1076 AGGCTACTGAAATATTATTTAT 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2098 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       876 AAAATTCTAAAATAGAAATGCAT 898
                                                                          APPLICANT: Rubin, Gerald M.
Pan, Duojia
Rooke, Jenny
Yavari, Reza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94104
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816 AGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTGA 875

Gaps 0

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121 GATATATAGTAGGCATTTGAAAGTTGAAAGATGAATTTCACACTAAACTCAGATAAGATG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          712 AAATCTTGGACAATAGCTTTTCCATAGAGAAACCGTGAGGAAAGGGAGTCGATACCATAA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        772 ATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AACACAATCAACCAAATGAATTCTAAAAACAAGAATTTTACTGGGGAAAAAAACGTTTCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             832 ATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 652 GACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAA 711
                                                                                                                                                                                                                                                                                                                                                                     592 AGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAAT 651
                                                                                                                                                                                                                                                                         Query Match 3.2%; Score 34.8; DB 1; Length 6877; Best Local Similarity 44.5%; Pred. No. 4.6; Matches 138; Conservative 0; Mismatches 172; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Obstein, Fodstad
APPLICANT: Hovig, Eivind
APPLICANT: Begebraaten, Olav
APPLICANT: Acrawal, Sudhil H.
APPLICANT: Acrawal, Sudhil
TITLE OF INVENTION: OREN, SPECIFIC OLIGONUCLEOTIDES AND
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JABER: US/08/602,036A
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US-08-602-036A-1
Sequence 1. Application US/08602036A
Fatent No. 579924B
GENERAL INFORMATION:
APPLICANT: OBystein, Fodstad
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6877 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
CRIGINAL SOURCE:
US-08-347-340-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: HALE AND DORR LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
FILING DATE: 16-FER
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: promoter; LOCATION: (1)..(1241); LOCATION: (1)..(1241); OTHER INFORMATION: n= a or g or c or t/u; OTHER INFORMATION: Act7 promoter polynucleotide sequence and intron US-09-737-698B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence I, Application US/08347340
Patent No. 5633439
GENERAL INFORMATION:
APPLICANT: WALTER, MICHAEL H
TITLE OF INVENTION: EXPRESSION OF GENES IN TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.4%; Score 36.4; DB 4; Length 1241; 59.8%; Pred. No. 0.79; tive 0; Mismatches 41; Indels 0.
        Patent No. 6462258

GENERAL INFORMATION:
APPLICANT: Fincher, Karen
APPLICANT: Fincher, Karen
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION: No. 6462258el Plant Expression Constructs
FILE REPERENCE: 38-21(51499)C
CURRENT APPLICATION UNBER: US/09/737,698B
PRIOR FILING DATE: 2000-12-15
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VORSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1090 ACCTAGTTTTCTCAATAATCAACATATGAAGCGATGTTTGAG 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 TCCCATGTTTATGAAAATTCAGAAATGAGGGATGTAGAAG 462
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COMPUTER: IBM PC compatible
COMPUTER: Patent PC Compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,340
FILING DATE: 06-DEC-1994
CLASSIFCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CTCTGB93/01098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/GB93/01098 FILING DATE: 27.MAY-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: 29-MAY-1992
ATTORNEY/AGENT INPORMATION: REGISTRATION NUMBER: 1992
ATTORNEY/AGENT INPORMATION: REGISTRATION NUMBER: 15772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9320/212448
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ADDRESSEE: CUGHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTEY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"TWPITER: IBM PC COMPATIBLE
"VSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 93.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/861-3000
TELEPHONE: 202/862-0944
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
OKGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 3.4;
Best Local Similarity 59.8
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                    1241
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US-08-347-340-1
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NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
     TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: genomic DNA
                                                                                         Query Match 3.2
Best Local Similarity 55.4
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                  ; ANTI-SENSE:
US-08-502-374A-1
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                                                                                                                                                                                                                                                                                                                                        470 ACGTGCCCTAAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTTATCGAGA 529
                                                                                                                                                                                                                        Query Match 3.2%; Score 34.6; DB 1; Length 10952; Best Local Similarity 55.4%; Pred. No. 6.5; Matches 67; Conservative 0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08502374A
Patent No. 5872007
Patent No. 5872007
GENERAL INFORMATION:
APPLICANT: Engelraaten, Olav
APPLICANT: Maraten, Olav
APPLICANT: Agrawal, Sudhir
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: HYZ-039CIP
TELECOMMUNICATION INCORMATION:
TELEPHONE: (617) 526-6000
TELEPHONE: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10952 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
                                                                                                                                                                              ; ANTI-SENSE: NO
US-08-602-036A-1
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US-08-502-374A-1
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                                                                                                                                                                                                                                                                  410 GTGAAGAGTCTTCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGC 469
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0
3.2%; Score 34.6; DB 2; Length 10952; 55.4%; Pred. No. 6.5; tive 0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
3.2%; Score 34.6; DB 2; Length 10952;
Best Local Similarity 55.4%; Pred. NO. 6.5;
Matches 67; Conservative 0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08642407A
Patent No. 5877308
GENERAL INFORMATION:
APPLICANT: Ocystein, Fodstad
APPLICANT: Howig, Elvind
APPLICANT: Howig, Elvind
APPLICANT: Maclandsmo, Gunhild H.
APPLICANT: Maclandsmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,407A
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CPDV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: NUCLEIC acid
TYPE: NUCLEIC acid
STRANDEDNESS: SING1E
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FITLE REFERENCE: CLOO0968
CURRENT APPLICATION NUMBER: US/09/741,150
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09784316
| Sequence 3, Application US/09784316
| Patent No. 6461843
| Patent No. 6461843
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
| TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES;
| TITLE OF INVENTION: THEREOF | FILE REPRENCE: CLO1139 |
| FILE REPRENCE: CLO1139 |
| CURRENT APPLICATION NUMBER: US/09/784,316 |
| CURRENT PILING DATE: 2001-02-16 |
| NUMBER OF SEQ ID NOS: 5 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 17216 ATTCTCTAGGGTGGTAGCTATTTAAAGGGACTGGCAATGAATCTTTCCAAACAGTAAAAA 17157
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                                                                                                                          1510 CYTTRCARAANARDAINGCCCARIGNARCAINCCDAINGINSWNARYTINARNARNACNG 1451
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                                           1570 INGCRCANCKNGTNGGNARNGCNARNSWNGCNGGNARRTANCKNACDATYTGNARDATNC 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 CATCCATICIAATITIGAAGIGAGITCTACCAGTICAICAAAAIGICITATIGAAAAIAA 138
                                                                                 728 CITITCCAIAGAGAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAG 787
668 AAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAAATCTTGGACAATAG 727
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3.1%; Score 33.8; DB 4; Length 65042;
Best Local Similarity 52.5%; Pred. No. 23;
Matches 74; Conservative 0; Mismatches 67; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-741-150-3/c
; Sequence 3, Application US/09741150
; Patent No. 6436689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 17156 GAATCCTTGTACGTTATGAAT 17136
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ORGANISM: Human
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                                                          548 ATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGGGGGCTACAAATCCTGAA 607
                                                                                                                   470 ACGIGCCCTAAAAGGICATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGA 529
                                 410 GIGAAGAGICTICCCAIGTITAIGAAAATICAGAAAAIGAGGAIGIAGAAGCCAAGGC 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Holloway, James
APPLICANT: Jelinck, Laura
APPLICANT: Durnam, Diane
APPLICANT: Blumberg, Hal
TITLE OF INVENTION: ROVEL NUCLEAR RECEPTOR POLYPEPTIDE
TITLE OF INVENTION: ZPPAR4
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL NUCLEAR RETITLE OF INVENTION: ZPPAR4
NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESSE: ADDRESSE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09106194
Partent No. 626234
GENERAL INFORMATION:
APPLICANT: HOLloway, James
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TELECOMMUNICATION INFORMATION:
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IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORING CALL.
NAME: Leith, Debra K
REGISTRATION NUMBER: 32,6
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SEQUENCE CHARACTERISTICS:
LENGTH: 2067 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 206-442-6674
TELEFAX: 206-442-6678
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
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COUNTRY: US
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US-09-106-194-11/c
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US-09-106-194-11
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895 TATGTTTATGTTTTTTAATATATTCTAAAAGTTTTTGTTTTATCTATAAAGGTACCTTCAC 836
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                                                                                                                                                                                                                                                                                                                   325 GCGTACAATÄGCGATCAGATTGCTTTGTAGGGTTTGTATGCGTTGTTTTTTACTAGGAAG 384
                                                                                                                                                                                                   265 ATATGCTTTTCTTCCTTCATGGTTTTCAATAAGTCCGCTTTCAACAGTAAACCAAAAGCA 324
                                                                                                                                                          0; Gaps
                                                                                                               DB 4; Length 112132;
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49.2%; Pred. No. 5;
tive 0; Mismatches 91; Indels 0.
                                                                                                          Ouery Match
3.18; Score 33.8; DB 4; Length 11
Best Local Similarity 51.0%; Pred No. 29; 77; Indels
Matches 80; Conservative 0; Mismatches 77; Indels
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OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DAYR:
APPLICATION NUMBER: US/08/938,546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fosberry, Andrew P.
APPLICANT: Lavlor, Elizabeth J.
APPLICANT: Nicholas, Richard O.
TITLE OF INVENTION: NO. 6004556el rsbU-1
CORRESPONDENCES: 5
CORRESPONDENCE ADDRESS:
; NAME/KEY: misc_feature
; LOCATION: (1)...(112132)
; OTHER INFORMATION: n = A,T,C or G
0S-09-741-150-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DICKINSON, TOAG O
REGISTRATION NUMBER: 28,354
REFERENCE/POCKET NUMBER: P505
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
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SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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nes 88; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskette
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US-08-938-546-1
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STREET: 40
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US-08-938-546-1/c
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985 GAGTGATTGGCTGTTCTGGAAGAAGAAGTGGAATTGTCTCAGCTTTAGAGCAATCT 1043
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3.1%; Score 33.4; DB 3; Length 1002;
Best Local Similarity 49.2%; Pred. No. 5;
Matches 88; Conservative 0; Mismatches 91; Indels 0; Gaps.
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                                                                                                                ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CTTY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,812
                                                                                                                                                                                                                                                                                                                 APPLICANT: Fosberry, Andrew P.
APPLICANT: LawLor, Elizabeth J.
APPLICANT: Micholas, Richard O.
TITLE OF INVENTION: No. 6111078e1 rsbU-1
CORRESPONDENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/938,546
FILING DATE:
                                                                                                                                                                                                                                             Sequence 1, Application US/09340812; Patent No. 6111078; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: DICKINSON, TOCK O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P54
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Philadelphia
STATE: PA
COUNTR: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: 215-994-2222
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US-09-340-812-1/c
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ADDRESSEE: Dechert Price & Rhoads
STRRET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
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FastSEQ for Windows Version 2.0
                                                                                                                                                                                            FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/340,812
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/938,546
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COUNTRY: US
ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
"~~noringER: IBM Compatible
"~~noringER: IBM Compatible
                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd 0
REGISTRATION NUMBER: 28,354
REPERENCE/DOCKET NUMBER: P50
TELECOMMUNICATION INFORMATION:
                                                                                                                                         : Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
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                                                                                                                                                                                                                    DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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OPERATING SYSTEM:
SOFTWARE: FASTSEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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US-08-938-546-5/c
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TOPOLOGY:
US-09-340-812-3
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                                                                                     COUNTRY:
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49.2%; Pred. No. 5;
tive 0; Mismatches 91; Indels 0;
                                                                                                                                                                                                                           ADDRESSEE: Dechert price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
STRY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09340812; Sequence 3, Application US/09340812; Patent No. 6111078; Persexa INFORMATION: APPLICANT: Leoberry, Andrew P. APPLICANT: Lawlor, Elizabeth J. APPLICANT: Nicholas, Richard O. TITLE OF INVENTION: No. 6111078el rsbU-1; NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSER for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,546
                                                                                                         APPLICANT: Fosberry, Andrew P.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Nicholas, Richard O.
TITLE OF INVENTION: No. 6004556el rsbU-1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                    Sequence 3, Application US/08938546 Patent No. 6004556 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Dickinson, Todd O
REGISTRATION UNMBER: 28,354
REFERENCE/DOCKET UNMBER: P55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEPHONE: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 1020 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 49.2
Matches 88; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: Diskett
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US-09-340-812-3/C
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STATE:
                     RESULT 17
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865 IAAGITITIGAAAAATICIAAAATAGAAAIGCATITIGIGICGAGCIAAAAGCIIGCIICIC 924
                                                                                                                                                                       913 TATGITTATGITTITTAATATATTCIAAAAGTTTTTGITTATCIATAAAGGTACCTTCAC 854
                                                                                                                                                                                                                                 925 ITTATITICCITITGIAGAAIGATICGGIAGTAGGAATATGGGGTCGAGTAIGCACGTIG 984
                                                                                                                                                                                                                                                                   985 GAGTGATTGCCTGTTCTGGAAGAACAGGGAAAGTGATTGTCTCAGCTTTAGAGCAATCT 1043
                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 1020;
   Ouery Match
3.1%; Score 33.4; DB 3; Length 16
Best Local Similarity 49.2%; Pred. No. 5;
Matches 88; Conservative 0; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fosberry, Andrew P.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Nicholas, Richard O.
TITLE OF INVENTION: No. 6004556el rsbU-1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Defeirt Frice & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Bacillus sp.
                                                                                                                                                                                            linear
                                                                                                                                                                                            ; TOPOLOGY:
US-09-340-812-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: Dechert Price & Rhoads
F: 4000 Bell Atlantic Tower, 1717 Arch Stre
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fosberry, Andrew P.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Nicholas, Richard O.
TITLE OF INVENTON: No. 6111078e1 rsbU-1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/340,812
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ATTORNEY AGENT INFORMATION:
NAME: Dickinson, Todd O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/938,546
                                                                                                                                                            NAME: DICKINSON, TOGG O
REGISTRATION NUMBER: 28,354
REFERENCE/POCKET NUMBER: P505:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 5, Application US/09340812; Patent No. 6111078; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHRACTERISTICS:
LENGTH: 3360 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
JYPELOLOGY: linear
US-08-938-546-5
                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DICKINSON, TOOR O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                           FILING DATE:
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US-09-129-727-1/C
US-09-149-727-1/C
Sequence 1, Application US/09149727
Patent No. 6391547
GENERAL INFORMATION:
APPLICANT: Jefferson, Richard A.
APPLICANT: Keese, Paul Konrad
TITLE OF INVENTION: USES THEROF
TITLE OF INVENTION: USES THEROF
TITLE OF INVENTION: USES THEROF
FILE REFERENCE: 190106-105
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3.1%; Score 33.4; DB 4; Length 6029;
Best Local Similarity 51.7%; Pred. No. 11;
Matches 76; Conservative 0; Mismatches 71; Indels 0;
                                                                                                                                                                                                                                                              Query Match

3.1%; Score 33.4; DB 3; Length 3360;
Best Local Similarity 49.2%; Pred. NO. 8.4;
Matches 88; Conservative 0; Mismatches 91; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/149,727
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: US 60/058,263
EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4240 ACAACGAACCCTTCTTTAGTAGCTAAA 4214
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TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3360 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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7299 AATTATTAAAGTGATCAGTTGTGATAAGCTTGTGAATCT--CTTTCCACACAATCCCATG 7356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   938 TGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTG 997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              878 AATICIAAAAIAGAAAIGCAIITIGIGICGAGCIAAAGCIIGCIICTITIAIIIICCIII 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
NUMBER OF SEQUENCES: 140
STREET: Two Embarcadero Center, Eighth Floor
STREET: Two Embarcadero Center, Eighth Floor
STREET: Califoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.0%; Score 33; DB 4; Length 10815; 48.6%; Pred. No. 18; tive 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                  ZIP: 94111-3834
COMPUTER READALEE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC COMS/MS-DOS
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFRATHARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/POOKET NUMBER: 38,400 P. REGISTRATION NUMBER: 30,3070-078810US TELEPOMNUNCATION INTERPORATION TELEPOMNUNCATION TELEPONS: 415,576-0200 TELEPONS SEQ ID NO: 21: SEQUENCE CHARACTERSTICS: LENGTH: 10915 base pairs TYPE: nucleic acid STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-7AN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 48.6
Matches 120; Conservative
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RESULT 23 US-09-004-838-87

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998 TICIGGAAGAACAGGGAAAGIGAIIGICICAGCITITAGAGCAAICTICAGAAIAIACTIT 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    818 CAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAA 877
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48.6%; Pred. No. 20;
tive 0; Mismatches 125; Indels 2
                                                      APPLICANT: Withelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Meyers: Blake
APPLICANT: Meyers: Blake
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                              COUNTRY: U. 2844

ZIP: 94111-384

COUNTRY: I. 1984

COMPUTER: I. 1987

APPLICATION NUMBER: I. 1987

ATTORNEY/AGENT INFORMATION:

RECISTRATION NUMBER: I. 38,440

RECISTRATION NUMBER: I. 38,440

RECISTRATION NUMBER: I. 38,440

RECISTRATION INFORMATION:

TELECHONE: (415) 576-0200

TELECHONE: (415) 576-0300

INPORMATION FOR SEQ. ID NO: B7:

SEQUENCE CHARACTERISTICS:

LENGTH: I. 13149 base pairs

COMPUTER: I. 19149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COCATION: 1.13149
COTHER INFORMATION: /note= "RG2A"
US-09-004-838-87
Sequence 87, Application US/09004838 Patent No. 6350933 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 48.6
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                                       HSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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APPLICANT: AGODS, Kenneth
APPLICANT: MCCOY, John
APPLICANT: MCCOY, John
APPLICANT: AGOTS, Lisa
APPLICANT: Marber, Lisa
APPLICANT: Merber, David
APPLICANT: Merber, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: EMCODING THEM
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPTRY: U.S.A.
ZIP: 0.2140

ZIP: 0.2140

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OCHEVER: FROM PC Compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA: US/08/702,080
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589 GGGAGCTACAAATCCTGAAACGGGATA 615
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Sequence 7, Application US/08702080 Patent No. 5654173 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 514
ATORNEY/AGENT INFORMATION:
NAME: BLOWN, SCOLT A.
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 498-8224
TELEFAX: (617) 498-8224
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 448 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                              Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: CDNA
US-08-702-080-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                       STREET: 87 Campa
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-858-830-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 CTAATTTTGAAGTGCAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAGTCTCTT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.0%; Score 32.8; DB 4; Length 806; Best Local Similarity 53.6%; Pred. No. 6.7; Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 GATATTTCTCTTGATTGTAAAGGGGAATTGATTCTAACAGACCTTGGTCGAGCATCCATT 86
                                                                                                          APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
APPLICANT: Bornham, Martin
APPLICANT: Hodgeon, John
APPLICANT: Hodgeon, John
APPLICANT: Knowles, David
APPLICANT: Knowles, Michael
APPLICANT: Nicholas, Richard
APPLICANT: Reschard, Richard
APPLICANT: Reschard, Richard
APPLICANT: Reschard, Nartin
APPLICANT: Rosenberg, Martin
APPLICANT: Rosenberg, Martin
APPLICANT: Nard, Judith
TITLE OF INVENTION: Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SmithKilne Beecham Corporation STREET: 709 Swedeland Road CITY: 1709 Swedeland Road CITY: 1709 Swedeland Road CITY: 1709 Swedeland Road CITY: 1709 Swedeland Road COMPATY: USA COMPATY: USA COMPATER READABLE FORM: MEDIUM TYPE: Diskettle COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: REASLED (FOR Windows Version 2.0 CURRENT APPLICATION UMBRE: US/08/936,165A FITTING DATE: 0.500-1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 98,991
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                Sequence 6, Application US/08936165A
Patent No. 6348582
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 806 base pairs TYPE: nucleic acid STRANDEDNESS: $1091e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-936-165A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610-270-5090
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RESULT 24
US-08-936-165A-6
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                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/0885830
Fatent No. 5965693
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: LAVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Spaulding, Vikki
APPLICANT: Second Maurice
APPLICANT: Beney, Maurice
APPLICANT: Selviding, Vikki
TTLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: IL
Query Match 3.0%; Score 32.6; DB 1; Length 448; Best Local Similarity 60.9%; Pred. No. 5.9; Matches 53; Conservative 0; Mismatches 34; Indels (Matches 53; Conservative 0; Mismatches 34; Indels (Matches 53; Conservative 0; Mismatches 34; Indels (Matches 54); Conservative 0; Matches 54; Conservative 0; Conservative 0;
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310 GATGA 314

RESULT 25 US-08-702-080-7/c

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3.0%; Score 32.6; DB 2; Length 448; 60.9%; Pred. No. 5.9; Live 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A. STREET: P. O. Box 2938
CITY: Minneapolis STATE: M. COUNTRY: USA
COUNTRY: USA
ZIP: 55402
COMPOTER READBLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION.

FILING DATE: 13.APR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATE: 800
PRIOR APPLICATION DATE: PCT/US96/04625
APPLICATION NUMBER: PCT/US96/04625
ATTORNEY/AGENT INFORMATION:
NAME: Embresson, Janet E.
REGISTRATION NUMBER: 99.665
REFERENCE/DOCKET NUMBER: 600.318US4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: TBM COMPALIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,285
FILLING DATE: 13.APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         589 GGGAGCTACAAATCCTGAAACGGGATA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 GGGTCTTATCCCACCTGCAACAGGAAA 116
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/858,834
                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/702,080
                                                                                                                                                                                                                                             NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 638 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 448 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 448 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-858-834-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                           FILING DATE:
                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 28
US-08-930-285-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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; Sequence 7, Application US/0885834
; Patent No. 598122
; GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Treacy, Maurice
APPLICANT: Spaulaing, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.0%; Score 32.6; DB 2; Length 448; 60.9%; Pred. No. 5.9; tive 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFRATM: Pc-Dos/Ms-DOS
OFFRATM: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,830
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Genetics Institute, Inc.
87 CambridgePark Drive
                 ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         589 GGGAGCTACAAATCCTGAAACGGGATA 615
                                                                                                                                                                                                                                                                                                                                                                                                                          FILLING APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: 08/702,080
FILING DATE: ATTORNEY TOWN
NAME: BLOWN, SCOCT A.
RESISTRATION NUMBER: 32,724
PELEPRONE (617) 498-821
TELEPHONE: (617) 498-821
INPORMATION FOR SEQ ID NO: 75
SEQUENCE FORMATISTICS: SEQUENCE TOWN AND TOWN
SEQUENCE TOWN AND TOWN AND TOWN
SEQUENCE TOWN AND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: LEAGSTICS:

LENGTH: 448 base pairs

TYPE: nucleic acid

STRANDENESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 60.9
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 87 CambridgePCITY: CambridgeSTATE: Massachusetts
                                                                          Cambridge
: Massachusetts
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
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                                                                                 CITY: Car
STATE: Ma
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Sequence 3, Application US/09851896
Patent No. 6410325
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
APPLICANT: Andrew T. Watt
APPLICANT: Andrew T. Watt
APPLICANT: ANDREW T. ANDREW T. ANDREW T. ANDREW T. TILLE OF INVENTION: EXPRESSION
TILLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                             645 ATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAAT 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             856 AACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTAAAGC 915
                                                                                                                                                                                                                                                                                                                                                                                                                                  585 GAIGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.0%; Score 32.4; DB 1; Length 5555;
Best Local Similarity 53.1%; Pred. No. 20;
Matches 69; Conservative 0; Mismatches 61; Indels 0;
Matches 69; Conservative 0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
3.0%; Score 32.2; DB 4; Length 3800;
Best Local Similarity 61.2%; Pred. No. 19;
Matches 52; Conservative 0; Mismatches 33; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-05-762-15
US-08-05-762-15
Sequence 15, Application US/08965762
Patent No. 6280963
GENERAL INFORMATION:
APPLICAMY: Rollin, Yigal
APPLICAMY: Rollin, Yigal
APPLICAMY: Rollin, Yigal
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
FILE REFERENCE: 07334/062001
CURRENT APPLICATION NUMBER: US/08/965,762
CURRENT FILING DATE: 1997-11-07
NUMBER OF SEG ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       916 TIGCTICTCTTTATTTTCCTTTTGT 940
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5555 base pairs
TYPRE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-08-965-762-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 ATAGTTCTCCTTATTGTTCTTTTT 87
                                                                                                                                                                                                                                         NAME/KEY: CDS
; LOCATION: 34..3210
US-08-484-438-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5543 AAAAAAAAA 5552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           705 CAAGAAAAA 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/0848438

Patent No. 5811098

Patent No. 5811098 5780031

GENERAL INFORMATION:
APPLICANT: Plowman, Gregory D.
APPLICANT: Culouscou, Jean-Atchel
APPLICANT: Siegall, Clay B.
APPLICANT: Riegard
APPLICANT: M. Ingegerd
APPLICANT: Hellstr m. Ingegerd
APPLICANT: Hellstr m. Marl E.
TILE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORPESSER: Pennie & Edmonds
                                                                                                                                                                                                                                    // Match 3.0%; Score 32.6; DB 4; Length 638; Local Similarity 52.6%; Pred. No. 6.9; nes 71; Conservative 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE PORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484.438
FILING DATE: 07-UUN-1995
CLASSIFICATION: NAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-0CT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10 NOV-1993
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5624-230
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET WUMBER: 565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            957 AGGAATATGGGGTCG 971
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                                                                                                                                       FRAGMENT TYPE:

/ ORIGINAL SOURCE:

US-08-930-285-16
                                                                                                                       ANTI-SENSE: NO
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Matches
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APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Well-dens, Thomas E.
TITLE OF INVENTION: AND PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERVIHROCYTE BINDING PROTEINS
                                                                                 APPLICANT: Sim. Kim L.
APPLICANT: Sim. Kim L.
APPLICANT: Sim. Kim L.
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Miller S.
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA A
APPLICATION NUMBER: US/08/568,459A
FILING DATE: 07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH121.001CP1
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; Patent No. 5993827
; GENERAL INFORMATION:
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US-08-568-459A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 11, Application US/08568459A Patent No. 5849306 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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Best Local Si
Matches 59,
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Sequence 2004, Application US/09134001C
Sequence 2004, Application US/09134001C
GENERAL INFORMATION:
TITLE OF INFORMATION:
TITLE OF INFORTION:
THE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         727 GCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAA 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      787 GGGAGIGCTIACAACAGCCAIATCAGIGGAGCAACCTICCCTTIGAITCTITGAIAAIGA 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32.2; DB 4; Length 70000;
Pred. No. 67;
0; Mismatches 98; Indels 0;
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                 FILE REFERENCE: RTS-0220
CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
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CRCANISM: Staphylococcus epidermidis
US-09-134-001C-2094
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 48.1%;
Matches 91; Conservative
                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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US-09-134-001C-2094
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US-08-568-459A-11
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APPLICANT: Childrie, Chetan
APPLICANT: Childrie, Chetan
APPLICANT: Childrie, Chetan
APPLICANT: Childrie, Chouls H.
APPLICANT: Wallens And S.
APPLICANT: Su, Xin-zhau APPLICANT: Su, Xin-zhau APPLICANT: Wallens, Thomas E.
APPLICANT: Wallens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Wemport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.9%; Score 32; DB 2; Length 8220; 56.7%; Pred. No. 31; tive 0; Mismatches 45; Indels
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BAP PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION WHOSER: US-SEP-1993
ATTORNEY AGENT INFORMATION:
NAME: Israelsen, Wed
NAME: Israelsen, Ned
NAME: Israelsen, Ned
NAME: ISPACION NUMBER: NH121.001CP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 235-0176
INFORMATION POR SEQ ID NO: 11:
SEQUENCE GIARACTERISTICS:
LENTH: 8220 base pairs
TYPE: Nucleicaid
STRANDENESS: Single
TOPOLOGY: linear
TOPOLOGY: Linear
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NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
US-08-487-826B-11
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 56.74
Matches 59; Conservative
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ORGANISM: Pla
                                                                                                                                                                     92660
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US-09-210-288-11
                                                                                                                                                  COUNTRY:
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Sequence 13, Application US/08487826B
Patent No. 599387
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitais, Chetan
APPLICANT: Miller Louis.H.
APPLICANT: But Xin-zham
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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2.9%; Score 32; DB 4; Length 8220;
Best Local Similarity 56.7%; Pred. No. 31;
Matches 59; Conservative 0; Mismatches 45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 TCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAAC 258
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATA:
CLASSIPTCATION:
MATCHER FOLLEY, MICHAEL
REGISTRATION NUMBER: 36,516
REFERENCE/DCCKET WINDER: 36,516
TELECOMMUNICATION INFORMATION:
TELECHONE: (619) 235-850
ITELEPHONE: (619) 235-850
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: Knobbe Martens Olson & Bear
F: 620 Newport Center Drive 16th Floor
Newport Beach
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: ISTBELSEN, NE
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                    . 8220 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
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US-08-487-826B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 62
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APPLICANT: Kondo, Keiji
APPLICANT: Kondo, Keiji
APPLICANT: Inouye, Masayori
TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
TITLE OF INVENTION: APPLICATIONS
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 GTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAACGGCTCCAT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 CTAATITIGAAGIGAGIICIACCAGIICAICAAAAIGICITATIGAAAAIAAAGICITT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 CTAATATGATAAAAGATTTATGAATCAATTAATTCGAGGTATTAAACATTGTCATTCTC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 GTGGAGTTGATGTATTGAAGGGAAGACGAATAATCTGATCCAATTCTAAAGGGAGAACAC 206
                                                        Draetta, Guilio
PENTION: Cell-Cycle Regulatory Proteins from
FENTION: Human Pathogens, and Uses Related Thereto
EQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 31.8; DB 1; Length 1002; Best Local Similarity 47.3%; Pred. No. 14; Matches 96; Conservative 0; Mismatches 107; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICACHUN: 4.2.
ATTORNEY, AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36.70
REFERENCE/DOCKET NUMBER: MIV032.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-129
TELEPHONE: (617) 832-700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPER: NUCLEIC acid
                                                                                                                                                                                                               E: Foley, Hoag & Eliot, LLP
One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,090B
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-667-276A-1/c
; Sequence 1, Application US/07667276A
; Patent No. 5470971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 ATGCTTTCTTCCTTCATGGTTT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542 ATGAAGTTGTCACTTTATGGTAT 564
Cottarel, Guillaume
                                 Veronique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1995
                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , NAME/KEY: CDS
, LOCATION: 43..993
US-08-463-090B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                APPLICANT: Draetta, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                      Boston
                                                                                                                                                                                                                                                                                                                                                                                    02109
                                                                                                                                                                                                                                                                                                                        MA
                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
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US-09-356-952-12/C

Sequence 12, Application US/09356952

Sequence 12, Application US/09356952

Sequence 12, Application Sequence 12, Application Sequence 12, Application Sequence 13, Application Sequence 13, Application Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 15, Applicant Bor-Sogi, Dafna

APPLICANT: Bor-Sogi, Dafna

APPLICANT: Bor-Sogi, Dafna

APPLICANT: Wargarit, S. M.

APPLICANT: Wargarit, M.

APPLICANT: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       b 32322 aaggattgatgccttcttgaataagaatattgaacatagttttgaaaatttgtaaaaac 32263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DD 32382 AATTGAAAGTGAAAAACCTTTCAGTTCATCTTCCAATATTGTGAAGTACTCATCGCGTA 32323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            831 GATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAAATAG 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             771 AATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTT 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
2.9%; Score 32; DB 2; Length 19124;
Best Local Similarity 56.7%; Pred. No. 44;
Matches 59; Conservative 0; Mismatches 45; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 10169 TACAAAAACGTCTTTTTACCTCCCGGAGGAGAACACATGTGTAC 10212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 TCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAAC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/08463090B; Patent No. 5801015; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Saccharomyces cerevisiae US-09-356-952-12
           TELEPHONE: (619) 235-8550
TELEFRAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1914 Dasse pairs
TYPE: nucloic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32262 TTCTGGAT 32255
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                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                         TOPOLOGY: linea
MOLECULE TYPE: CE
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                       , ANTI-SENSE: NO
US-08-487-826B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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Matches
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OTHER INFORMATION: corresponds to base -474 of the sequence listed in
OTHER INFORMATION: Figure 4 of the application"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1296 AATTGTCAAGAAAGGAAACATTTCTTACGGATTGGGAAGAAGCACTAATCTCGAAAAAGA 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         666 CTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAAT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   726 AGCITITCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   606 AAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.9%; Score 31.8; DB 1; Length 1584;
Best Local Similarity 51.9%; Pred. No. 17;
Matches 95; Conservative 0; Mismatches 87; Indels 1; Gaps
                                                                                                                                                                     COMPUTER READABLE FLORM;
COMPUTER: IBM PC compatible
CLASSIFICATION NUMBER: US/O/7667,276A
TILING DATE: 11-MAR-1991
CLASSIFICATION NUMBER: 377.531P
TELETATION UNBER: 377.531P
TELETATION UNBER: 377.531P
TELETAMION UNBER: 215-875-8394
INFORMATION FRED: 215-875-8394
INFORMATION FRED: A15-875-8394
INFORMATION FRED: UN NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: UNKNOWN
MOLECULE TYPE: NNA (genomic)
HYPOTHETICAL: NO
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREFT: 230 S. Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: Saccharomyces cerevisiae
S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 40
US-08-642-274D-51
Sequence 51, Application US/08642274D
Patent No. 6200749
GENERAL INFORMATION:
                                                             CITY: Philadelphia
STRATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         internal
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LOCATION: 475..1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
FRAGMENT TYPE: in
ORIGINAL SOURCE:
ORGANISM: Sacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1117 AGG 1115
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APPLICANT: Shiloh, YOSEÍ
TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO
TITLE OF INVENTION: SCREEN FOR A PARTIAL A-T PHENOTYPE
FILE REFERENCE: 229000033
CURREWY APPLICATION NUMBER: US/08/642,274D
CURREWY APPLICATION 1996-05-03
NUMBER OF SEQ ID NOS: 220
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 51
LENGTH: 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 AAGTTTGCAATAGTTCATATAATTTAGCTATGTATATATGTATATAGTTAAATTTTAG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               926 TTATTTTCCTTTTGTAGAATGATTCGGTAGGAATATGGGGTCGACTATGCACGTTGG 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 TGTATTACCTTAATTTGAGTGATTCTTTAGATGTATTTAGTATTTGTAAATATAAATTTAA 202
                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: genomic US-08-642-274D-51
                                                                                                                                                                                                                                                                                                                                                                                                                     2.9%; Score 31.6; DB 4; Length 679; 50.0%; Pred. No. 13; tive 0; Mismatches 79; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: GRANIA TELANGIECTASIA GENE AND ITS
TITLE OF INVENTION: GENOMIC ORGANIZATION
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 6265158thwestern Hwy., Suite 410
CITY: Farmington Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,014C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   986 AGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGATTG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 ATTGGTTGTGTTTTCTTGAAGGCAGTAGAAGTTGCTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2290.00028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 51, Application US/08952014C; Patent No. 6265158; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: KÖNN, Kenneth I.
REGISTRATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 2290.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 810-539-5050
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 50.09
les 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 679 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Michigan COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-952-014C-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-952-014C-51
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                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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143 ICITGIGGAGTIGATGTATTGAAGGGAAGACGAATAATCTGATCCAATTCTAAAGGGAGA 202
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                                                            203 ACACGIACGITAICAAIGAAAGCGIGICCAAGIICCIGAGGAGAACIGAIAAGAACGG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31.6; DB 3; Length 1734;
                                                                                                                                                                                   GEOUL.

Sequence 2, Application US/09200284

Sequence 2, Application US/09200284

Sequence 2, Application US/09200284

Sequence 2, Application US/09200284

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: OF INVENTION: HUMAN 3-HVDROXXISOBUTYRUL-COENZYME ATTILE OF INVENTION: HYDROLASE

NUMBER OF ENQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
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UNETWARE: FASTESO for Windows Version 2.0
APPLICATION NUMBER: US/APLICATION DATE:
FILING DATE:
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/858,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J. REGERRATION NUMBER: 36,749 REFERENCE/DOCKET WUMBER: PF-TELECOMMUNICATION INFORMATION: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1734 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.98;
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Best Local Similarity 54.2%;
Matches 64; Conservative
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TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Palo Alto
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US-09-484-970B-60
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                                                                                                                                                 83 AAGTITGCAATAGTICATATAATITAGCTAGCTITTATATGTATATAAGTTAAATITTAG 142
                                                                                                                                                                                               926 TTATTTTCCTTTTCTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTTGG 985
                                                                                                                                                                                                                                 143 IGTATTACCTTAATTIGAGTGGATTCTTTAGATGTATTTAGTATTTGTAAATATAATTTAA 202
                                                                                                               0; Gaps
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1 Similarity 54.2%; Pred. No. 20;
64; Conservative 0; Mismatches 54; Indels 0.
                             Query Match 2.9%; Score 31.6; DB 4; Length 679; Best Local Similarity 50.0%; Pred. No. 13; Matches 79; Conservative 0; Mismatches 79; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2. Application US/08858052
| Sequence 2. Application US/08858052
| Patent No. 5849498
| GENERAL INFORMATION:
| APPLICANT: Bandman, Olga | APPLICANT: Guegler, Karl J. APPLICANT: Corley, Nell J. APPLICANT: Corley, Nell J. TITLE OF INVENTION: HUMAN 3-HYDROXYISOBUTYRUL-COENZYME A TITLE OF INVENTION: HYDROLASE
                                                                                                                                                                                                                                                                               986 AGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGATTG 1023
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APPLICATION WUBBR: US/08/858,052
FILLING DATE: Herewith
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STREET: 3174 Porter Drive
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1734 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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LIBRARY: U937NOT01
CLONE: 1187
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CORRESPONDENCE ADDRESS:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.9%; Score 31.6; DB 4; Length 13977; Best Local Similarity 46.1%; Pred. No. 50; Matches 106; Conservative 0; Mismatches 124; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 12047 CTAATAGAAAGAAATTACTTCTAGTCAGTCATCCAGGCTTACCTGCTTGG 12096
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jones, Karen A.
APPLICANT: Jones, Karen A.
APPLICANT: Walker, Michael G.
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL PROGRAM
SEQ ID NO 60
LENGTH: 13977
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Patent No. 6410712
SCENERAL INFORMATION:
APPLICANT: Bergilind Ran Olafsdottir
APPLICANT: Deffrey Gulcher
TITLE OF INVENTION: HUMAN NARCLEPSY GENE
FILE REFERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 1
Sequence 60, Application US/09484970B Patent No. 6426186 GENERAL INFORMATION:
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(95252)...(95430)
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ORGANISM: Homo Sapiens
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US-09-426-290-1
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NAME/KEY:
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                                                                                                                                   Query Match

2.9%; Score 31.6; DB 4; Length 168575;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 105; Conservative 0; Mismatches 104; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cheng, Kuo-Joan
APPLICANT: Liu, Jin-Hao
APPLICANT: Tsai, Cheng-Feng
APPLICANT: Hsu, Yih-Chin
TITLE OF INVENTION: CELLULASE ENZYMES
FILE REFERENCE: 08919/03601
CURRENT APPLICATION NUMBER: US/09/428,034
CURRENT PETLING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78297 TTGCAGACTTGTGAGGTGGTTAAATAACAA 78326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/09428034; Patent No. 6428996; GENERAL INFORMATION:
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NAME/KEY: CDS
LOCATION: (127009)...(127130)
                                             ; NAME/KEY: CDS
; LOCATION: (128910)...(129139)
US-09-426-290-1
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Best Local Similarity 52.74
Matches 68; Conservative
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; LOCATION: (1)...(1128)
US-09-428-034-1
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US-09-428-034-1/c
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SEQ ID NO 1
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US-09-004
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63 RNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SCOSLEA, Jack W.
APPLICANT: ROBERTS, RICHARD W.
APPLICANT: ROBERTS, RICHARD W.
APPLICANT: APPLICANT: RICHARD W.
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: PUSIONS;
FILE REFERENCE: 00706/350007
CURRENT APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER PLING DATE: 1997-01-27
EARLIER PLING DATE: 1997-01-27
EARLIER PLING DATE: 1997-01-27
EARLIER PLING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASSED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 31.2; DB 4; Length 289; Best Local Similarity 9.3%; Pred. No. 12; Matches 26; Conservative 111; Mismatches 142; Indels
APPLICANT: Liu, Rihe
TITLE OF INVENTION: FUSIONS
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: 05/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 60/064,491
BARLIER APPLICATION NUMBER: 1997-01-27
EARLIER APPLICATION NUMBER: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTHARE: FASTESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

; LOCATION: (1)...(289)

; OTHER INFORMATION: n = A,T,C or G

US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: Artificial Sequence
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SEQ ID NO 17
LENGTH: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4390 AATTATTAAAGTGATCAGTTGTGATAAGCTTGTGAATCT--CTTTCCACAAACCCATG 4447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4448 TCTATACTGCATCATCATGAAGAGCTTGAAGTCGAGAATTGTGGTTCCATTGAATCGTTA 4507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           818 CAACCTTCCCTTTGATTCTTTGATAATGACAAGATGAACAAGAGTAAGTTTTTGAAA 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      938 TGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTG 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       998 TICTGGAAGAACAGGGAAAGTGATTGTCTCAGCTTTAGAGCAATCTTCAGAATATACTT 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 31.4; DB 4; Length 7521; Best Local Similarity 48.5%; Pred. No. 43; Matches 116; Conservative 0; Mismatches 121; Indels 2;
                                                  APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCES ADDRESS:
ADDRESSEB: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REPERBNIC/POCKET NUMBER: 023070-078810US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
FILING DATE: 10-JAN-1997
ATTORNEY AGRAT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | NAME/KEY: | LOCATION: | LOCATION: | LOCATION: | TOCATION: | OTHER INFORMATION: /note= "RG2N" | US-09-004-838-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09007005B patent No. 625858 GENERAL INFORMATION:
              APPLICANT: Michelmore, Richard W. APPLICANT: Shen, Kathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LEWGHH: 7521 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA
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US-09-007-005-17
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Search completed: January 9, 2003, 11:51:00 Job time : 476 secs

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPLEMENTIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DEPLEMENTIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UNDERS. US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 1809
LENGTH: 999
TUBBER OF SEQ ID NOS: 5674
TWOFF DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 RNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             688 GAAAGCTTCTAAGTAATCAAGAA-AAAATCTTGGACAATAGCTTTTCCATAGAGAAAACC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 AACAGTAAACCAAAAGCAGCGTACAATAGCGATCAGATTGCTTTGTAGGGTTTGTATGCG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 TTGTTTTTACTAGGAAGACCTTGTACTTTTCTATGACTTTAGTGAAGAGTCTTCCCAT 426
                                                                                                                                                                                                                                                                                                                              508 GGAGAAATTATCTTTATCGAGAGTTCGCATTACAGAGGCAATGGGAAAGTAACGGTCCTG 567
                                                                                                                                                                                                                                                                                                                                                                                                                              568 CAACAGAGACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATG 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628 TGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACC 687
                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                            3 RGRGRARCRARARURURARCRURARURURURARCRARARURURARCRARARURGRNRNRS 62
                                                                                                                                                                                                                            Query Match
2.9%; Score 31.2; DB 4; Length 289;
Best Local Similarity 9.3%; Pred. No. 12;
Matches 26; Conservative 111; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.9%; Score 31.2; DB 4; Length 999; Best Local Similarity 53.2%; Pred. No. 21; Matches 66; Conservative 0; Mismatches 58; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747 GTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAA 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Translation template FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 50
8.09-13-001C-1809
; Sequence 1809, Application US/09134001C
; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1809
                                                                                                              COCATION: (1) ...(289)
COTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
ORGANISM: Artificial Sequence
                                                                                                  NAME/KEY: misc_feature LOCATION: (1)...(289)
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| AL105023 Drosophil<br>AL106628 Drosophil<br>BJ345426 BJ345426<br>BJ345414 BJ345414<br>AL065781 Drosophil | BJJ35240 BJJ35240<br>ALO98379 DIOSOSPhil<br>BJ340295 BJ340360<br>BJ340295 BJ340295<br>AU038515 AU038515<br>BJ3400438 BJ3400438<br>BJ302020 BJ34002020 | BJ341943 BJ341943 BJ341943 BJ341943 BJ398603 BJ376868 BJ376868 BJ376868 BJ401886 BJ402538 BJ402538 C93147 C93147 Dict | BJ343976 BJ344976<br>BJ375941 BJ375941<br>BJ401060 BJ401060<br>BJ434901 BJ434901<br>BJ401293 BJ401293<br>BJ3939159 BJ399159                                | BJ341290 BJ341290<br>BJ401883 BJ401883<br>BJ400818 BJ400818<br>BJ401195 BJ401195<br>BJ341261 BJ341261<br>BJ342890 BJ343890<br>BJ339243 BJ3739243<br>BJ347280 BJ34739243<br>BJ347280 BJ34739243 | BJ371948 BJ371948 AL066743 Drosophil AL066801 Drosophil AL166896 Drosophil AZ550321 ENTEMPTER AZ57921 ENTEG17TR AZ67921 ENTEG17TR AZ69917 ENTHG5TR AZ69917 ENTHG5TR AZ649336 ENTED2ZTR AL104338 Drosophil BJ344899 BJ344899 C93903 C93903 Dict | ALO7972 Drosophil BM416099 OP21184 M ALO56899 Drosophil ALO781186 Drosophil ALO69797 Drosophil AL523778 AL523778 AL055406 Drosophil AL065567 Drosophil AL065567 Drosophil AL07172 Drosophil AL107172 Drosophil AL566489 AL566489   | AL514453 AL514453 AL071208 Drocsophil AL02961 clone BAO AL062781 Drocsophil AL104216 Drocsophil AL106773 Drocsophil BE84853 ux37f05.y BE631807 BE631807 AL069127 Drocsophil BE601807 Brocsophil BE601807 Brocsophil BE601807 Brocsophil BE601807 Brocsophil BE1600924 G03249264 BJ141956 BJ141956 AL54421 AL514421 BH596443 BGGCK93TF   |
|--|---|---|--|--|--|--|---|
| 48.2 4.4 1001 17<br>47.2 4.3 615 13<br>47.2 4.3 635 13   | 45.6 4.3 588 17<br>45.2 4.2 588 13<br>45 4.1 485 13<br>45 4.1 485 13<br>45 4.1 529 9<br>45 4.1 549 13<br>45 4.1 549 13                                | 45 4.1 562 13<br>45 4.1 584 13<br>45 4.1 590 13<br>45 4.1 596 13<br>45 4.1 597 13<br>45 4.1 653 14                    | 45 4.1 654 13<br>45 4.1 663 13<br>45 4.1 664 13<br>45 4.1 665 13<br>45 4.1 675 13<br>45 4.1 688 13   | 455 411 698 13<br>455 411 698 13<br>455 411 722 13<br>455 411 722 13<br>455 411 732 41<br>455 411 742 13<br>45 411 742 13  | 444<br>444<br>646<br>646<br>646<br>646<br>646<br>646<br>646<br>646   | 43.4<br>43.2<br>43.2<br>43.2<br>42.8<br>42.8<br>42.8<br>42.8<br>42.6<br>42.6<br>42.6<br>42.7<br>42.2<br>42.2<br>42.2<br>42.2<br>42.2<br>42.2<br>42.2<br>42.2<br>42.2<br>42.3<br>42.4<br>42.4<br>42.4<br>42.4<br>42.4<br>42.4<br>42.4<br>42.4<br>42.4<br>42.4<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7<br>42.7 | 65 42 3.9 877 9 AL514453<br>67 41.8 3.8 1101 17 CNSO0FVE<br>68 41.6 3.8 1001 17 CNSO04G<br>61 41.6 3.8 1001 17 CNSO14J2<br>70 41.6 3.8 1102 17 CNSO14J2<br>71 41.4 3.8 567 12 BE848353<br>72 41.4 3.8 567 12 BE848353<br>73 41.4 3.8 1101 17 CNSO18IN<br>74 41.2 3.8 1001 17 CNSO05FI<br>75 41.2 3.8 1067 13 BIGOD59<br>76 41.2 3.8 1067 13 BIGOD59<br>77 41 3.8 748 13 BJ141956<br>78 41 3.8 757 9 AL514421<br>79 41 3.8 772 17 BH596443 |
|  | me 1940 Seconds<br>lignments)<br>11lion cell updates/sec  | ctcgcagtagtgcac 1086  |  | 1 M M M M M M M M M M M  |  |  | have a ng printed,  |
| GenCore version 5.1.3<br>Copyright (c) 1993 - 2003 Compugen Ltd  | nucleic - nucleic search, using sw model on: January 9, 2003, 06:35:28; search (without; 9066.133; US-09-438-185A-1 COPY 1199590_120067               | core: 1086 1 ttggcaaagtacctcaaaac able: IDENTIY_NUC Gapop 10.0 , Gapext 1.0   | Searched: 10124000 Segs, 0097743570 Lesidues Total number of hits satisfying chosen parameters: Minimum DB Seq length: 0 Maximum DB Seq length: 2000000000 | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 150 summaries Listing first 150 summaries EST:* 1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estin:*                    | 5: em_estpl:.* 7: em_estpl:.* 8: em_estpl:.* 9: gb_est1:* 10: gb_est2:* 12: gb_est3:* 13: gb_est3:* 13: gb_est4:* 14: gb_est5:* 15: em_estfun:*  | 17; 9b_gss:* 18: em_gss_lum:* 19: em_gss_lun:* 20: em_gss_pln:* 21: em_gss_pln:* 22: em_gss_fun:* 23: em_gss_fun:* 24: em_gss_lun:* 25: em_gss_lun:* 26: em_gss_lun:* 27: em_gss_lun:*   | Pred. No. is the number of results predicted by chance to score greater than or equal to the score of the result beland is derived by analysis of the total score distribution    Summaries   |

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Page 2

| ALIGNMENTS              | 1 1<br>39G/c                        | LOCUS CNS0039G 1101 bp DNA linear GSS 03-JUN-1999 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK08K10 of RPCI-98 library from Drosophila melanogaster (fruit | ACCESSION 1177 9540MIL SULVEY SEQUENCE: VERSION AL063921.1 GI:4941778 KRYWORDS GSS. | SM                     | Eukaryota: Metazoa: Arthropoda; Hexapoda; Insecta; Pterygota;<br>Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha;<br>Ephydroidea; Drosophilidae; Drosophila. | CE<br>RS               | JOURNAL Submitted (02-JUV-1999) Genoscope - Centre National de Sequencage : | br 191 91000 Evri Cedex - France (E-mail : segret@enoscope.cns.ir<br>- Web : www.genoscope.cns.ir<br>- Dotomination of this process consists of the constant of the |  | melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila | melanogaster BAC library was prepared by Kazutoyo Osoegawa and<br>Aaron Mammoser in Dieter de Jone's laboratory in the Department of | Cancer Genetics at the Nowell Park Cancer in Stitute in Buffalo, NV mho library is named DDCT-08 and use constructed by narrial | ECORI digestion of Drosophila DNA provided by the BDGP from the | isogenic strain y2; on bw sp, the same strain used for the BDGP's<br>Pl and EST libraries. A more detailed description of the library | and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be | found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.<br>Location/Onalifiers |          | /organism="brosophila melanogaster"<br>/db_xref="taxon:7227" | /clone="BACRU8K10"<br>/clone_lib="RPCI-98" | RASE COINT 2013 64 C 131 0 202 t 503 others |                    | Query Match 5.6%; Score 61; DB 17; Length 1101; | Local Similary 1979, free No. No. les 98; Conservative 270; Mismat | Qy 353 AGGTTTGTATGCGTTGTTTTTACTAGGAAGAGCTTGTACTTTTCTATGACTTTAGTG 412 | Db 1096 WGDDTWDRDTRKDDWDWTKWWTWWKDRADDRRWAGDADRWAWDDGAGTWWTATWWWWWW 1037 | Qy 413 AAGAGTCTTCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACG 472 | Db 1036 WATWDTWWDKWWWATAAKTDTAWTWWRTAWRADWAGRDRGAGKRDRDAUGAGRRD 977 | Qy 473 TGCCCTAAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTT 532 | Db 976 GGRKRKDRKDGDDDK-KGGKRKKAARAARWATKWWDDWDWDKDWKWDGAKDRKADDD 918 | 533 CGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGGA | DD 91/ DGAGJKDDDGKGKKDADDDIDGTKDDDKDKWDDWDKAKGTWGDATWAWAATDWWWWWAD 858 | QY 593 GCTACAAATCCTGAAACGGGATAATAGGAAAATGTGTTTCTAATTCGAAGAATTTAATG 652 ::::  ::  :: ::: ::: ::: ::: ::: ::: :: |
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| 1823                    | 0487<br>1721<br>9035                | A2692378 ENTGLOITF<br>AZ531880 ENTCO37TF<br>AL065906 Droscophil<br>A106591 Proceedii   | AV955881 AV955881<br>AV860727 AV860727<br>AV880960 AV880960                         | 991                    | 0010<br>1729<br>7406   | 168                    | 1618  | AV900393 AV900393<br>AV897732 AV897733<br>AV907690 AV907690   | 3746                                   | 5824<br>3569   | 1435   | AL272927 TELTSOCON AL08761 Processity   | BE554967 SP83b01.Y  | 331 ,<br>9199   | 5604  | 537   | 3987     | ALUBZU49 DIOSOPALI<br>BM911712 AGENCOURT                     | 1211                                       | AQ379091 RPCI11-16<br>AL064634 Drosophil    | 1646               | 5758  | 9674   | 3222   | ALIUDIZI DIOSODNII<br>AZG74289 ENTMITATR<br>AIO7026 DAGGGGGG             | 7309   | 3018  | ALICOSSS DIOSOPILI<br>AV72030 AV72030                                   | 7563   | 3934   | AL108/02 Drosophil<br>AL077748 Drosophil                               | AL078714 Drosophil<br>BM926208 AGENCOURT<br>BQ398645 NISC_m009   |
| .8 1101 17<br>.8 480 17 | .8 486 17<br>.8 687 17<br>.8 696 12 | .8 850 17 AZ692378<br>.8 873 17 AZ531880<br>.8 938 17 CNS006TJ<br>.0 10A7 17 CNS016AD  | .7 477 10<br>.7 530 10<br>.7 568 10   | .7 579 10<br>.7 648 10 | .7 670 14<br>.7 675 10<br>.7 684 10  | .7 688 10<br>.7 689 14 | .7 693 10<br>.7 697 17  | 7 721 10  | ., , , , , , , , , , , , , , , , , , , | .7 1156 17<br>.7 635 13  | .7 698 13  | 7 878 17  | .7 350 10   | .7 510 9 .7 .7 1031 17  | .7 1061 17<br>.7 1179 10  | .7 570 17   | 7 943 17 | .7 1234 14   | .6 457 17                                  | 6 634 17                                    | 6 848 17           | .6 580 17<br>6 982 17                           | .6 1028 17<br>.6 1101 17   | 6 1111 13  | .6 888 17<br>6 1059 17   | .6 1101 17   | .6 1300 13  | .6 465 10   | .6 544 17<br>6 581 17  | 6 606 17   | .6 1101 17   | .6 1101 17<br>.6 1113 14<br>.6 486 14  |
| 41                      | 82 40.8<br>83 40.8<br>84 40.8       | C 85 40.8 3 C 87 40.8 3 C 87 40.8 3  | 89<br>90<br>44<br>40.6<br>60.6  | 40.6                   | 4 4 4 4 0 . 6<br>6 0 . 6 6   | 40.6                   | 40.6<br>00 40.6   | 0.02<br>4 4 0.00<br>6 0.00  | 0.04 40.6<br>0.5 40.6                  | 06 40.4<br>07 40.2   | 08 40.2<br>09 40.2   | 110 40.2  | 12 40   | 13 40<br>14 40  | 15 40<br>16 40  | 17 39.8<br>18 39.8  | 39.8     | 21 39.8  | 22 39.6<br>23 39.6                         | 24 39.6<br>25 39.6                          | 26 39.6<br>27 39.6 | 128 39.4  | 130 39.4   | 32 39.4  | 134 39.2   | 36 39.2  | 138 39.2  | 38.8  | 142 38.8   | 144 38.8   | 47 38.8  | 38.8<br>38.8<br>38.6   |

653 ACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAA 712

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Direct Submission

Submitted (23-ULL-1999) Genoscope - Centre National de Sequencage : Submitted (23-ULL-1999) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (F-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr |
Determination of this BAG-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - Http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC |
Library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding project grant. The DNA was prepared from embryos by Alain Bucheton and Geneviewe Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 26-JUL-1999
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Drosophila melanogaster.
Eukaryota, Metanogaster
Eukaryota, Metanogaster
Eukaryota, Metanogaster
Enkaryota, Metanogaster
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Ephydroidea; Drosophilae; Drosophila.

[ Pases 1 to 1101)
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BP 191 91006 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr

- Web: www.genoscope.cns.fr

- Gold boration with the Berkeley Drosophila genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruitfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutcyo Osoegawa and

Aaron Mammoser in Pleter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

BCORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

pl and BCST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 997)
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Drosophila melanogaster genome survey sequence SP6 end of BAC BAC BACN37F10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     614 TAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              705 AAAAAAAAAAAAADAGGKRKWKKGDGKDGKAIKIAAWAKGRKDWGTAIAWWIWDAIWADIWK 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         674 TCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTC 733
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Buxosophila melanogaster.

Buxaryota; Metanogaster

Eukaryota; Metanogaster

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                               11arity 20.4%; Score 51.2; DB 17; Length 1101; Pred. No. 0.022; Conservative 209; Mismatches 249; Indels 2;
                                                                                                         358 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   974 TATGCACGTTGGAGTGATTGGCTGTTCTGGAAGAACAG 1011
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/clone="BACN37D10"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
                                                                        /note="end : SP6"
268 c 128 g
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- Web : www genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a

Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRT.-cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

REFERENCE AUTHORS

JOURNAL

COMMENT

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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -
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collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37A07 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 GGAAGAGCTTGTACTTTTCTATGACTTTAGTGAAGAGTCTTCCCATGTTTATGAAAAAT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440 TCAGAAAATGAGGGATGTAGAAGCCAAGGCACGTGCCCTAAAAGGTCATGGATGAGATCA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         988 WWRDTDWWDKWDTKWKDDRWTKRWATRGDGRAGRAKRRDDRRGDRGRRRRRRRTRKWRWW 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             500 GGAGTTAAGGAGAAATTATCTTTATCGAGAGTTCGCATTACAGAGGCAATGGGAAAGTAA 559
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Boptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidae; Drosophilidae; Drosophila.
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    .1101
    /organism="Drosophila melanogaster"
    /db_xref="taxon:7227"

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Conservative 135; Mismatches 181;
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                                                                                                                                                                                                                                                                               /clone="BACN37F10"
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/note="end: SP6"
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Drosophila melanogaster genome survey sequence SP6 end of BAC BACN13023 of DrosBAC library from Drosophila melanogaster (fruit 11), genomic survey sequence.
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
By 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1017 AKADDAAKAKAKAKABABAKAKAAKRAAKRABABAAKAKAKABDBABAKAKAKABABABAK 1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               720 GACAATAGCITITCCATAGAGAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGAT 779
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Bukaryota Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                  480 AAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTTCGCATTA 539
                                                                                                                                                                                                                                                                                                                                                                                                        661 ARKDKDTAKDAWKWDKATKAKAKKKAAKAKAKARAAAKTATGKDARKAKAKAKAKAK----ATK 716
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                                                                                                                                                                                                                                                                 4.5%; Score 48.4; DB 17; Length 1101;
ilarity 19.4%; Pred. No. 0.11;
Conservative 178; Mismatches 163; Indels 4;
                                                                                                                                                                                                       501 others
                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                         175 t
                                                                                     /db_xref="taxon:7227"
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/clone_lib="DrosBAC"
/plasmid="pBeloBACI1"
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Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEBH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Submitted (23-Jul-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
        http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/db_xref="taxon:7227"
/clone="BACN37A07"
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Local Similarity 30.5%; Pred. No. vies 96; Conservative 77; Mismatch
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/plasmid="pBeloBAC11"
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d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence 17 end of BAC
BACN15A12 of DrosBAC library from Drosophila melanogaster (fruit
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                      232 others
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                                                                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN13C23"
/clone_lib="prosBAC"
/plasmid="pBeloBAC11"
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EWR cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Project Gentre Project Gentre Project Prant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          889 AAAKKKDKKDAADKKAAARDAAKKKKDKAAKAADKDAAKKWDKKKKAGGAARAAAKGKK 830
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1 (bases 1 to 615)
                                                                                                                                                                                                                                                                                                                                                                                                                            312 others
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                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:727"
/db_xref="taxon:727"
/clone="PacN15a12"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
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Center For Genetic Resource Information
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18.28; Pred. No. (
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By 19 91000 EARL CHECKA LARGE CONTROLL OF MANY GENOROPE CARE AND A SECTION OF THIS BACTON Sequence was carried out as part of a Determination of this BACTON Sequence was carried out as part of a Determination of this BACTON Sequence of the Drosophila The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACS. For further information melanogaster genome using these BACS. For further information please see http://www.fruitfly.org the BDGP Drosophila please see http://www.fruitfly.org the BDGP Drosophila melanogaster BAC library was prepared by Kazucyo Googeawa and Azono Manmoser in Picter Ge Jong's laboratory in the Department Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Escapic Strain v2: on bw sp., the same strain used for the BDGP's I and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genome survey sequence T7 end of BAC # 18ACR14J19 of RPCI-98 library from Drosophila melanogaster (fruit fly). genomic survey sequence.
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                         253 AAGAACGCCTCCATATGCTTTCTTCCTTCATGGTTTTCAATAAGTCCGCTTTCAACAGT 312
                                                                                                            Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Erachycera; Muscomorpha; Ephydroidas; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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/note="end : T7"
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Drosophila melanogaster
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BJ345414 GI:19215921
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Lobases 1 to 615)

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostellum discoideum at the aggregation
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/clone="dda23117"
/clone_lib="bictyostelium discoideum cDNA library, AF"
/sex="nat A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Tadasu Shin-i
Center For Genetic Resource Information
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                 /organism="Dictyostelium discoideum"
                            National Institute of Genetics Ill Yate, Mishina Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-685 Email: tshini@genes.nig.ac.jp. Locatlon/Qualifiers
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95 c 105 g 218 t
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94 c 103 g 210 t
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Location/Qualifiers
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Dictyostelium discoideum
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Best Local Similarity 59.83
Matches 79; Conservative
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Caenorhabditis elegans

Eukaryota, Metazoa; Nematoda, Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

( Passa 1 to 588)

Kohara, Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.
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//dev_stage="L1"
//note="The AD-vermeDNA library was generated with poly(A)+
RNA is="The AD-vermeDNA library hromphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
a 112 c 131 g 179 t
                                                                                           637 AAATAAAAAAAADKAKWKAAAWTATAAAAATTGTAGTWAWTAKTAAAAAATATAAAAA 696
                                                                       821 CCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAGAGTAAGTTTTTGAAAAAT 880
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/clone="ykl097h08"
/clone.lib="unpublished oligo-capped cDNA library, C.
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  761 CGATACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAA
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59.1%; Pred. No. 0.56;
tive 0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A complementary view of the C.elegans genome Unpublished (2002)
Contact: Tadasu Shin.oi
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Fax: 81-559-81-6856
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/tissue_type="whole animal"
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                                                                                                                                          881 TCTAAAATAGAAATGCATTTGTGTCGA 907
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Drosophila melanogaster genome survey sequence SP6 end of BAC BAC BACN03604 of DrosBAC library from Drosophila melanogaster (fruit 11y), genomic survey sequence.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk · This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DRA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 WTWTTTTGWKKWDTKTKTKWKDDDGTTWTDTWKDWKTDKDTDKTWTDVWADNAGWWTDKD 522
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                                                                                                                                                                                                                                                                                        Drosophila melanogaster.

Burosophila melanogaster.

Bukaryotia metanogaster.

Bukaryotia Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroida; Drosophilidae; Drosophila.
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Dictyostellum discoideum
Dictyostellum discoideum
Libraryota, Mycelocoa; Dictyostellida; Dictyostellum.
Libraryota, Mychana, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Morio, T., Urushihara, H., Pi, M., Saito, T., Takemoto, K., Yasukawa, H., Wallinama, J., Maeda, M., Takeuchi, T., Ochiai, H. and Tanaka, Y.
Williama, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
The Dictyostellum developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of development.
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/ 78 c 79 g 175 t
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E 9915627
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Fax: 10-24460e8biol.tsukuba.ac.jp
PROJECT - 'Dictyostelium discoideum cDNA project in Japan'.
Icee 1.529
                                                                                                                                                                                                                                  /clone="dda12a18"
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                                                                                                                                                                                                                                                                                                                                                                                                 th 4.1%; Score 45; DB 13; Length 485; L Similarity 61.5%; Pred. No. 0.79; 72; Conservative 0; Mismatches 45; Indels
Center For Genetic Resource Information National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855
Fax: 81-559-81-6855
Fax: 1-559-81-6855
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                                                                                                                                                                                                   /strain="AX4"
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BJ340295
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Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the aggregation
                                                                                                                                                                                                                                    BJ340360 BST 07-MAR-20 BJ340360 Dictyostellum discoideum cDNA library, AF Dictyostellum discoideum cDNA conce ddal2b22 3', mRNA sequence.
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Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 348)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
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                                                                                   837 TIGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATA 889
                                                                                                               Match 4.1%; Score 45; DB 13; Length 348; Local Similarity 61.5%; Pred. No. 0.77; Local T; Conservative 0; Mismatches 45; Indels
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411,8540, Japan
Tat: 81-559-81-6856
Fax: 81-559-81-6855
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50 c 53 q 137 t
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Location/Qualiflers
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SM Dicryostelium discoideum.

Elarryota: Myctosca; Dicryostellida; Dicryostellium.

E Larryota: Myctosca; Dicryostellida; Dictyostellium.

1 (bases 1 to 546)

1 (bases 1 to 546)

1 (bases 1 to 546)

2 (burbhhara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

1 (bases 1 to 540)

2 (bases 1 to 540)

3 (bases 1 to 540)

4 (bases 1 to 540)

5 (bases 1 to 540)

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8 (
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/db_xref="taxon:44689"
/clone="dds13e07"
/clone=lib="pictyostelium discoideum cDNA library, SF"
/sex="mat A"
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Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota, Mycetoza, Dictyosteliida; Dictyostelium.
1 (bases 1 to 547)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Pull length cDNA of Dictyostelium discoideum at the slug stage
Unpublished (2002)
Contact: Tadasu Shin-i
                                               208 TACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAACGGCTCCATA 267
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tive 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Dictyostelium discoideum"
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84 c 95 g 184 t
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Location/Qualifiers
1. 546
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BJ376869 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc30g10 3', mRNA sequence.
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1 (bases 1 to 562)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Ax4"
/db_xref="taxon:44689"
/clone="dds20n04"
/clone="dbs20n04"
/clone="lib="pictyostelium discoideum cDNA library, SF"
/sex="mat A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 TACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAACGGCTCCATA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.1%; Score 45; DB 13; Length 547; 61.5%; Pred. No. 0.79; tive 0; Mismatches 45; Indels
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                                                                                                                                                                                                                                                Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. :47
/organism="Dictyostelium discoideum"
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Contact: Tadasu Shin-i
Contact: For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Exar: 81-559-81-6855
Exar: 81-559-81-6855
Email: tshiniqqenes.nig.ac.jp.
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
TT: 81-559-81-6856
Fax: 81-559-81-6855
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84 c 93 g 192 t
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84 c 94 g 185 t
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BJ376869.1 GI:19286252
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Best Local Similarity 61.5.
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EST 08-MAR-2002
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Dictyostellum discoideum
Dictyostellum discoideum
Eukaryota.i Mycetoza: Dictyostellida; Dictyostellum.
Eukaryota.i To 596)
1 (bases 1 to 596)
Urushihara.i H. Tanaka.y., Kohara.y. and Shin-i,T.
Full length cDNA of Dictyostellum discoideum at the culmination
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/clone="ddsln01"
/clone="ddsln01"
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Pred. No. 0.8;
0; Mismatches 45; Indels
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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89 c 97 g 205 t
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Pred. No.
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Location/Qualifiers
1. .596
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshinil@genes.nig.ac.jp.
Location/Qualifiers
1. .590
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BJ376868.1 GI:19286251
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Local Similarity 61.5%;
Les 72; Conservative C
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Dictyostellum discoideum.
Dictyostellum discoideum
Eukaryota: Mycetcoa: Dictyostellida; Dictyostellum.
Eukaryota: Mycetcoa: Dictyostellida; Dictyostellum.
I (bases 1 to 590)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length CDNA of Dictyostellum discoideum at the slug stage Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
Mational Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                   Dictyostelium discoideum.
Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 584)
1 (bases 1, Yanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
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                                                 267 IGCTCTAATTGTATCACTTCTTTACATATCCAAATTCAACTGTAAACCAATAAACA 323
                             268 IGCITITCITCCTTCATGGTTTTCAATAAGTCCGCTTTCAACAGTAAACCAAAAGCA 324
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11arity 61.5%; Pred. No. 0.8;
Conservative 0; Mismatches 45; Indels
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Contect: Tadasu Shin-i
Contect For Genetic Resource Information`
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
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91 c 101 g 192 t
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Location/Qualifiers
1. .584
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Unpublished (2002)
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es 72; Conserve
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BJ341943
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Dictyostellum discoideum.

Eukaryota: Mycetozoa; Dictyostellida; Dictyostellum.

Eukaryota: Mycetozoa; Dictyostellida; Dictyostellum.

(bases 1 to 653)

Morio,T., Uushihara,H., Salto,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshiho,R., Mitra,B.N., Pi,M., Saco,T., Takemoto,K., Yasukawa,H., Yoshilams,A., Macda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.

The Dictyostellum developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
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/clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
1. .598
//organism="DictyOstellum discoldeum"
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/db_xref="taxon:44689"
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/clone=lb="intyOstellum discoldeum cDNA llbrary, SF"
/sex="mat A"
/dev_stage="Slug stage"
/dev_stage="Slug stage"
/dev_stage="Slug stage"
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PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
POLXA=No.
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ilarity 61.5%; Pred. No. 0.8;
Conservative 0; Mismatches 45; Indels
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DNA Res. 5 (6), 335-340 (1998)
9915627
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennodal, Tsukuba
Tel: 81-298-53-4664
Fax: 81-298-53-6614

    653
    /organism="Dictyostellum discoideum"

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/db_xref="taxon:44689"
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107 c 98 g
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SM Dictyostellum discoideum.

Dictyostellum discoideum.

E Ubtyostellum discoideum

E Utakaryota: Mycetozoa; Dictyostellida; Dictyostellum.

E Utushinari, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostellum discoideum at the slug stage

L Unpublished (2002)

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Fax: 81-559-81-6855
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BJ402538 Dictyostellum discoideum cDNA library, SF Dictyostellum
discoideum cDNA clone dds17c11 3', mRNA sequence.
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/clone_lib="Dictyostelium discoideum cDNA library, SF"
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1 (bases 1 to 598)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostellum discoideum at the slug stage Unpublished (2002)
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Tel: 81-559-81-6855
Fax: 81-59-81-6855
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nlarity 61:58; Pred. No. 0.8; Conservative 0; Mismatches 45; Indels
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88 c 99 g 2
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Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Dictyostelium discoideum
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SM Dictyostelium discoideum.

Dictyostelium discoideum.

Bukaryota: Mycetozoa: Dictyosteliida; Dictyostelium.

E (bases 1 to 664)

Cuchinhara.H., Tanaka,Y., Kohara,Y. and Shin-i,T.

SG Gurahihara.H., Tanaka,Y., Kohara,Y. and Shin-i,T.

Curahitara.H., Tanaka,Y., Kohara,Y. and Shin-i,T.

Full length cDNA of Dictyostelium discoideum at the slug stage

Unpublished (2002)

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Fmail: tshinidgenes.nig.ac.jp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="nictyostelium discoideum cDNA library, SF"
/scx="mat A"
/scx="mat A"
/d-_stage="$\]
/d-_112 g 231 t lothers
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ilarity 61.5%; Pred. No. 0.8;
Conservative 0; Mismatches 45; Indels
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Pred. No. 0.8;
0; Mismatches 45; Indels
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                                                                             /organism="Dictyostelium discoideum"
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/clone="dds22c02"
                   Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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ilarity 61.5%;
Conservative
Fax: 81-559-81-6855
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1 (bases 1 to 663)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                            BJ343976 Bictyostelium discoideum cDNA linear EST 06-MAR-20 BJ343976 Dictyostelium discoideum cDNA library, AF Dictyostelium discoideum cDNA clone dda17e22 3', mRNA sequence.
BJ343976  GI:19214483
                                                                                                                                                                                                                                                             Dictyostellum discoideum.
Dictyostellum discoideum
Eukaryostellum discoideum
Eukaryote, Mycetoza; Dictyostellida; Dictyostellum.
1 (bases 1 to 654)
Uturshihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:44689"
/clone="dda17e22"
/clone_lib="Dictyostelium discoideum cDNA library, AF"
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Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Tadasu Shin-i
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Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: Linini@qenes.nig.ac.jp.

    . 654
    /organism="Dictyostelium discoideum"
/strain="AX4"

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Dictyostelium discoideum
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BJ375941
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BJ343976
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BJ343093
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BJ399159
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                              BJ434901 BJCtyostellum discoideum cDNA library, VF Dictyostellum discoideum cDNA library, VF Dictyostellum discoideum cDNA clone ddv25jll 3', mRNA sequence.
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SM Dictyostelium discoideum.

Bukaryota: Mycetozoa: Dictyosteliida; Dictyostelium.

E l (bases 1 to 675)

S Urushihara; H., Tanaka; Y., Kohara; Y. and Shin-i, T.

Full length conva of Dictyostelium discoideum at the slug stage to 10 to 1
                                                                                                                                                                                                                            Dictyostellum discoideum.
Dictyostellum discoideum.
Blictyostellum discoideum
Eukaryota: Mycetoca; Dictyostellida; Dictyostellum.
1 (bases 1 to 665)
1 (bases 1 to 665)
1 (bases H., Tanaka, Y., Sohara, Y. and Shin-i, T.
Purshihara, H., Tanaka, Y. of Dictyostellum discoideum at the vegetative
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/clone_11b="Dictyostelium discoideum cDNA library, VF"
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4.1%; Score 45; DB 13; Length 665;
Best Local Similarity 61.5%; Pred. No. 0.8,
Matches 72; Conservative 0; Mismatches 45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
Contact: Tadasus Shin-i
Contact: Tadasus Shin-i
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fat: 81-559-81-6856
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99 c 113 g 230 t
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Location/Qualifiers
1. .665
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BJ401293.1 GI:19314210
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Dictyostellum discoideum.
Dictyostellum discoideum
Eukaryota; Wycetozoa; Dictyostellida; Dictyostellum.
1 (bases 1 to 680)
Urushihara, Y., Kohara, Y., and Shin-i, T.
Full length CDNA of Dictyostellum discoideum at the aggregation
                     /strain="AX4"
/db_xref="taxon:44689"
/clone="dds22d23"
/sex="mat.h" lictyostelium discoideum cDNA library, SF"
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/clone="eda22c04"
/clone_lin="Dictyostelium discoideum cDNA library, AF"
/sex="mat A"
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4.1%: Score 45; DB 13; Length 680;
Best Local Similarity 61.5%; Pred. No. 0.81;
Matches 72; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                               DB 13; Length 675;
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Best Local Similarity 61.5%; Pred. No. 0.81;
Matches 72; Conservative 0; Mismatches 45; Indels
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/organism="Dictyostelium discoideum"
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99 c 122 q 232 t
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101 c 119 g 2;
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Location/Qualifiers
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SM Dictyostellum discoideum.

Eukaryota, Mycetozea; Dictyostellida; Dictyostellum.

Eukaryota, Mycetozea; Dictyostellida; Dictyostellum.

Eukaryota, Mycetozea; Dictyostellida; Dictyostellum.

Full length cDNA of Dictyostellum discoideum at the slug stage.

Londact: Tadasu Shin-i

Contact: Tadasu Shin-i

Contact: Tadasu Shin-i

Contact: Tadasu Shin-i

Contact: Tadasu Shin-i

Tal: Bal-SS-81-6856

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BJ400818 BJ400818
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BJ401883. GI:19314800
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/strain="AX4"
/strain="A34"
/clone="das19p14"
/clone=lib="Dictyostelium discoideum cDNA library, SF"
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/clone="dda6d03"
/clone_lib="Dictyostelium discoideum cDNA library, AF"
/sex="mat A"
                                                                                                                                                                                                                                                                                                   208 TACGTTATCAATGAAAGCGTGTCCCAAGTTCCTGAGGAGAACTGATAAGAACGGCTCCATA 267
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Best Local Similarity 61.5%; Pred. No. 0.81;
Matches 72; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                        4.1%; Score 45; DB 13; Length 691;
ilarity 61.5%; Pred. No. 0.81;
Conservative 0; Mismatches 45; Indels
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                                                                                       /dev_stage="Aggregation stage"
101 c 121 g 238 t
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103 c 119 g 2
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Matches 72; Conserv
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BJ400818
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BJ401883
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                   688 bp mRNA linear EST 10-MAR-2002
BJ399159 Dictyostellum discoideum cDNA library, SF Dictyostellum
discoideum cDNA clone dds4pl0 3', mRNA sequence.
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Full length cDNA of Dictyostelium discoideum at the slug stage of the contact: Tadasu Shin-i,T.

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Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases I to 691)
1 (bases I to 691)
1 Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
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Pred. No. 0.81;
0; Mismatches 45; Indels
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Fax: 1-559-81-6856
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102 c 114 g 240 t
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BJ341290.1 GI:19249652
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Local Similarity 61.5%;
hes 72; Conservative (
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BJ400818.1 GI:19313735

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BJ341261 Dictyostelium discoldeum cDNA library, AF Dictyostelium discoldeum cDNA library, AF Dictyostelium BJ341261 Dictyostelium cDNA clone dda5120 3', mRNA sequence.
BJ341261 GI:19249633
EST.
BJ341261 GI:19249633
Dictyostelium discoldeum.
Dictyostelium discoldeum
Usukaryotas, Mycetozoa; Dictyosteliida; Dictyostelium.
Urushihara, H., Tanaka,Y., Kohara,Y. and Shin-1,T.
Full length cDNA of Dictyostelium discoldeum at the aggregation
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3734 bp mRNA linear EST 06-MAR-2002
413438990 Dictyostelium discoideum cDNA library, AF Dictyostelium
discoideum cDNA clone dda17d13 3', mRNA sequence.
                                                                                                         208 TACGITATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAACGGCTCCATA 267
                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 TACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAACGGCTCCATA 267
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4.1%; Score 45; DB 13; Length 722;
Best Local Similarity 61.5%; Pred. No. 0.81;
Matches 72; Conservative 0; Mismatches 45; Indels
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4.1%; Score 45; DB 13; Length 724;
Best Local Similarity 61.5%; Pred. No. 0.81;
Matches 72; Conservative 0; Mismatches 45; Indels
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Unpublished (2002)
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/organism="Dictyostelium discoideum"
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106 c 124 g 251 t
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Location/Qualifiers
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BJ341261
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BJ343890
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        SM Dictyostellum discoideum.

SM Dictyostellum discoideum.

Eukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.

Eukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.

Surshiharara.H., Tanaka,Y., Kohara,Y. and Shin-i,T.

Full length CDNA of Dictyostelium discoideum at the slug stage

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BJ401195.1 GI:19314112
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SM Dictyostelium discoideum.

Bukaryota: Mycetozoa: Dictyosteliida: Dictyostelium.

E Ukaryota: Mycetozoa: Dictyosteliida: Dictyostelium.

S Grushihara H. Tanaka, Y. Kohara, Y. and Shin i, T.

L Upublished (2002)

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                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:44689"
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/dev_stage="Slug stage"
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/dev_stage="Slug stage"
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                                                                                                                                                                                                                                                                                                       /organism="Dictyostelium discoideum"
/strain="AX4"
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105 c 122 g 2
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Location/Qualifiers
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DJ401342 Dictyostelium discoideum cDNA linear EST 10-MAR-2002 BJ401342 Dictyostelium discoideum cDNA library, SF Dictyostelium discoideum cDNA clone dds22019 3', mRNA sequence.
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Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota, Wycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 744)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
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                                                                                                                                         268 IGCITITCTTCCTTCATGGTTTTCAATAAGTCCGCTTTCAACAGTAAACCAAAAGCA 324
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Dictyostelium discoideum
Eukaryota Mycetoca; Dictyosteliida; Dictyostelium.
1 (bases 1 to 760)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
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Best Local Similarity 61.5%; Pred. No. 0.81;
Matches 72; Conservative 0; Mismatches 45; Indels
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Fax: 81-559-81-6855
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105 c 127 g 262 t
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/clone="dda26k16"
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Location/Qualifiers
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BJ401342.1 GI:19314259
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BJ347280.1 GI:19217787
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SM Dictyostellum discoideum.

Dictyostellum discoideum

Dictyostellum discoideum

E Ukaryota: Mycetozoa: Dictyostellida; Dictyostellum.

E Ubases 1 to 742)

S Urushihara H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDnA of Dictyostellum discoideum at the slug stage

Unpublished (2002)

Contact: Tadasus Shin-i

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/clone="dda17d13"
/clone_lib="Dictyostellum discoideum cDNA library, AF"
/sox="mat A"
         Eukaryota; Mycetozoa; Dictyosteliida; Dictyostellum.
1 (bases 1 to 734)
Urushihara H. Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the aggregation
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                                                                                                                                                                                                                                                                                                            /organism="Dictyostelium discoideum"/strain="AX4"
                                                                                                                 Contact: Tadasu Shin-i
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Tel: 81-559-81-6856
Fax: 81-559-81-6856
Email: tshiniqqenes.nig.ac.jp.
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105 c 126 g 256 t
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105 c 126 g 2
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Location/Qualifiers
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les 72; Conserv
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/clone="dds22019"
/clone_lib="Dictyostelium discoideum cDNA library, SF"
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/sex="mat A"
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4.1%: Score 45: DB 13; Length 765;
Best Local Similarity 61.5%; Pred. No. 0.81;
Matches 72: Conservative 0; Mismatches 45; Indels
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1 (bases 1 to 76)
Orushihara H., Tanaka,Y., Kohara,Y. and Shin-i,T.
                                                                                                                                                                                                                                                                                                                                                       1 others
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Location/qualifiers
1.765
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Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tahini@qenes.nig.ac.jp.
                                                                                                                                                                                                                 /organism="Dictyostelium discoideum"
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113 c 126 g 268 t
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109 c 127 g 2
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Print Jacob Evaluation of this Evaluation of this process.

- Web : www.genoscope.cos.france (E.Malli : Sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration with the Barkeley Drosophila Genome Project (BDCP). The BDGP is constructing a physical map of the Drosophila melanogaster agenome using these BACs. For further information please see http://www.fruitily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is amed RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; or bw sp. the same strain used for the BDGP's and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR14E13 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                   623 AAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGG 682
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Drosophila melanogaster.

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Meoptera: Endopterygota: Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

( bases 1 to 988)
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                                                                                                                                     268 IGCTITICTICCTICATGGTTTTCAATAAGTCCGCTTTCAACAGTAAACCAAAAGCA 324
                                                                                                                                                                             4.1%; Score 44.6; DB 17; Length 988; 39.3%; Pred. No. 1;
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/db_xref="taxon:7227"
/clone="BACR14E13"
/clone="lane:lib="RPC1-98"
/note="end : TET3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        fly), genomic survey sequence. AL066743
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Best Local Similarity
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Web: www.genoscope.cns.fr)
Determination of this Bac-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Forject (EDEP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Biland at CEPH (Centre drough the Option of the Centre droporthisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                  GSS 26-JUL-1999
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submitted (13-101-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mall : segref@genoscope.cns.fr
                                                                                                                               CNSO16LI
Drosophila melanogaster genome survey sequence T7 end of BAC
BACM16D22 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         913 AGCTTGCTTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGA 972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             935 TAATWAWAWATAAITWIWWTWTWIWAWIWAWIAATAIWATWAAMIAATWWWAWHAWWWT 876
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                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Poptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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71; Mismatches 206; Indels
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. Organism="Drosophila melanogaster"
./db_xref="taxon:7227"
./clone="BACN16D22"
./clone="baCN16D22"
./plasmid="pab-loBAC11"
./note="end : T7"
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Best Local Similarity 28.6%;
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                                                                                            RESULT 45
CNS016LI/C
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Direct Submission

Direct Submission

Direct Submission

Submitted (O2-UNW-1999) Genoscope - Centre National de Sequencage :

Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of an angagater genome using these BACs. For further information please see http://www.fruitfly.org the BDGP brosophila melanogaster BAC library was prepared by Kazutcyo Coscogawa and Aaron Mammoser in Pieter Ge Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcokI digestion of Drosophila DNA provided by the BDGP from the EcokI digestion of Drosophila DNA provided by the BDGP from the Stand EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found the hyp://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                            CNS0074D 958 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR14F23 of RPCI-98 library from Drosophila melanogaster (fruit
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Bukaryota; Metanogaster.

Eukaryota; Metanogaster.

Eukaryota; Metanogaster.

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

[ Pass 1 to 958)
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Matches 115; Conservative 11; Mismatches 163; Indels
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//organism="backli27"
/clone="backli4F23"
/clone_lib="RRGI-98"
/note="end: TET3"
/lice="end: TET3"
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                                                                                            780 AAAAAMAATYTYCCAAAAAAAAAACTWAAAYT 811
                                            863 AGTAAGTTTTTGAAAATTCTAAAATAGAAAT 894
                                                                                                                                                                                                                                                                                            tly), genomic survey sequence. AL066801
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CNS0074D/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /graniam="Entamoeba histolytica"
/strain="Miniimss"
/db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/rlone_"vector: pHOS1; Site_1: Bst I: Constructed at The
/note="vector: pHOS1; Site_1: Bst I: Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond, Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
fight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                              SM Entamobeb histolytica

Eukaryota: Entamoebidae; Entamoeba.

Eukaryota: Entamoebidae; Entamoeba.

Eukaryota: Entamoebidae; Entamoeba.

Softus, B., Van Aken, S. and Fraser, C.

Determination of Clone end sequences from Entamoeba histolytica
HMI:HMSS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

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The Institute for Genomic Research

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Tel: 301 838 0208

Fax: 301 838 3543

Email: blioftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
                                            A2550349 896 bp DNA linear GSS 14-NOV-2000 ENTEM/9TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 36
High quality sequence stop: 844.
Location/Qualifiers
1. .896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA library
Seq primer: M13-Forward
Class: shotgun
                                                                                                                                     AZS50349.1 GI:11175650
                                                                                      genomic, DNA sequence.
AZ550349
                                                                                                                                                                               Entamoeba histolytica.
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Best Local Similarity 52.5%
Matches 96; Conservative
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ORIGIN
                                                                                                                                                                                                    ORGANISM
RESULT 46
AZ550349
                                                                                                                                                                                                                                                                          AUTHORS
TITLE
                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                   REFERENCE
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/organism="Entamoeba histolytica"
/strain="Whi: IMSS"
/db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Steel: Bst I: Constructed at The Note: "Vector: pHOSI: Site_l: Bst I: Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Dlamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Wenter, J.C. (Making small insert libraries for whole genome shequm sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
AZJZ/YZ1 BRITAMOGDA HISTOLYLICA Sheared DNA EntamogDa HISTOLYLICA SPECOMIC. DNA Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bjloftusetigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seg primer: M13.Reverse
Class: shotgun
                                                                                                                                                                                                                                                                                                     Eukaryota; Entamoeblae; Entamoeba.

1 (bases 1 to 899)
Loftus B., Van Aken,S. and Fraser,C.

Loftus B., Van Aken,S. and Sequences from Entamoeba histolytica HMI:MSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 TCGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGG 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           652 GACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAA 711
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4.0%; Score 43.8; DB 17; Length 899;
Best Local Similarity 52.5%; Pred. No. 1.7;
Matches 96; Conservative 0; Mismatches 87; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence start: 15
High quality sequence stop: 808.
Location/Qualifiers
                                                                                                                                                                               AZ527921.1 GI:11080094
                                                                                                                                                                                                                                                    Entamoeba histolytica.
Entamoeba histolytica
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genomic, DNA sequence.
AZ690917
AZ690917.1 GI:11828063
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ORIGIN
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AZ549336
                                                        DEFINITION
                                                                                                                                                                                                                                        ORGANISM
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TITLE
                                                                                                                    ACCESSION
                                                                                                                                                VERSION
KEYWORDS
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AZ690917
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Astrain

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                 BNTLYTYE Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                               Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 914)

1 (bases 1 to 914)

1 oftus, B., Van Aken, S. and Fraser, C.

1 oftus, B., Van Aken, S. and sequences from Entamoeba histolytica

Determination of Clone end sequences from Entamoeba histolytica

HMI: IMSS sheared DNA library

Unpublished (2000)

1 oftus

Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence start: 7
High quality sequence stop: 869.
Location/Qualifiers
1. 914
/organism="Entamoeba histolytica"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13-Forward
                                                                                                                                                                                          AZ687856.1 GI:11825002
                                                                                                                                                                                                                                                   Entamoeba histolytica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA library
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                     RESULT 48
AZ687856/c
                                                                                                      DEFINITION
                                                                                                                                                                                                                                                          SOURCE
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TITLE
                                                                                                                                                                     ACCESSION
                                                                                                                                                                                              VERSION
KEYWORDS
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/strain-"whilinws:
/db xrafa"-whilinws:
/db xrafa"-whilinws:
/clone_lib-"Entamocba histolytica Sheared DNA"
/clone_lib-"Entamocba histolytica Structed at The
/note="wector: pHOSI; Site_li Bst I; Constructed at The
/note="wector: pHOSI; Site_li Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of B. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamocba histolytica: a
method for isolate identification. Exp. Parasitol.
// 7.450.) The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
tight size distribution (-2 kb). The v + i method used
for the library construction is described in detal in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, coxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Englands Canomics
Department of Englands Canomic Research
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0508
Fax: 301 838 554
Email: Dilottus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shootgun
High quality sequence start: 85
High quality sequence stop: 895.

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1.924
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A2690917 924 bp DNA linear GSS 14-DEC-2000 ENTHV65TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                        Entamoeba histolytica.
Entamoeba histolytica.
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 924)
Loftus, E., Van Aken, S. and Fraser, C.
Determination of Clane end sequences from Entamoeba histolytica
HMI: MSS sheared DNA library
Unpublished (2000)
Contact: Erendan J Loftus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               592 AGCTACAAATCCIGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAAT 651
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Best Local Similarity 52.5%; Pred. No. 1.7;
Matches 96; Conservative 0; Mismatches 87; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
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us-09-438-185a-1\_1199590\_1200675.rst

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/dlone_lib=Tentamoeba histolytica Sheared DNA"
/dlone_lib=Tentamoeba histolytica Sheared DNA"
/note Tentamoeba Histolytica Sheared Former Down Strain Streel Former F
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Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 944)

1 (bases 1 to 944)

1 Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HMI:MSS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

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Popartment of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0548

Fax: 301 838 543

Email: bjloftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared

DNA library

Seg primer: MJ Reverse

Class: shotyen
944 bp DNA linear GSS 14-NOV-2000
ENTED27TRB Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, DNA sequence.
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Matches 96; Conservative 0; Mismatches 87; Indels 0;
Matches 96; Conservative 0; Mismatches 97; Indels 0;
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High quality sequence stop: 907.
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652 GACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAA 711 

completed: January 9, 2003, 11:40:55 ne: 1961 secs

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592 AGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAAT 651

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|---|--|---|--|---|--|---|--|---|--|---|--|--|---|--|--|--|--|--|
| :<br>GenCore version 5.1.3<br>Copyright (c) 1993 - 2003 Compugen Ltd. | OM nucleic - nucleic search, using sw model              | Run on: January 9, 2003, 05:32:32; Search time 251 Seconds (without alignments) 9743.706 Million cell updates/sec | Title: US-09-438-185A-1_COPY_1199590_1200675 Perfect score: 1086 Sequence: 1 ttggcaaagtacctcaaaacgttctctcgcagtagtgcac 1086 | Scoring table: IDENTITY_NUC . Gapop 10.0 , Gapext 1.0     | Searched: 2185239 seqs, 1125999159 residues Total number of hits satisfying chosen parameters: 4370478 | Minimum DB seq length: 0<br>Maximum DB seq length: 2000000000 | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 150 summaries | Geneseq_101002:<br>/SIDS2/gcgdata<br>/SIDS2/gcgdata<br>/SIDS2/gcgdata | /SIDS2/gcgdate<br>/SIDS2/gcgdate<br>/SIDS2/gcgdate<br>/SIDS2/gcgdate                     | <ol> <li>/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*</li> <li>/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*</li> <li>/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*</li> <li>/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*</li> <li>/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*</li> </ol> | /SIDS2/gcgdat/SIDS2/gcgdat/SIDS2/gcgdat/SIDS2/gcgdat/                                    | /SIDSZ/gcgdat<br>/SIDSZ/gcgdat<br>/SIDSZ/gcgdat          | <ol> <li>/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*</li> <li>/SIDS2/gcgdata/geneseq/geneseqn-embl/NA199.DAT:*</li> <li>/SIDS2/gcgdata/geneseqveneseqlyoneseqn-embl/NA2000.DAT:*</li> <li>/SIDS2/gcgdata/geneseqlyoneseqn-embl/NA2001a.DAT:*</li> <li>/SIDS2/gcgdata/geneseqlyoneseqn-embl/NA2001b.DAT:*</li> <li>/SIDS2/gcgdata/geneseqlyoneseqn-embl/NA2001B.DAT:*</li> </ol> | /SIDS2/gcgdata/geneseg, the number of results pre              | derived by analysis of the total score di                | j 1  | 1086 100.0 1089 24<br>46.6 4.3 1642 21<br>43.4 4.0 6089 24<br>41.4 2 817 21  | 41 3.8 868 20 AAZI7250<br>41 3.8 9504 24 AAZI7250<br>7 40.6 3.7 5152 24 ABL92307<br>8 40.6 3.7 37184 24 ABG67077 |

Buchnera sp. genom Human immune syste chemically pretrea Human immune syste by A transcription Genomic fragment # Human immune syste Arabidopsis thalia Arabidopsis thalia S. epidermidis gen Human immune syste Human immune syste Arabidopsis thalia S. epidermidis gen Human immune syste Human immune famena Human secreted pro Human secreted pro Human secreted pro Human secreted pro Human immune/haema Human immune syste Chemically treated Human immune syste Human immune syste Ilisteria innocua c Human gene regulat signal transductiol can Chemically treated Human prostate exp Human prostate exp Human metastasis a chemically treated Human immune syste Human immune syste Human metastasis a chemically treated Human immune syste Human gene regulat signal transductiol can chaman immune syste Human gene regulat signal transductiol can simune syste Human cardiovascul

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continuous ABB90526-ABB90715 represent novel proteins from Chlamydia predences ABB90526-ABB90715 represent novel proteins from Chlamydia continuous fatrain CWL029), and ABL91184-ABL91373 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia cuseful in vaccine production and for diagnostic purposes. Chlamydia commoniae is a common cause of respiratory disease in humans, and is a state into involved in the development of cardiovascular diseases such as the development of cardiovascular diseases such as the process of the invention continuous stroke. The proteins and nucleic acids of the invention or treatment of chlamydial infections, particularly chlamydia preumoniae infections. The proteins may also be used in PCR, branched CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched commoniae, and the nucleic acids may be used in PCR, branched preumoniae gene expression. The present sequence represents a specifically claimed DNA which encodes a Chlamydia pneumoniae protein of the invention.
                                                                                                                                                                                                                                                                                                                                                          Chlamydial infection, antigen; immunogen; vaccine; diagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carotid artery stenosis; myocardial infarction; cerebrovascular disease; aortic aneurysm; claudication; stroke; strain CWL029; open reading frame; ORF; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes
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RESULT 1
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ID ABL91284 standard; DNA; 1089 BP.
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21-JUL-2000; 2000GB-0017047.
07-AUG-2000; 2000GB-0019368.
18-AUG-2000; 2000GB-0020440.
14-SEP-2000; 2000GB-002583.
10-NOY-2000; 2000GB-0027549.
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Score 1086; DB 24; Length 1089; Pred. No. 1e-283;

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Query Match Best Local Similarity

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                                                                                                  181 CTGATCCAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTG 240
                                                                                                                                       GCTTTCAACAGTAAACCAAAAGCAGCGTACAATAGCGATCAGATTGCTTTGTAGGGTTTG 360
                                                                                                                                                                                                                 TATGCGTTGTTTTTTACTAGGAAGAGCTTGTACTTTTTCTATGACTTTAGTGAAGAGTCT 420
                                                                                                                                                                                                                                                           667
                                                                                                                                                                                                                                                                             TCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACGTGCCCTAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 ATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGA 67
                                                     TAACAGACCTTGGTCGAGCATCCATTCTAATTTTGAAGTGAGTTCTACCAGTTCATCAAA 120
                                                                                         121 ATGICTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATAAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGGCAAAGTACCICAAAAACCAGAAAGATAITITCICITGAITGIAAAGGGGAATIGAIIC 60
                                                                                                                                                                                                                                                                                                                          AGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGGGAGCTACAAA
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  Mismatches
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   Matches 1086; Conservative
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The present sequence is the cod-5 gene from Caenorhabditis elegans. Cod-5 is the aromatic amino acid hydroxylase that synthesises serrotonin froom precursor Ltryptophan. The cod-5 gene was knocked out to produce mutants precursor Ltryptophan. The cod-5 gene was knocked out to produce mutants completely lacking in serotonin. These mutants were found to have defects in metabolic control. A number of c. elegans proteins that have defects can mamalian homologues acting in the insulin signalling pathway were also remained in PI 3-kinase whilst daf-2 encodes a homologue of the mammalian proceptor. The C. elegans ART kinase and PKB kinase act downstream of insulin signalling. The C. elegans PFEN lipid phosphatase homologue.

Co fad-2 and age-1, just as their mammalian homologues act downstream of consulin synalling pathway. This discovery has enabled mammalian PFEN action to be mapped to the insulin signalling pathway. Conserved DAF motifs can be used to design probes to redisposition towards the development of glucose intolerance conditions,
                                                                                                                                                                                                                                                                                                                                           ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing and treating obesity and impaired glucose tolerance using modulators of daf-18 expression and/or activity -
                                                                                                                                                                                                                                                                 Caenorhabditis elegans; cod-5; daf-18; insulin signalling pathway; daf-2; age-1; insulin receptor; PI 3-kinase; PKB kinase; PTEN lipid phosphatase; antidiabetic; anorectic; obesity; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1642 BP; 479 A; 347 C; 351 G; 465 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
44..1642
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 42; 402pp; English.
                                                                                                                                                                                                                Caenorhabditis elegans cod-5 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Cod-5"
AAA91624 standard; DNA; 1642 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                such as obesity and diabetes.
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Matches 249; Conservative
                                                                                                                                          (first entry)
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P-PSDB; AAB13327.
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1464 TCTTCAAAATTTCTAGTATAGAAATACGCTGGAAAGTAGTAATGAGAACATTCTTGC 1405
                                                                                                                                                                                                                                                                                                  1344 AACTCGCCAGCACTGCTCAGAAGTCCTGCTCCGTATACTTTTAAATCTTTCATGATTTGAT 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1284 CCATTITCTTTTACTGGAG-AATCGGCAGCGTCATCAGACGAGAGACCAAATTCAATGGA 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1173 GAAGCTAATCCAATCTCTTGAGAAACTGAGCAAAATCTGGATCAGCGAATAGAGCCATG 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1113 TGACCCATGACCTCGTGAACGGTGTCTGGAGTGTAAAATGGATCGGCATGATGG 1054
                                                                                                                                                                                                                       233 AGTICCIGAGGAGAACIGATAAGAACGGCTCCATAIGCTTTTCTTCCTTCATGGTTTTCA 292
                                                                                                                                                                                                                                                                                                                                                                         293 ATAAGTCCGCTTTCAACAGTAAACCAAAAGCAGCGTACAATAGCGATCAGATTGCTTTGT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 AAGAGTCTTCCCATGTTTATGAAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACG 472
                                                                      473 TGCCCTAAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTT 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              533 CGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGGA 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1053 CGAACGTATTGAGTGCAGAAGACACGATATGCAAGACCTGCCAAGAATCACGAGCT 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis; heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation; antidiabetic; cytostetic; anticonvulsant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human chemically modified disease associated gene SEQ ID NO 271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN80254 standard; DNA; 6089 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG.
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ABN80234

ABN8023

AC ABN802

XX ABN802

XX ABN802

DT 15-JUL

XX Human;

KW Haman;

KW Howarti,

KW ANTIGHS

ANTI
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADFN, or AFDI and comprising one of 35 cequences (ABNT9984-ABN80333) or their complements. The invention is sequences (ABNT9984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with compension or therapy of diseases sasociated with congenital heart disease, epilepsy, diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to historie deacetylation; Currarino syndrome, diseases related with the development of the brain and limb girdle muscular dystrophy and dwarfism. Oligomers specific to each of the genes are useful for detecting the complements requences, as primer oligonuclectides for (II) and their complementsy sequences, as primer oligonuclectides for the amplification of the 350 sequences, (II) and/or their complements and as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs).

C Note: The sequence data for this patent did not form part of the printed specification but is based on sequence information supplied to berwent by the complements of the model.
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associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 621 AAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATTCAGAAA 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     681 GGAGACCGAAAGCTTCTAAGTAATCAAGAAAAAATCTTGGACAATAGCTTTTCCATAGAG 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 741 AAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAGGGAGTGCTTACAA 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          861 AGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTAAAGCTTGCT 920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.0%; Score 43.4; DB 24; Length 6
Best Local Similarity 45.8%; Pred. No. 0.24;
Matches 149; Conservative 0; Mismatches 176; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6089 BP; 1262 A; 219 C; 1585 G; 3023 T; 0 other;
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                                                                                             Claim 1; SEQ ID NO 271; 27pp; English.
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The present sequence is a Caenorhabditis elegans cod-5 knockout cDNA.

Most of the cod-5 gene has been deleted and this has caused a frameshift
in the remaining coding region. Cod-5 is the aromatic amino acid
the cod-5 gene was knocked out to produce mutants completely lackfing in
cod-5 gene was knocked out to produce mutants completely lackfing in
cod-5 gene was knocked out to produce mutants completely lackfing in
cod-5 gene was knocked out to produce mutants completely lackfing in
cod-5 gene was knocked out to produce mammalian homologues acting in
the insulin signalling pathway were also identified. The C. elegans age-1
cancedes a homologue of the mammalian PI 3-kinase whilst daf-2
encodes a homologue of the mammalian pisulin signalling. The C. elegans
codes a homologue of the mammalian issulin signalling. The C. elegans
codes a homologue act downstream of insulin signalling. The C. elegans
code mammalian homologues act downstream of insulin signalling pathway. Conserved DAF mottls can
code mapped to the insulin signalling pathway. Conserved DAF mottls can
code be mapped to the insulin signalling pathway. Conserved DAF mottls can
code used to design probes to identify mammalian DAF homologues and thus to
definity individuals with a predisjoosition towards the development of
glucose intolerance conditions, such as obesity and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 TCATCAAAATGTCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 639 TCTTCAAAATTTCTAGTATAGAAATACGCTGACTGGAAAGTAGTAATGAGACATTCTTGC 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          579 TCAACAACACGATCCGGATCAAAACGAATAATGGTTGCACTACCCTCAACGGCATGTTGC 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 ATAAGTCCGCTTTCAACAGTAACCAAAAGCAGCGTACAATAGCGATCAGATTGCTTTGT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 AGGGTTTGTATGCGTTGTTTTTACTAGGAAGAGCTTGTACTTTTTCTATGACTTTAGTG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 AAAGAAGTAGAGGTTGCAAGCTTCTTCAAA------TCTTCCTCTGATGCTCCAAGA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 AAGAGTCTTCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing and treating obesity and impaired glucose tolerance using modulators of daf-18 expression and/or activity ^{\rm -}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 AGTICCIGAGGAGAACTGATAAGAACGGCICCATAIGCITITCTICCTICAIGGITITCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 3.8%; Score 41.4; DB 21; Length 8 Best Local Similarity 45.2%; Pred. No. 0.39; Matches 239; Conservative 0; Mismatches 281; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 817 BP; 214 A; 197 C; 166 G; 240 T; 0 other;
                                                                                           /product= "Cod-5 frameshift mutant"
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                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 43; 402pp; English
                                                                                                                                                                                                                                                                  98US-0205658.
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                                                                                                                                           WO200033068-A1.
                                                                                                                                                                                                                           02-DEC-1999;
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Synthetic.
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ1253 to AAA17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ1779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an
                                       473 TGCCCTAAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTT 532
                                                                               288 TGACCCATGAGCICGTGAACGGTGTCTGGTTCTGGAGTGTAAAATGGATCGGCATGATGG 229
                                                                                                                    533 CGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGGGA 592
                                                                                                                                                          228 CGAACGTATTGAGTGCAGAAGAAGACACGATATGCAAGACCTGCCAAGAAATCACGAGCT 169
348 GAAGCTAATCCAATCTCTTGAGAAAACTGAGCAAAATCTGGATCAGCGAATAGAGCCATG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene expression product cDNA sequence SEQ ID NO:4721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cia PD, Garcia V, Giese K, Innis MA;
m A, Kennedy GC, Kita D, Labat I;
owitz D, Pot D, Radazzo F, Reinhard C;
Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                    593 GCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGA 641
                                                                                                                                                                                                                                         168 GATAAGTATCCGGCGACTGGGCGAACACGGAATCCAGTTTTTGACACTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dickson M, Drmanac R, Drmanac S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 2243; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                AAZ17250 standard; cDNA; 868 BP.
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98US-0080114.
98US-0080515.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escobedo J, Garcia PD,
Jones WL, Kassam A, Kel
Lamson G, Leshkowitz D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-494092/41
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24-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                       AAZ17250;
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encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased listene in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and ing cancer, phe polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 446 AATGAGGATGTAGAAGCCAAGGCACGTGCCCTAAAAGGTCATGGATGAGATCAGGAGTT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      575 AGNGNNNGANGANAAAATAAANNANAAGNNGAANAANANTGAGANNAAAANAGAGGNT 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 AAGGAGAAATTATCTTTATCGAGAGTTCGCATTACAGAGGCAATGGGAAAGTAACGGTCC 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        515 TAGGAGNNANAAANANANANAGAGNNNANNNTAGNNANTAAATGGNAAANTGGANANNN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455 ANTNAGGNANANAGNTNNGAGNNNNGAGGNATGANANATTGANAGAANTNANNNNNAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    626 TGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGA 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 NNNATNAATTATNAATGNNNNGNGAAGNGANANGAAAAANTTAAAANNANTATNAATAAGN 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  566 TGCAACAGAGACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 20; Length 868;
Pred. No. 0.51;
0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                     Sequence 868 BP; 148 A; 148 C; 32 G; 284 T; 256 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 CCGAAAGCTTCTAAGTAATCAAGAAAAA 714
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                                                                                                                                                                                                                                peptide analogues and antagonists.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK28408 standard; DNA; 9504 BP
                                                                                                                                                                                                                                                                                                                                                                                  3.8%;
1 Similarity 33.1%;
89; Conservative (
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30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK28408;
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sazary syndrome, memaclogical disorders, immunological disorders, where syndrome, chemically acids and developmental disorders, psoriasis, sporiasis, developmental disorders, psoriasis, syndrome, numeran-tick disease, mylologyplutamine disorders, solid tumours of infarction, hypertension, anglogenesis, erythropolesis, congenital heart disease, HDNR syndrome, arthritis, polyglutamine disorders, solid tumours associated genomic DNA molecules of the invention.

Note: The sequence data for this patent did not form part of the printed syndrome patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8971 ATTGTTATTGTGTTTTTTAGATTTTTTATTGAAAAGGAAAGTGAGGGTTAGGTTTAGAG 9030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA repair; cytosine methylation; PMS2L1; PMS2L12; PMS2L2; PMS2L3; PMS2: L4; PMS2L5; PMS2L6; MGMT; MSH2; NUDT1; TDG; INPPL1; RFC4; DDIT1L; FNC6; Atcaxia telangiectasia; aging; Bloom's syndrome; Cockayne syndrome; Nijmegen breakage syndrome; Werner syndrome; immunodeficiency; trichthiodystrophy; Fanconi's anaemia; solid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            922 CTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACG 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                       New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumours or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemically treated DNA repair gene fragment complementary to#58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.8%; Score 41; DB 24; Length 9504; 53.4%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9504 BP; 2775 A; 138 C; 2348 G; 4243 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9031 AGATAGTGTTTTTGTTTTTAGGGGAATAAGGATATTAATT 9071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.2;
0; Mismatches
                                                                                                                                                    Claim 1; SEQ ID No 282; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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The invention relates to nucleic acids containing a sequence of at least

18 nuclectides of chemically treated DNA of genes associated with DNA

18 nuclectides of chemically treated DNA of genes associated with DNA

19 cepair, and their complements. The invention also relates to nucleic

20 cepair, sasociated with DNA repair selected from PNSZLL,

21 PMSZL2, PMSZL3, PMSZL3, PMSZL5, PMSZL6, MGMT, MSRZL, NUCPT1, TDG, INPPL1,

22 PMSZL2, PMSZL3, PMSZL6, PMSZL6, MGMT, MSRZL, NUCPT1, TDG, INPPL1,

23 RFC4, DDITIL, FANUB, Or XRC68. Nucleic acids of the invention and related

24 cliquency, are useful for diagnosis of diseases associated with gene

25 cliquency, specifically attain the angle-taskin, aging, Bloom's syndrome,

26 clockayne syndrome, Nijmegen breakage syndrome or Wentner syndrome,

27 clockayne syndrome, Nijmegen breakage syndrome or Wentner syndrome,

28 clockayne syndrome, Nijmegen breakage syndrome or Wentner syndrome,

29 clockayne syndrome, Nijmegen breakage syndrome or Wentner syndrome,

20 clockayne syndrome, Nijmegen breakage syndrome or Wentner syndrome,

20 clockayne syndrome, Nijmegen breakage syndrome or Wentner syndrome,

20 clockayne syndrome, Nijmegen breakage syndrome or Wentner syndrome,

20 clockayne syndrome, Nijmegen paterns may allow development of individualised

21 chemically pre-treated DNA fragments from genes associated with DNA

22 chemically pre-treated DNA fragments from genes associated with DNA

23 content of the sequence data for this patent is not represented in the

24 content of the syndrome, SNA fragment is not represented in the

25 content of the syndrome or SNA fragment is not represented in the

26 content of the syndrome or SNA fragment is not represented in the

27 content of the syndrome syndrome.
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                                                                                                                                                                                                                                                                                                                                                  New nucleic acid derived from genes associated with DNA repair, useful for diagnosis, e.g. of ataxia telanglectasia, by determination of cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644 AATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      704 TCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGATCGA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        764 TACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCT 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 ATTTTTTTTTTTTTTAGAGGAATAAATTTTAGAATAAGATATTTAAATGTTAGGATTTG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        824 TCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGGGGTAAGTTTTTGAAAAATTCT 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  384 AAAATAGAAATGCATTTGTGTCGAGCTAAAGCTTGCTTCTCTTTATTTTCCTTTTGTAGA 943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 TGTTGGGGTGGGAGGATTATTTATTTGAGTTTAGGAATTTGAAATTGTAGTGAGTCGTGA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 GTATTTTAGTTTGGGTAATAGTGTGAGATTTTGTTATAAAATAAGATTAGTTTAGTATAA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 116; 25pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5152 BP; 1608 A; 36 C; 965 G; 2543 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.3;
0; Mismatches 249;
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                                                                                                                                                                                                                                                                 Berlin K;
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Matches 201; Conservative
                                                                                              07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                  06-APR-2001; 2001WO-EP03972.
                                                                        06-APR-2000; 2000DE-1019058.
                                                                                                                                                                                                                                                              Olek A, Piepenbrock C,
                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                   WPI; 2002-034446/04.
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The invention relates to nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation, selected from 94 genes (ABL49301-ABL49394) and/or complementary sequences associated with DNA replication, CENPB, DNA2L, ATR, CHDIL, ERCC3, SNRPAL, RAD50 and Ling2. The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hypridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences and method are useful in the cytosine methylations. The DNA sequences and method are useful in the cytosine methylations. The passociated with DNA replication and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes. They are especially useful in diagnosis and therapy of eigh Ataxia telanniectusia, ATR-X, Bloom's syndrome, solid tumours and cancer.

Complementation and was supposed to be available directly from WIPO at the wipo. Intypub/published_pct_sequences. However, the sequence data did contour correspond to that referred to in the specification. The present data is taken from EPO data for the patent.
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                                                                                                                                                                                                                                                                                                                                                   Human, cytostatic; neuroprotective; nootropic; immunostimulant; gene regulation; DNA replication; CRNBB; DNAZL; ATR; CHDLL; ERCC3; SNRPAl; RAD50; LIG2; cytosine methylation; Ataxia telangiectasia; ATR; ATR; Bloom's syndrome; tumour; cancer; methylation; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          584 TGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAG 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid sequences from chemically modified genes associated with DNA replication, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. Ataxia telangiectasia
432 GIGITITTACGAAAAAAAATATAATGITTTTAATTITTTAAGIGTTATAATITTTAGT 491
                                                                                                                                                                                                                                                                                                              Human polynucleotide associated with DNA replication SEQ ID NO 74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40.6; DB 24; Length 5152;
Pred. No. 1.3;
0; Mismatches 249; Indels 1;
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                                         1004 AAGAACAGGGAAAGTGATTGTCTCAGCTTTA 1034
                                                                    492 TAATTTCGTAAGAAATTTTTTAGATTTTA 522
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                                                                                                                                                                                         ABL49374 standard; DNA; 5152 BP.
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Similarity 44.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2001; 2001WO-EP03971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-dUN-2000; 2000DE-1035529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                       01-MAY-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek A, Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                     ABL49374;
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                                                                                                                                                  RESULT 8
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                                                                                                                                                                                                                                                                                                                                               The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (I) having sequences (ABQ66971-ABQ67178) or their complements. (I), also
                                                                                                                                                                                                                                          944 ATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTGTTCTGG 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human: angiogenesis; methylation; eye disease; glaucoma; tumour; infilammation; rheumatoid arthritis; diabetuc retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
133 GTATTTTAGTTTGGGTAATAGTGTGGGATTTTGTTATAAAATAAGATTAGTTTAGTATAA 192
                                                                        TCAAGAAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGA 763
                                                                                                               764 TACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCT 823
                                                                                                                                    253 ATTTTTATTTTTTTTTTTAGAGGAATAAATTTTAGAATAAGATATTAATGTAATGTAGGATTTG 312
                                                                                                                                                                                                               644 AATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAA 703
                                                                                           193 GATTTTAAAATTTTTAATATTTTTTTTTTTTTTTAGGGAAAGTGGAAAAATAAGGAACGC 252
                                                                                                                                                                            824 TCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                     Human angiogenesis associated polynucleotide SEQ ID NO 107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 107; 41pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                  1004 AAGAACAGGGAAAGTGATTGTCTCAGCTTTA 1034
                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                        ABQ67077 standard; DNA; 37184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-2001; 2001WO-EP14320.
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiarteriosclerotic; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-2002.
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                                                                                                                                                                                                                                                            printed
om WIPO
related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in andiogenesis related genee, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatiol arthritis, diabetic retinopathy, macula undepensation caused by neovascularisation, psoriasis, arterlosclerosis, inflammatory bowel diseases, ulcers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                834 TCTTTGATAATGACAGAAGATGAACAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAA 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the pr
specification, but was obtained in electronic format directly from
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchnera; cockroach-symbiotic bacterium; cockroach extermination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 24; Length 37184;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37184 BP; 8680 A; 717 C; 9540 G; 18247 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
3.7%; Score 40.6; DB
Best Local Similarity 57.5%; Pred. No. 2.7;
Best Ches 73; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buchnera sp. genomic DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA92787 standard; DNA; 640681 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-APR-2000; 2000JP-0107160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6362 AGGAGGA 6368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            954 AGTAGGA 960
                                                                                                                                                                                                                           disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          circular; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-2001.
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                                                                                                                                                                                                                           Crohn's
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Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation

Berlin K;

Piepenbrock C,

olek A,

WPI; 2002-130909/17

01-SEP-2000; 2000DE-1043826

(EPIG-) EPIGENOMICS AG

Claim 1; SEQ ID NO 1120; 32pp + Sequence Listing; German

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                                                                                                                                                                                                                                                                                                                                                           D 190182 ATAGTGCCTAAAAAAATTAAAAAATAATTTTTTCTCAATTATAGCCTGTATTCCTTGG 190241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 190422 GTAGATGTTTTTTAAATGTTTTTAAATTGTAATGTGAATCGTAGTAAAGTGAAGTGTATT 190481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the expression protein of the objective protein is collected from the resultant culture. The DNA is useful for developing agricultural chemicals for exterminating cockraches. The present sequence represents the specifically claimed Buchnera sp. genomic DNA sequence, from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 190242 AATCGAAACATCGTAACAACACGTGTAATAGATCTTTTTAATTTTTTAATTATACAACAT 190301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 190302 ACTAATTTAGTACAAAAAAAAAATCATATCATAGAAGAAATAATTATTCGATACGCAT 190361
                                                                                                                                                                                                                                                                                            299 CCGCTTTCAACAGTAAACCAAAAGCAGCGTACAATAGCGATCAGATTGCTTTGTAGGGGTT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 CTTCCCATGTTTATGAAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACGTGCCCT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 AAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTTCGCATT 538
                                                                                                                                                                                                                                                     119 AAATGTCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATA 178
                                                                                                                                                                                                                                                                                                                                     179 ATCTGATCCAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant, optinalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosts; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                              Sequence 640681 BP; 237522 A; 83822 C; 84757 G; 234580 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24; Length 640681;
                                                                                                                                                                  Score 40.6; DB 24; Length (Pred. No. 7.8; O; Mismatches 244; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune system associated gene SEQ ID NO: 1120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL33147 standard; DNA; 6740 BP.
                                                                                                                                                                  3.7%; Scc
Similarity 43.4%; Pre
37; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2001; 2001WO-EP07537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 ACAGAGGCAAT 549
                                                                                         present invention.
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                                                                                                                                                                                                                Matches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL33147;
                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell cycle; human; CpG dinucleotide; cytosine methylation, HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft versus host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemically pretreated complementary DNA associated with cell cycle #49
                                                                                                                                                                                                                                                                                                                                                                                                                                                       984 ATATAAGTTTTTTTTTTGATGAAGCGTATATTTTTAAAAGGTGGATTTTTTGGTTATTAT 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 ATGACTITAGIGAAGAGICITCCCAIGITTAIGAAAAATICAGAAAAIGAGGGAIGIAGA 460
                                                                                                                                                                                                                                                                                                                                                                                                                             341 AGATTGCTTTGTAGGGTTTGTATGCGTTGTTTTTACTAGGAAGAGCTTGTACTTTTTCT 400
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                  DB 24; Length 6740;
                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                      Sequence 6740 BP; 1717 A; 76 C; 1496 G; 3451 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                     3.7%; Score 40;
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                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS45393 standard; DNA; 17419 BP.
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20000E-1019058.
20000E-1019173.
20000E-1032529.
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                                                                                                                                                                                                                                                                                                                                                                                   58.3%;
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nes 70; Conservative
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06-APR-2000; 2
07-APR-2000; 2
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01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CPG dinuclectides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be secretained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadventageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, arteriosclerosis, solid tumours and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            972 AGTATGCACGTTGGAGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGATTGTCTCAGCT 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2266 ATTATTAGGTTGGAGTGTAGTGATGTAATTATAGTTTATTGTAATTTTTATTGGG 2325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 912 AAGCTTGCTTCTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                852 GATGAACAAAGGGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                  Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Immune system disease; cytosine methylation; antiasthmatic; antianteriosclerofic; antianaemic; cytostatic; nootropic; neuroprotective; antianteriosclerosic; anticonvalsant; ophthalmological; antitrheumatic; antiarthritic; antidiabetic; antipsoriatic; antiframmatory; cancer; eye disease; arteriosclerosis; anemia; acute myeloid leukaemia; Alzheimer's disease; AlDis epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17419 BP; 5015 A; 311 C; 3864 G; 8229 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune system associated gene SEQ ID NO: 1268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.6%; Score 39.6; DB 22; Best Local Similarity 49.5%; Pred. No. 3.7; Matches 102; Conservative 0; Mismatches 104;
                                                                                                                                              Claim 1; SEQ ID No 98; 28pp; English.
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                                                                                                    associated with cell cycle -
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albriemer's diseases, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA, cytosine methylation state; SNP; retroviral infection; gene; ds; single nuclectide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezsty syndrome; haematological disorder; tuberculosis; immunological disorder; Werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; nourological disorder; erythropolesis; neurodegenerative disorder; wardenburg syndrome; Niemann-Pick disease; mayelodysplastic syndrome; wyocardial infarction; hypertension; arthritis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy; polyglutamine disorder; solid tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2266 ATTATTTAGGTGGAGTGTAGTGATGTATATAGTTTATTGTATTTTATTTTGG 2325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     852 GATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTGTCGAGCTA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   912 AAGCTTGCTTCTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGGAATATGGGGGTCG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 24; Length 17419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA transcription associated complementary genomic DNA #56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17419 BP; 5015 A; 311 C; 3864 G; 8229 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1268; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.7;
0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39.6; Di
Pred. No. 3.7;
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                                                                                                                         Berlin K;
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Local Similarity 49.5%;
les 102; Conservative (
                30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                    Piepenbrock C,
                                                                              (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                          for diagnosis and tre
cytosine methylation
                                                                                                                                                               WPI; 2002-130909/17.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid, which comprises a segment of the chemically pretradted DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligomucleotide cor peptide nucleic acid (PNA)-oligomer that hybridises to or is identical cor peptide nucleic acid (PNA)-oligomer that hybridises to or is identical cor the chemically pretreated DNA of genes associated with DNA cranscription. The set of oligomer probes are useful for detecting the crytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deliciency, virsal infection, retroviral infection, serary syndrome, contrological disorders, immunological disorders, Merner syndrome, tuberculosis, developmental disorders, psoriasis, Reger's syndrome, contrological disorders, immunological disorders, manological disorders, morodagenerative disorders, marchemburg contrological disorders, and angoquensis, explorome, mycocardial concer. Sequences ABK28127-ABK28472 represent DNA transcription associated genomic DNA molecules of the invention.

Concern Sequence deata for this patent did not form part of the printed concerns better of the concern of the printed concerns better of the concern of the printed concerns better of the concerns of the printed concerns between the concerns of the concerns of the printed concerns between the concerns of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              852 GATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     912 AAGCTTGCTTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumours or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.6%; Score 39.6; DB 24; Length
49.5%; Pred. No. 3.7;
ive 0; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 112; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                               Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF28550 standard; DNA; 99629 BP.
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Matches 102; Conservative
                                                                             06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1035529.
01-SEP-2000; 2000DE-1043826.
06-APR-2001; 2001WO-EP03973.
                                                                                                                                                                                                                                                                                                                                                                                               Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Patent Office.
                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-090046/12.
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The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAR78814-AAR78814). The library has a number of uses described in the specification e.g. is useful for aldentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large acrobic, gram-negative diplococcus, normally found among the bacterial flocalised infections and as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis and meningitis.
                                                                        Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8570 GCCATATTGGCGATGGCAATTTACATTTAAATATTCTAAAACCTGCCAATTTGACCAAAG 8511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      803 GCCATATCAGTGGAGCAACCTTCCCTTTGATTGATAATGACAGAAGATGAACAAAG 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HV; anticonvulsant; opthhalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                              Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.6%; Score 39.6; DB 22; Length 99629; 61.8%; Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 99629 BP; 29233 A; 19222 C; 21909 G; 29264 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune system associated gene SEQ ID NO: 306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 391-415; 545pp; English.
                                                                                                                                                                                                                                                                                                                                 Patterson C, Berg KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL32333 standard; DNA; 8895 BP
                                                                                                                                                                                                                                                                                                   (INCY -) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                16-JUN-2000; 2000WO-US16649.
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             04-APR-2001 (first entry)
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                                                                                                                              Moraxella catarrhalis.
                                             Genomic fragment #37.
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-041427/05.
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                                                                                                                                                                 WO200078968-A2.
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                                                                                                                                                                                                                                                                18-JUN-1999;
                                                                                                                                                                                                   28-DEC-2000.
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albriemer's diseases, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7066 AAAAAAAAAAAAAAAAAAAAAAAA 7007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7006 AAAAAAAAATAAAATAATATCGAAAAACCTAAAAATACTACTACCTAAAAACCCTCTTACAT 6947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6946 CTCCCAAAACCACTTTTACCCATCTATAAAACAATAACCAATCTAACTTTAATATTCTAA 6887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          695 TCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAA 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          755 AGGAGTCGATACCATAAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCCATATCAGTG 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         815 GAGCAACCTTCCCTTTGATTCTTTGATGACAGAGATGAAGAGAAGAAGAAGTTTTTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             635 AATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCT 694
                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 3.6%; Score 39; DB 24; Length 88 Local Similarity 46.2%; Pred. No. 4.2; nes 129; Conservative 0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8895 BP; 2269 A; 62 C; 1898 G; 4665 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 306; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               875 AAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTAAA 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate expression marker cDNA 61117
                                                                                                                                                                                                                                                                                                                          Berlin K;
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                                                                                                                                                                                                                      2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                              02-JUL-2001; 2001WO-EP07537
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                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-130909/17
                                                                                               WO200200928-A2
                                                                                                                                                                                                                      30-JUN-2000;
01-SEP-2000;
                                                          Homo sapiens
                                                                                                                                       3-JAN-2002
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                                                                                                                                                                                                                                                                                                                        olek A,
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient;

(g) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             735 ATAGAGAAAACCGTGAGGAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGC 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  795 TTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGAT 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855 GAACAAAGAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTAAAG 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 11610; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                         Schlegel R, Endege WO, Monahan JE;
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                                                                                                                                                                                                      16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
9-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219907P.
13-DEC-2000; 2000US-255281P.
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                                                                                                                                                  20-FEB-2001; 2001WO-US05171.
                                                                                                                                                                                     17-FEB-2000; 2000US-183319P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                         WO200160860-A2
                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a nucleic acid comprising a sequence (I) of at least 18 bases in length of a segment of chemically pre-treated genomic DNA whitch has any one of the sequences of (ABKA31919-ABKA4032) or its complement. Also included are an oligonuclectides which hybridises to (I), probes for detecting oytosine methylation or single-complements (SNP) in (I), an array of oligomers to (I), probes for detecting oytosine methylation states of the CpG dinuclectides of (I). The array is useful cor peptide nucleic and/or epigenetic parameters, classification, differentiation, grading, staping, treatment and/or diagnosis of attroxycomas, or the predisposition to astrocycomas by analysing openetic and/or epigenetic parameters, classification, differentiation, involves obtaining a biological sample containing genomic C methylations, involves obtaining a biological sample containing genomic C methylations, involves obtaining a biological sample containing genomic C methylations, involves obtaining a biological sample containing genomic C NNA, extracting the genomic DNA, converting cytosine bases which are unethylation to astrocycomas by analyting second or containing a biological sample containing genomic C NNA, extracting the genomic DNA, converting cytosine bases which are another base which is dissimilar to cytosine in terms of hybridisation cannot base which is dissimilar to cytosine in terms of hybridisation content or more data sets. The genomic DNA is the cytosine positions by reference to confer more data sets. The genomic DNA is of particular interest in astrocytom or bisulphite, hydrogen sulphite of or disulphite. The amplificates are detachable most of one or more cytosine positions or bisulphite, hydrogen sulphite or disulphite. The amplificates are detachable most of one or more cytosine positions or tissues, as opposed to background DNA. The amplificates are detachable most of one or more cytosine position or conference to an elected by matrix assisted laser desorption/indicy having a lectrometer. Con
                                                                                                                                                                                                           Human; ds; astrocytoma; cytostatic; staging; cysteine methylation; CpG; bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry; matrix assisted laser desorption/ionization mass spectrometry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel chemically modified genomic DNA sequences, useful in the characterisation, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                      Human DNA for staging of Astrocytomas #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 31; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP07538.
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01-SEP-2000; 2000DE-1043826.
                                                      18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG.
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopethy, neovascular glaucoma and macular degeneration, arteriosclerosis, anemia, cancer, acute myeloid leukaemia, Albahimer's disease, AlbS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                     0;
                                                                                                                                                                                         856 AACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTAAAGC 915
                                                                                                                                                                         916 TTGCTTCTTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGGTCGAGTA 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, immune system disease; cytosine methylation; antiasthmatic; antiatteriosolerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV, anticonvulsant; ophthalmologic; antirheumatic; antiarhritic; antidiabetic; antipsoriatic; antiframmatory; cancer; eye disease; arteriosolerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                     DB 24; Length 18997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18997 BP; 4675 A; 299 C; 4016 G; 10007 T; 0 other;
Sequence 18997 BP; 4675 A; 299 C; 4016 G; 10007 T; 0 other;
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 543; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 543.
                                                                     :99
                                       Score 38.4; DI
Pred. No. 8.2;
                                                                         0; Mismatches
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                                       3.5%;
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2000DE-1043826.
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cytosine methylation
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                                                   Local Similarity
nes 78; Conserv
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                    ABL32570;
                                       Query Match
Best Local S
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                                                                             Matches
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New isolated polynucleotide, a polymorphic variant of glutamate receptor, metabotrophic 3 (GRM3) gene for expressing GRM3 protein isoform to screen drugs to treat GRM3 activity-related disease -
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                                                                                                                                                     Example 1; Fig 1; 165pp; English.
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AAD26437 standard; DNA; 50000
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4192
                           WPI; 2002-090198/12.
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AAD26437/
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/note= "Nucleotide R is present at this location in the
sequence shown in sequence listing of the specification"
4667..4528
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/*tag= c
//octe= "Nucleotide R is present at this location in the squence shown in sequence listing of the specification" 4529..28175
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                                                                                                                                                                                             916 TIGCTICTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTA 975
                                                                                   856 AACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTAAAGC 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; glutamate receptor metabotrophic 3; GRM3; neuroprotective; nootropic; gene therapy; neurotransmitter; chromosome 7q21.1-q21.2; drug screening; neurological disorder; polymorphism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human glutamate receptor, metabotrophic 3 (GRM3) gene fragment #1.
Query Match 3.5%; Score 38.4; DB 24; Length 18997; Best Local Similarity 54.2%; Pred No. 8.2; Matches 78; Consery Vative 0; Mismatches 66; Indels 0; Matches 78; Conservative 0; Mismatches 66; Indels 0;
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/partial
replace (26157, A)
/*tag= h
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replace (4006, A)
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                                                                                                                                                                                                                                                          976 TGCACGTTGGAGTGATTGGCTGTT 999
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/*tag= d
^<176..26031
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AAD 26400/Cc
ID AAD 26400/Cc
ID AAD 26400/Cc
XX AAD 2641
XX HUMAN;
XW HUMAN;
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The invention relates to an isolated polynucleotide which is a polymorphic variant of glutamate receptor, metabotrophic 3 (GRM3) is a receptor for glutamate, the major excitory neurotransmitter in the mammalian central nervous system. Human GRM3 located on chromosome 7421.1-q21.2 is expressed in human focatal and adult whole brain especially in the caudate nucleus and corpus collosum. GRM3 hole brain especially in the caudate nucleus and corpus collosum. GRM3 function of GRM3. GRM3 polypeptide is used for screening and expression and recombinant non-human organism is used to study expression of GRM3 or vivo screening and testing of drugs targetted against GRM3 protein, and for testing the efficacy of therapeutic agents and compounds for neurological disorders in a biological system. GRM3 enablotypes are for treating diseases associated with GRM3 activity, e.g., neurological disorders. The present sequence is human GRM3 gene fragment containing polymorphic sites.
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//note= "This degenerate base represents polymorphic site
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//ore= "This degenerate base represents polymorphic site
(PS) 2.
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28-AUG-2002 (first entry)
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δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polynucleotide which is a polymorphic variant of glutamate receptor, metabotrophic 3 (GRM3) is areaptor for glutamate, the major excitory sequence GRM3 is a receptor for glutamate, the major excitory neurotransmitter in the mammallan central nervous system. Human GRM3 located on chromosome 7421.1.421.2 is expressed in human foretal and adult whole brain especially in the caudate nucleus and corpus collosum. GRM3 of MA is useful in gene therapy and also for studying the expression and for inciton of GRM3. GRM3 polypeptide is used for screening drugs. A recombinant non-human organism is used to study expression of GRM3 GC in vivo, for in vivo screening and testing of drugs targetted against compounds for neurological disorders in a biological system. GRM3 compounds for treating diseases associated with GRM3 and protypes are for treating diseases associated with GRM3 activity, neurological disorders. The present sequence is an alleitc variant containing polymorphic sites (PS):
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/note= "This degenerate base represents polymorphic site
(PS) 4"
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note= "This degenerate base represents polymorphic site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 50000 BP; 15337 A; 9554 C; 9287 G; 15818 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.5%; Score 38.4; DB 24; Length 500 Best Local Similarity 51.9%; Pred. No. 12; Matches 110; Conservative 0; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41233 ATACAAACCTTGTTTTTTTTTTTTTTTTT 41202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 135-153; 165pp; English.
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                                                                                                                                                                                                                                                                                                                                                                              Tanguay DA;
                                                                                                                                                                                                                                                                                                                                       (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                  16-JUN-2000; 2000US-212328P.
                                                                                                                                                                                                                                                              18-JUN-2001; 2001WO-US19447
                                                           3"
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                                                                                                                                                                                                                                                                                                                                                                              Finkel K, Koshy B,
                                                                                    misc_feature
         misc_feature
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ABQ67094
ID ABQ671
XX
AC ABQ671
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The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of anglogenesis-associated genes (II) having sequences (ABG6691-ABG67118) or their complements. (I) also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in anglogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, necvascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, ediabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease. Complement of this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; anglogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatold arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarteriosclerotic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404 ACTTIAGTGAAGAGTCTTCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGC 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 TICCITIGIAGGGTITGIAIGCGTIGITTTTTACTAGGAAGACCTIGIACTTTTTCTAIG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid fragments from chemically treated anglogenesis associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.5%; Score 38.4; DB 24; Length 83391; Best Local Similarity 52.5%; Pred. No. 14; Matches 84; Conservative 0; Mismatches 76; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 83391 BP; 24547 A; 665 C; 16953 G; 41209 T; 17 other;
Human angiogenesis associated polynucleotide SEQ ID NO 124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 124; 41pp. + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS46333 standard; DNA; 7667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2000; 2000DE-1061338.
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                                                                                                                                                                                                                                                                                                       Homo sapiens
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2794 TAGAAACTAATTATTAAAGGAAATGTAGAGAAAATATTGTTATTAAGATAAAGGG 2853
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                                                                                                                                                                                             ABL32294;
                                                                                                                                                                                                                                                                                                                                                                                                         gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chamically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences complementary to (Ss). The nucleic acid may be peptide nucleic acid coligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the oytosine methylation state and cumours. The probes can also be used in a method for ancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases associated with CpG dinucleotides e.g. canneers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific compared to another set of genetic and/or epigenetic parameters may be differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                              Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; cytos dinucleotide; single-nucleotide polymorphism; SNP; cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2674 TGTATTAATAAAAATTTTATTTTAGAATTTTTTAATTTTGGGAGAAAATAAGATAAA 2733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2734 AATATGATAAGTTAAATGATTTTAAAATATATAAATTTTTAAGATAGATAGATATGAGG 2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566 TGCAACAGAGACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAA 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    626 TGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGA 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 686 CCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAAC 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
              Tumour suppressor gene derived chemically modified sequence #55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uvery watch 3.5%; Score 38.2; DB 22; Length 7667; Best Local Similarity 49.7%; Pred. No. 6.6; Matches 97; Conservative Autches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7667 BP; 2446 A; 63 C; 1493 G; 3665 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 55; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Berlin K;
                                                                                                                                                                                                                                                       06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1035529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                          15-MAR-2001; 2001WO-EP02955.
                                                                                                                                                                                                                                           2000DE-1013847
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                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG.
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                                                                                                                                             WO200168912-A2
                                                                                                               Homo sapiens
                                                                                                                                                                                                                                          15-MAR-2000;
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albriemer's disease, AlbS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic; antiatrefioscierofic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant: ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antifilammatory; cancer; eye disease; arterioscialorosis; anaemia; acute myeloid leukaemia; Albeimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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Best Local Similarity 48.8%; Pred. No. 7.1;
Best Local Similarity 48.8%; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 267.
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                                                                                                                                                                                          RESULT 24
ABL32294/c
ID ABL32294 standard; DNA; 9415 BP.
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01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002 (first entry)
                                                                       2854 AGAGAGAGAGATT 2868
746 CGTGAGGAAAGGAGT 760
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WO200200926-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albrahimer's disease, AlbS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/alcerative bowel diseases. The present sequence is a gene of the invention.
                       606 AAACGGGATAATAGGAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
715 TCTTGGACAATAGCTTTTCCATAGAGAAACCGTGAGGAAAGGAGTCGATACCATAAATT 774
                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic; antiatrefiosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmologici; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antianamatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                   Human immune system associated gene SEQ ID NO: 440.
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Pred. No. 8.
                                                                                                  3869 AAAAATAAAAATAATTATAAATAAATCC 3839
                                                                   775 CCGATTAAAAAGGGAGTGCTTACAACAGCC 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin K;
                                                                                                                                                                        467/c
ABL32467 standard; DNA; 15373 BP.
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2000DE-1043826.
                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 145;
                                                                                                                                                                                                                                                    26-MAR-2002
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666 CTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAAATCTTGGACAAT 725

10266 AAACTTTATACAAAAAAAAAACTAACTTCTCGCTCTACTTCATCCACCACTATTTT 10207

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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonoclectides and/or PNA oligomers of conferencing the cytosine methylation state (ppd islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible compinations. Invervious expenses of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and sequences of different genes associated with signal transduction, or their complementary sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction
                                           10146 CITCICCICACAAAAAAAAAAAAAAAAAAAAAAAAAATIACCIAAITCAAAATAAITIC 10087
                                                                                                                               10086 CICTATAAACTCCAAATTATAAAACGTTAAACTAACCATAACTATACTTTTACATTACT 10027
                                                                                                                                                                                                    786 AGGGAGTGCTTACAACAACCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATG 845
                                                                                                                                                                        846 ACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTC 905
726 AGCTITICCATAGAGAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal transduction associated gene modified DNA #177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 353; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berlin K;
                                                                                                                                                                                                                                                                                                           9966 ATACTAACTTATTTCATATTAA 9944
                                                                                                                                                                                                                                                                  906 GAGCIAAAGCITGCITCTTIA 928
                                                                                                                                                                                                                                                                                                                                                                                                                      ABK31510 standard; DNA; 47108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2001; 2001WO-EP07472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
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ABL34174;
                                                                                                                                                           Query Match
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    888888888888
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                           43962 TAAAAAATTCTTCATAAAATTTAAAATTTTTCGATATAAAACTTTTCAATATCGCATTTA 43903
                                                                                                                                                                                                                                                                                                                                        614 TAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAA 673
                                                                                                                                                                                                674 TCAGAAAGGAGCCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTC 733
                                                                                                                                                                                                                                                       734 CATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTG 793
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Immune system disease; cytosine methylation; antiasthmatic; antiatratiosclarofic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmologici; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiarthritic; artidabetic; antipsoriatic; antifammatory; cancer; eye disease; arteriosclarosis; anaemia; acute myeloid leukaemia; Alraheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                              794 CTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAAGA
                                                                                    Length 47108;
                                                          Sequence 47108 BP; 13283 A; 429 C; 9740 G; 23656 T; 0 other;
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1456; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune system associated gene SEQ ID NO: 1456.
                                                                                     DB 24;
                                                                                                                 0; Mismatches 143;
                                                                                     Score 38.2; I
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                         43782 TCTACCATATACTACCATTTAATAAAT 43756
                                                                                                                                                                                                                                                                                                                                                                    854 TGAACAAAGAGTAAGTTTTTGAAAAT 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL33483 standard; DNA; 17213
                                                                                     3.58;
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2000DE-1043826.
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                                                                                                                 Conservative
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                                                                                    Query Match
Best Local Similarity
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01-SEP-2000;
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                                                                                                                 Matches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL33483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dene; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 27
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ID ABL3
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albriemer's disease, AlbS, eplilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                             13766 TTTGAGTTTAGTGTATATTGTTAAGGTGATAGATGTATTAGAATTTTATAAATTATATATAT 13825
                                                                                                                                                                                                                                                                                                                                                                                                                                                 13826 AAAGAATTTAGTTAGGTAGGGCGTAGTTTATGTTATTATTTTAGTATTTTGGGAGGT 13885
                                                                                                                                                                                                                                                                                                                                    828 TTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAATTCTAAAA 887
                                                                                                                                                                                                                                                                                                                                                                                                                          888 TAGAAATGCATTTGTGTCGAGCTAAAGCTTGCTTCTTTATTTTCCTTTTGTAGAATGA 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                           DB 24; Length 17213;
                                                                                                                                                                                                    Sequence 17213 BP; 5148 A; 333 C; 3659 G; 8073 T; 0 other;
                                                                                                                                                                                                                                                                                          65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 2147; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated gene SEQ ID NO: 2147.
                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                               3.5%; Score 38;
54.2%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13886 TAAGGTAGGTAGATTATGAGGT 13907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL34174 standard; DNA; 113515 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                948 TTCGGTAGTAGGAATATGGGGT 969
                                                                                                                                                                                                                                                                                       0
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                   Local Similarity
nes 77; Conserv
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2689 AATCAAATTTAAAAACTAAAAATAATATAAAAAACTTTATTTCCTTAATTTTAACGTT 2630
                                                                                                                                                                                              2629 TCTAAAAAAAAAAAATATAATAAAAAAAAAAAAAATATAACGTTCTATAACAATTTAAA 2570
                                                                                   672 AATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAAATCTTGGACAATAGCTTT 731
                                                                                                                                                           732 TCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAG 791
                                                                                                                                                                                                                                   792 TECTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
          DB 24; Length 7690;
                                             117; Indels
                                                                                                                                                                                                                                                                                                                                                 2509 AACAAAAAGGCAAAAACAACAATAATAACTAATACTTCGAAATCC 2465
                                                                                                                                                                                                                                                                                                              852 GATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGC 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana DNA fragment SEQ ID NO: 29351.
      Score 37.8; DB; pred. No. 8.5; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC40730 standard; DNA; 870 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
99US-0127462.
99US-0127462.
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99US-0132486.
99US-0132487.
             3.5%;
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99US-0134218
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                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
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                                Similarity
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30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1999,
05-MAR-1999,
09-MAR-1999,
23-MAR-1999,
25-MAR-1999,
01-APR-1999,
08-APR-1999,
16-APR-1999,
16-APR-1999,
16-APR-1999,
16-APR-1999,
16-APR-1999,
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               Query Match
Best Local Simi
Matches 108;
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                                                                                                                                                                                                                                                           including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/dulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                        343 ATTGCTTTGTAGGGTTTGTATGCGTTGTTTTTTACTAGGAAGAGCTTGTACTTTTTCTAT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic; antiatrefiosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmologica; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiinfammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzhoimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                             Sequence 113515 BP; 31803 A; 1174 C; 24020 G; 56518 T; 0 other;
                                                                                                                                                Score 38; DB 24; Length 113515;
Pred. No. 21;
0; Mismatches 40; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7690 BP; 1804 A; 225 C; 2151 G; 3510 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1095; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                      Human immune system associated gene SEQ ID NO: 1095.
                                                                                                                                                                                                                                                                                                     403 GACTTTAGTGAAGAGTCTTCCCATGTTTATGAAAATTCAGA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin K;
                                                                                                                                                ch 3.5%; Scc
1 Similarity 60.8%; Pre
62; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                ABL33122/c
ID ABL33122 standard; DNA; 7690
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL33122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; ds.
                                                                                                                                                       Query Match
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 29
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| 99080146538<br>99080146538<br>99080146538<br>99080147324<br>99080147324<br>99080147325<br>99080147335<br>99080147335<br>99080147335<br>99080147335<br>99080147335<br>99080147335<br>99080147335<br>99080149725<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>99080149726<br>9908015936<br>9908015936<br>9908015936<br>9908015926<br>9908015926<br>9908015926<br>9908015926<br>9908015926<br>9908015929<br>9908015929<br>9908015929<br>9908015929<br>9908015929<br>9908015929<br>9908015929<br>9908015929<br>9908015929<br>9908015929<br>9908015929<br>9908015929<br>9908015929<br>9908015929<br>9908015929<br>99080160044   | to to to to to to  |
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| 990x-0135124<br>990x-0135333<br>990x-0135332<br>990x-0135322<br>990x-0137724<br>990x-0137724<br>990x-0137724<br>990x-0137724<br>990x-0137724<br>990x-0139453<br>990x-0139454<br>990x-0139454<br>990x-0139454<br>990x-0139454<br>990x-0139454<br>990x-0139458<br>990x-0139458<br>990x-0139458<br>990x-0139458<br>990x-0139458<br>990x-0139458<br>990x-0139458<br>990x-0139458<br>990x-0140834<br>990x-0140834<br>990x-0141287<br>990x-0141287<br>990x-0141287<br>990x-0141287<br>990x-0141287<br>990x-0141287<br>990x-0141287<br>990x-0141287<br>990x-0141287<br>990x-0141287<br>990x-0141287<br>990x-0141287<br>990x-0141287<br>990x-0141287<br>990x-0141331<br>990x-0144331<br>990x-0144335<br>990x-0144335<br>990x-0144335<br>990x-0144335<br>990x-0144335<br>990x-0144335<br>990x-0144335<br>990x-0144335<br>990x-0144335<br>990x-0144552   | 99US-014527<br>99US-014527<br>99US-014591<br>99US-014591<br>99US-014591  |
| 20 - MAY 1999; 25 - MAY 1999; 25 - MAY 1999; 25 - MAY 1999; 26 - MAY 1999; 26 - MAY 1999; 27 - MAY 1999; 28 - MAY 1999; 28 - MAY 1999; 29 - MAY 1999; 20 - M   | - JUL - 19<br>- JUL - 19<br>- JUL - 19<br>- JUL - 19<br>- JUL - 19   |
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Sequence 6237 BP; 2071 A; 77 C; 1289 G; 2800 T; 0 other;
                                                       0; Mismatches
                              Score 37.4;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin K;
                                                                                                                                                                                                                                                                                                                               ABL32530 standard; DNA; 7644 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000DE-1032529.
2000DE-1043826.
                                 3.4%;
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                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002 (first entry)
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-130909/17
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                2062 AAT 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
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                                                                                                                                                                                                                                        522 TAT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2002.
                                                          92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; ds.
                                                                                                                                                                                                                                                                                                                                                          ABL32530;
                                  Query Match
                                                 Local
                                                                                                                                                                                                                                                                                                         RESULT 32
                                                            Matches
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                                                                                                 0;
                                                                                                                                                   168 ATTICITCCGGTGGTGGAGGCGACGCCGTACCAAGGAATCTAGAGGAGCGAGTCATTTG 109
                                                                                                                                                                            90 ATTITICAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAAGTCTCTTGTG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                   Gaps
                                                                                                                                                                                                    108 TITIGGITITIGAGITCIGITITIAGGGGAAGAGGAAATGIGAAAGACAGAAGGAAGAAGAGA 49
                                                                                                                         30 ATTICICITGATIGIAAAGGGGAATTGATTCIAACAGACCITGGTCGAGCATCCATTCTA 89
                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Immune system disease; cytosine methylation; antiasthmatic; antiatrefiosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant: ophthalmologici; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiframmatory; cancer; eye disease; arteriosclerosis; anaemia, acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                   .,
                                                                         DB 21; Length 870;
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  claim 1; SEQ ID NO 332; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                               150 GAGTTGATGTATTGAAGGGAAGACGAATAATCTGATCCAATTCTAAA 196
                                                                                                                                                                                                                                              48 ACTTTGTTGTTTTAGAGGAGAAGAAGAATCTGATCCAAGTTATAA 2
                                                                                                                                                                                                                                                                                                                                                                                                   Human immune system associated gene SEQ ID NO: 332.
                                                                                                   81;
                                                                                       4.8;
                                                                                                   Mismatches
                                                                         3.4%; Score 37.4;
51.5%; Pred. No. 4.
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0
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990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                   86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-130909/17.
                                                                                        Similarity
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 26-OCT-1999;
28-OCT-1999;
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29-OCT-1999;
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arterlosclerosis, anomana, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002 TITAAAATIGATATGAAAAAATIAATGTATAAGATAATTAAAATITAAAGTIAYAGT 2061
                                                                                                                                                                                       402 TGACITIAGIGAAGAGICITCCCAIGTITATGAAAAATTCAGAAAATGAGGGATGTAGAA 461
                                                                                                                                           342 GATIGCTITGTAGGGTTTGTATGCGTTGTTTTTACTAGGAAGAGCTTGTACTTTTTTA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant: ophthalmologicil; antitherumatic; antiarthritic; artidlabetic; antipsoriatic; antifilammatory; cancer; eye disease, arteriosclerosis; anemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                           462 GCCAAGGCACGTGCCCTAAAAGGTCATGGATGAGAGTTAAGGAGAAATTATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising fragment of chemically modified gene, usfor diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                     0
Length 6237;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 503; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune system associated gene SEQ ID NO: 503.
    DB 24;
                                                                     91;
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990S - 0139452
990S - 0139452
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990S - 0139465
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990S - 014519
990S - 014518
                                                          990S-0137528
990S-0137502.
990S-0137724.
990S-0138094.
990S-0138540.
      99US-0136782
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99US-0147204
28 - MAY - 1999;
01 - JUN - 1999;
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29.70L-1999;

20.70L-1999;

20
                                                                                                                                                                                                                                                                       338 ATCAGATTGCTTTGTAGGGTTTGTATGCGTTGTTTTTACTAGGAAGAGCTTGTACTTTT 397
                                                                                                                                                                              0; Gaps
                                                                                                                Query Match 3.4%; Score 37.4; DB 24; Length 7644; Best Local Similarity 60.2%; Pred. No. 11; Matches 62; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
      diseases. The present sequence is a gene of the invention.
                                                             Sequence 7644 BP; 2187 A; 53 C; 1625 G; 3779 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                              398 ICTAIGACTTTAGIGAAGAGTCTTCCCAIGTTTAIGAAAATT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana DNA fragment SEQ ID NO: 14105.
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AAC36518 standard; DNA; 522 BP
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9905 - 0123548
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25-MAR 10999
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ó
                                                        90 ATTTTGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAGTCTCTTGTG 149
                       Gaps
                                                                                                  30 ATTICICITGATIGIAAAGGGGAATTGATICIAACAGACCTTGGTCGAGCATCCTA 89
                    0;
                                                                                                                                                                                                                                                                                                     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
Query Match 3.4%; Score 37.2; DB 21; Length 522; Best Local Similarity 51.9%; Pred. No. 4.5; Matches 84; Conservative 0; Mismatches 78; Indels 0;
                                                                                                                               Arabidopsis thaliana DNA fragment SEQ ID NO: 67351.
                                                                                                                                                                                                       .121/c
AAC51121 standard; DNA; 869 BP.
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990S-0132484
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9905-0135529.
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990S-0130077.
990S-0130449.
990S-0130891.
990S-0132048.
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99US-0123180.
99US-012548.
99US-0126264.
99US-0126264.
99US-0126285.
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05-MAR-1999;
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| 99US-0147204.<br>99US-0147302.<br>99US-0147302.<br>99US-0147303.<br>99US-01474316.<br>99US-0147431.<br>99US-0147431.<br>99US-0148319.<br>99US-0148319.<br>99US-0148319. | 9905-0149176:<br>9905-0149426:<br>9905-0149422<br>9905-0149902:<br>9905-0149902:<br>9905-0150884:<br>9905-0150884:<br>9905-0151066:<br>9905-0151080:<br>9905-0151080:<br>9905-0151080:<br>9905-0151080:<br>9905-0151080:<br>9905-0151080:<br>9905-0151080:<br>9905-0151080:<br>9905-0151080:<br>9905-0151080:   | 9905-0155139<br>9905-0155486<br>9905-0155458<br>9905-0156458<br>9905-0157137<br>9905-0157753<br>9905-0158029<br>9905-0158232<br>9905-0158232<br>9905-0158239<br>9905-0159239<br>9905-0159330<br>9905-0159331 | 9905-0160741. 9905-0160741. 9905-0160767. 9905-0160815. 9905-0160816. 9905-0160980. 9905-0161405. 9905-0161406. 9905-0161360. 9905-0161360. 9905-0161360. |
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|   | 117-MUG-1999;<br>18-MUG-1999;<br>20-AUG-1999;<br>20-AUG-1999;<br>23-AUG-1999;<br>23-AUG-1999;<br>27-AUG-1999;<br>27-AUG-1999;<br>27-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-AUG-1999;<br>31-A |  |   |
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Sequence 3152 BP; 995 A; 616 C; 431 G; 1110 T; 0 other;
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                                                                                            3.4%;
ilarity 47.1%;
Conservative
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                                                                                                                                    Similarity
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                                                                                                                                                                           Matches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH54004;
                                                                                                         Query Match
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0
                                                                                                                                                                                                                                                                                                                                                                         90 ATTITGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAGTCTCTTGTG 149
                                                                                                                                                                                                                                                                                                  166 ATTICITCCGGTGGTGGTGGCGACGCCGTACCAAGGAATCTAGAGGAGCGAGTCATTTG 107
                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                30 ATTICTCTTGATTGTAAAGGGGAATTGATTCTAACAGACCTTGGTCGAGCATCCATTCTA 89
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    S. epidermidis genomic polynucleotide sequence SEQ ID NO:4056.

                                                                  Length 869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                  ch 3.4%; Score 37.2; DB 21; Length 8 I Similarity 51.9%; Pred. No. 5.4; 84; Conservative 0; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 GAGTIGALGIALIGAAGGGAAGACGAALAAICIGAICCAAIT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 ACTITGITGITGITAGAGGAGAAGAATCIGAICCAAGI 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-NOV-2000; 2000WO-US30782.
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    99US-0162142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccination; endocarditis;
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        29-OCT-1999;
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                                                                                   Query Match
                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                        1886 GITTAATTAAGTGTGAAATTCTTCTTCATCATATTTTCTGATAAAAAATAACCTGGGAC 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1766 ATAAAAAATTGCATATAGATCCTCCGTTCCTCATTCTGTATAACAATAATTATAAGTTAT 1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 694 TICTAAGTAATCAAGAAAAATCTIGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               754 AAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGT 813
                                                                                                                                                                      574 AGACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTC 633
                                                                                                                                                                                                                                                                                                                                         634 TAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGC 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis
                                                                                                    Gaps
                                                                                          0
Score 37.2; DB 22; Length 3152; Pred. No. 8.8; 0; Mismatches 128; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S. epidermidis genomic polynucleotide sequence SEQ ID NO:3368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
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AAH55090 represent specifically claimed S. epidermidis genomic DNA polymucleotide sequences from the present invention. AAH55091 to AAH5509B represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polymucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present for SEQ ID NO:4455 to 4472,
                                                                                                                                                                                                                                                                                                                          2911 ATAAAAATTGCATATAGATCCTCCGTTCCTATTCTGTATAACAATAATTATAAGTTAT 2970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2971 GAACACCCCAATATTAAACAAAACCACTTTTTACTCTAACTCTAAATAAAAACCACTTTT 3030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3031 GTTTAATTAAGTGTGAAATTCTTCTTCATCATATTTTTCTGATAAAAATAACCTGGGAC 3090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      754 AAGGAGTCGATACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGT 813
                                                                                                                                                                                                                                                                                                 574 AGACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTC 633
                                                                                                                                                                                                                                                                                                                                                                         634 TAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGC 693
                                                                                                                                                                                                                                                                                                                                                                                                                                              694 TICTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAAACCGTGAGGA 753
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, immune system disease; cytosine methylation; antiasthmatic; antiateriosclerotic; antianaemic; cytostatic; noctropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmologica; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antianamatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Albaimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                         3.4%; Score 37.2; DB 22; Length 3345; 47.1%; Pred. No. 9;
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                         Sequence 3345 BP; 1108 A; 485 C; 551 G; 1201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 775.
                                                                                                                                                                                                                                            Pred. No. 9;
0; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL32802 standard; DNA; 6113 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                             Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-130909/17
                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3151 TG 3152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              814 GG 815
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                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 37
ABL32802
ID ABL32
        88888888888888888
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                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albrahier's disease, AlbS, epllepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                        860 AAGAGTAAGTTTTGAAAAATTCTAAAATAGAAATGCATTGTGTGGAGCTAAAGCTTGC 919
                                                                                                                                                                                                                                                                                                                                                                                                           920 TICTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCA 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, immune system disease; cytosine methylation; antiasthmatic; antianteriosclerotic; antianaemic; cytostatic; nootropic; nouroprotective; anti-HIV; anticonvulsant: ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiframmatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Altheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
Nucleic acid comprising fragment of chemically modified gene, usfor diagnosis and treatment of diseases associated with abnormal cytosine methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, us-
for diagnosis and treatment of diseases associated with abnormal
cytosine methylation -
                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                     DB 24; Length 6113;
                                                                                                                                                                                                                                                                                                   3.4%; Score 37.2; DB 24; Length (53.4%; Pred. No. 11;
tive 0; Mismatches 68; Indels
                                                                                                                                                                                                                                                                  Sequence 6113 BP; 1487 A; 157 C; 1487 G; 2982 T; 0 other;
                                                                   Claim 1; SEQ ID NO 775; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune system associated gene SEQ ID NO: 1693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    980 CGTTGGAGTGATTGGCTGTTCTGGAA 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457 TTTATACGIGITIGCGTGTTTGTGAA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL33720 standard; DNA; 7190 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                         Ma.
Local Sim.
78;
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                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 38
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ID ABL
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Claim 1; Page 10116; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Partial dnaN gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAY49071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-1998;
22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                            RESULT 40
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                              The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlbS, epilepsy, neurofibromatosis, rheumatoid arthritis, psorlasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                               957 AGGAATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTGTTCTGGAAGAACAGGGAAA 1016
                                                                                                                                                                                                           6830 GGAAGIGIGGGGGAAGGIGGAAGIGATTITATGIATTGITAGTAGAAGTTACGITAGA 6889
                                                                                                                                                                                             837 TTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGC 896
                                                                                                                                                                                                                                         897 ATTICICICGAGCIAAAGCIIGCIICCITITATITITCCITITGIAGAAIGATICGCIAGI 956
                                                                                                                                                    DB 24; Length 7190;
                                                                                                                               Sequence 7190 BP; 1434 A; 310 C; 2114 G; 3261 T; 71 other;
                                                                                                                                                                          Indels
               Claim 1; SEQ ID NO 1693; 32pp + Sequence Listing; German.
                                                                                                                                                                          92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate expression marker cDNA 52120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                          0; Mismatches
                                                                                                                                                     Score 37.2; I
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                         ABV52129 standard; cDNA; 619 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-2113144P.
2000US-219007P.
                                                                                                                                                      3.4%;
ilarity 49.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2001; 2001WO-US05171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmacogenomic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-662795/76.
                                                                                                                                                                Similarity
90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                1017 GT 1018
                                                                                                                                                                                                                                                                                                                                                    6950 TT 6951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                               ABV52129;
                                                                                                                                                       Query Match
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Matches
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        comprising
                                                                                                                                                                                     (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated dnaE, dnaX and dnaB genes from Gram positive bacteria, used to develop screening assays for identifying antibiotic compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 CAATAGCGATCAGATTGCTTTGTAGGGTTTGTATGCGTTGTTTTTTACTAGGAAGAGCTT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
The invention relates to an isolated nucleic acid molecule (I) comp a nucleotide sequence given in Tables 1-9 (ABNO010-ABN05213) of this specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the prostato of procestate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patient;
(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.4%; Score 37; DB 23; Length 619; 60.4%; Pred. No. 5.4; tive 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 619 BP; 265 A; 95 C; 107 G; 149 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390 GTACTTTTCTATGACTTTAGTGAAGAGTCTTCCCATGTTT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 TTTGTTTTACATATTTGTAGTCAAGCTTTGTCTTATGTTT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "Dna N gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O'Donnell ME, Zhang D, Whipple R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ31005 standard; DNA; 1134 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0074522.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 60.4 61; Conservative
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This sequence is the partial dnaN gene of Staphylococcus aureus. The invention relates to a number of isolated DNA molecules from Gram positive bacterium, corresponding to dnaR molecules from Gram positive bacterium, corresponding to dnaR dnaN molecules from Gram (AAZ31002).and dnaB Gram and and East corresponds to the about of the Escherichia coli, DNA polymerase III holoenzyme, alpha subunit of the Escherichia coli, DNA polymerase III holoenzyme, dnax corresponds to the gamma and tau subunits, and dnaB corresponds to the particular to the gamma and tau subunit is the actual DNA polymerase, the gamma complex forms the clamp loader and tau is a "glue protein". Dnax encodes both gamma and Tau III is the product of the gram is the product of the gene. DnaN forms the belta subunit which forms the silding clamp, and dnaG encodes a primase. The DNA sequences of the invention can be used to identify agents that invention can be used to identifying pharmacological agents or lead compounds for agents active at the level of a replication protein can be used compounds for agents active at the level of a replication protein as antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dnaE; Gram positive bacteria; polC; dnaE; holA; holB; dnaX; dnaN; ssb;
dnaG; dnaB; antiblotic; replication; cell growth; cell death;
bacterial infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 TGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAGTCTCTTGTGGAGT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      894 TGTTGAATTATCTTCTACATCACCAGAAATTGGTACTGTAAAAGAAGAAGAAGTTGATGCAAA 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               834 CTCTTTATTAGCACGTGAAGGTGGTAATAACGTTATTAAATTAAGTACAGGTGATGACGT 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 CTCTTGATTGTAAAGGGGAATTGATTCTAACAGACCTTGGTCGAGCATCCATTCTAATTT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20; Length 1134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1134 BP; 411 A; 176 C; 194 G; 353 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.4%; Score 37; DB ilarity 50.3%; Pred. No. 6.8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of a dnaN polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "dnaN protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                Example 8; Page 30; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF54735 standard; DNA; 1134 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200109164-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 A 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF54735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF54735
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Human; secreted protein; proliferative disorder; cancer; foctal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; appidogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour; cell culture; chemotaxis; food additive; binding partner identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a dnaN polypeptide. The specification describes DNA molecules from Gram positive bacteria, which comprise a coding region from a polC, dnaE, hola, holB, dnaX, dnaN, ssb, dnaG or a dnaB gene. These sequences encode proteins that replicate the chromosome of Gram positive bacteria. They are used for sequencing and amplification of DNA and in drug discovery to identify compounds which have antibiotic activity through interference with replication. They are used in methods for identifying compounds that are active at the level of DNA replication and result in arrest of cell growth or cell death of bacteria to treat bacterial infections in animals.
                                                                                                                                                              Isolated DNA molecule from a Gram positive bacterium encoding DNA replication proteins used to identify compounds which have antibiotic activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 TGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAAGTCTCTTGTGGGAGT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 CTCTTGATTGTAAAGGGGAATTGATTCTAACAGACCTTGGTCGAGCATCCATTCTAATTT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein gene 27 cDNA clone HJAAJ58, SEQ ID NO:100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 1134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 6.8;
0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1134 BP; 411 A; 176 C; 194 G; 353 T; 0 other;
                                                                          Whipple R;
                                                                                                                                                                                                                                      Disclosure; Page 39-40; 239pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.4%; Score 37;
                                                                        O'Donnell ME, Bruck I, Zhang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            611/c
AAH32611 standard; cDNA; 1075 BP.
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Best Local Similarity 50.3%;
99US-0146178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-AUG-2001 (first entry)
                                      (UYRQ ) UNIV ROCKEFELLER.
                                                                                                         WPI; 2001-147453/15.
                                                                                                                             P-PSDB; AAB31935
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WO200134628-A1.

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ANH3252-AAH32627 represent CDNAs corresponding to 35 human secreted protein genes, and AAG73346-AAG73448 represent the proteins they encode.

Encoded and AAG73346-AAG73448 represent the proteins they encode and their corresponding secreted proteins are useful for preventing, and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the mouth of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of the protein in the new genes. Specific uses are described for each of the CS genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of the interpretative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, deseases of the immune system, and includent disorders (e.g., profilated are proteins and action of the interpretation of architists), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, atherosales, and action of an action of an infections. The proteins can also be used to aid wound the hand infections. The proteins can also be used to aid wound contain and epithelial cell proliferation, to prevent skin aging due to culture of primary tissues, to regenerate tissues, to cidentify their cognate ligands or binding partners, and in chemotaxis, and can be used in disorders specific for a protein of the invention can be used in disorders specific for a protein of the disorders mentioned above, and indianoschem tassay (ELISA). The present sequence represents a human con a manning and protein of the invention or expersents a human con a manning and protein of the invention or expersents a human contains and contains an action of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  694 TTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 TIGITITGIAAAAAAATAAACAAAATTAACAAAIGTTTAGCTAAACAAAGTAAGAAAAAG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       754 AAGGAGTCGATACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGT 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 1075;
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                                                                                                                                                                                                                                                                       Ruben SM, Komatsoulis GA, Birse CE, Ni J, Moore PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36.8; DE
Pred. No. 7.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         preventing, diagnosing and/or treat
disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 504; 604pp; English.
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                                                                                                                                            12-NOV-1999; 99US-0164735.
27-JUL-2000; 2000US-0221193.
                                                                                                 08-NOV-2000; 2000WO-US30653.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3est_Local Similarity 52.6
4atches 103; Conservative
                                                                                                                                                                                                                                                                                                                       2001-329066/34.
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                                                17-MAY-2001.
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AMH33522-AAH32627 represent cDNAs corresponding to 35 human secreted protein grade and AAG73346-AAG7348 represent the proteins they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes and their corresponding secreted protein are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be disgnosed by determining the mount of the new protein in a sample or by determining the presence of mutations in the new protein in a sample or by determining the presence of mutations in the new protein in a sample or by determining the presence of mutations in the new protein in a sample or by determining the presence of mutations in the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the soft of the protein of a disgnosis or treatment of the protein of a disgnosis or treatment of a hormalities, hemantopoietic disorders, foetal and developmental abortein disorders (e.g., Alzhelmer's disease) candiovascular disorders (e.g., rheumatoid arthritis), inflammation, alternative disorders (e.g., poorlasis), sepsis, diabetes, atherosclerosis, skin disorders, and infections. The proteins can also be used to aid wound clooning and epithelial call proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell collure of primary tissues, to regenerate tissues, to identify their conducte ligands or binding partners, and in chemotaxis, and can do an be used on a trobedies specific for a protein of the invention can be used in
                                                                                                                                                                     Human secreted protein-encoding gene 27 cDNA clone HJAAJ58, SEQ ID NO:98
                                                                                                                                                                                                                Human; secreted protein; proliferative disorder; cancer; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allorgy; neurological disorder; Alzheimer's disease; skin disorder; psoriasis; sepsils; diabetes; atherosclerosis; skin disorder; psoriasis; sepsils; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM, Komatsoulis GA, Birse CE, Ni J, Moore PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 503; 604pp; English.
                                        AAH32609 standard; cDNA; 1724 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-2000; 2000WO-US30653.
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27-JUL-2000; 2000US-0221193.
                                                                                                                                  10-AUG-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                     AAH32609;
RESULT 43
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2000US - 0226868 2000US - 0227182 2000US - 0227009 2000US - 0228924 2000US - 0229343 2000US - 0229344 2000US - 0229345 2000US - 0229345

20000S-0225757. 20000S-0225758. 20000S-0225759. 20000S-0226279. 2000US-0226681. 200005-0229513 20000S-0230437 20000S-0230437 20000S-0231243 20000S-0231244 20000S-0231414 20000S-0231414

2000US-0232397. 2000US-0232398. 2000US-0232399. 2000US-0232400.

2000US-0232401

2000US-0233064. 2000US-0233065. 2000US-0234223. 2000US-0234274. 2000US-0234997.

14 ANG - 2000)
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15 ANG - 2000)
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2000US-0235834. 2000US-0235836. 2000US-0236327. 2000US-0236367. 2000US-0236368.

2000US-0236369 2000US-0236370 2000US-0236802 2000US-0237037

Fri Jan 10 12:01:27 2003

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alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding CDNA of the invention.
                                                                                                                                                                                               1009 AAAGACTCAAATRAAATGAAAATGAAAAAGGAGACATGACAATTGATACCACAGA 950
                                                                                                                                                                                                                                            754 AAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGT 813
                                                                                                                                                                                                                                                                                                        814 GGAGCAACCTTCCCTTTGATTCTTTGATAATGACAAGA-TGAACAAAGAGTAAGTTTT 872
                                                                                                                                                                                694 TTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune; haematopoletic; immune/haematopoletic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                              Query Match 3.4%; Score 36.8; DB 22; Length 1724; Best Local Similarity 52.6%; Pred. No. 9; Matches 103; Conservative 0; Mismatches 92; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23239.
                                                                                                                                                                                                                                                                                                                          Sequence 1724 BP; 433 A; 242 C; 279 G; 770 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK68427 standard; DNA; 1761 BP.
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2000005-01969874
2000005-01969874
2000005-0196123
2000005-0205155
2000005-02056467
2000005-0216880
2000005-0216880
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2000005-0217486
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20000S-0224519.
20000S-0225213.
20000S-0225214.
20000S-0225266.
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2000US-0184664
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4-FEB-2000; 2
02-FEB-2000; 2
10-MAR-2000; 2
11-MAR-2000; 2
11-MAY-2000; 2
11-MAY-2000; 2
11-JUL-2000; 2
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2000US-0237040. 2000US-0239935. 2000US-0239937. 2000US-0240960.

2000US-0241786 2000US-0241787

2000US-0241221

2000US-0241809 2000US-0241826 2000US-024617 2000US-0246474 2000US-0246476

2000US-0246525 2000US-0246525 2000US-0246526

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) amino acid sequences given in AAM81701 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynuclectics may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynuclectides may be used to produce the secreted (1). by inserting protein calls into a host cell and culturing the cell to express the protein. (1) proteins and polynuclectides may be used to produce the secreted (1). by inserting cancers and cancer metastases of haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703 to AAK876494 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK87642 to AAK876950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 23239; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1761 BP; 809 A; 297 C; 253 G; 402 T; 0 other;
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05-JAN-2001; 2001US-0259678.
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2000US-0249300
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                                    754 AAGGAGTUGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGT 813
                                                                       814 GGAGCAACCTTCCTTTGATTCTTTGATAATGACAGAAGA-TGAACAAAGAGTAAGTTTT 872
                                                                                                           694 TTCIAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGA 753
                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23240.
        1; Gaps
       92; Indels
Best Local Similarity 52.6%; Pred. No. 9;
Matches 103; Conservative 0; Mismatches
                                                                                                                                                                                                        AAK68428 standard; DNA; 1761 BP.
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200005-0209515.
200005-0209467.
200005-021886.
200005-021886.
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20000S - 0220963
20000S - 0220964
20000S - 022518
20000S - 0225213
20000S - 0225213
20000S - 0225214
20000S - 0225268
20000S - 0225268
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                                                                                                                                                                                                                                                                                                                                                                    17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                              06-NOV-2001 (first entry)
                                                                                                                                         873 TGAAAATTCTAAAAT 888
                                                                                                                                                          879 AGTAAAAATGTATAAT 894
                                                                                                                                                                                                                                                                                                                                 WO200157182-A2.
                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                            AAK68428;
                                                                                                                                                                                        RESULT 45
AAK68428
                                                                                                                                                                                                                             οp
                                                                                                                       οp
                                                                                                                                          δy
                                                               δy
                                                                                                    δλ
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20000S-0228928
20000S-0229344
20000S-0229345
20000S-0229513
20000S-0229513
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20000S-0239513
20000S-0231244
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20000S-02312464
20000S-02312466
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20000S-02312466
20000S-02312466
20000S-02312466
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2000US - 0.24 1826.
2000US - 0.24 6474.
2000US - 0.24 6476.
2000US - 0.24 6476.
2000US - 0.24 6477.
2000US - 0.24 6477.
2000US - 0.24 6523.
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2000US-0246613.
2000US-0249207.
22 - Aug. - 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 20000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 2000 | 200
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) amino acid sequences given in AAM81210 to AAM91921. (1) have cytostatic acitivity, and can be used in gene therapy and vaccine production. (1) proteins and con be used in gene therapy and vaccine production. (1) proteins and polymuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polymiclectides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polymuclectic-derived cells. AAK64010 cancers and cancer metastases of haematopoietic-derived cells. AAK6401 to AAK8764 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK87642 to AAK67650 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  694 TICTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 23240; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.4%; Score 36.8; DB 22; Length 1761; Best Local Similarity 52.6%; Pred. No. 9; Matches 103; Conservative 0; Mismatches 92; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1761 BP; 809 A; 297 C; 253 G; 402 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Barash SC, Ruben SM
                                         17-NOV-2000; 20000S-0243529; 17-NOV-2000; 20000S-02435210; 17-NOV-2000; 20000S-0249211. 17-NOV-2000; 20000S-0249211. 17-NOV-2000; 20000S-0249213; 17-NOV-2000; 20000S-0249214; 17-NOV-2000; 20000S-0249218; 17-NOV-2000; 20000S-0249218; 17-NOV-2000; 20000S-0249245; 17-NOV-2000; 20000S-0249295; 17-NOV-2000; 20000S-0249299; 17-NOV-2000; 20000S-0249299; 17-NOV-2000; 20000S-0259391; 17-NOS-2000; 20000S-0259391; 17-NOS-2000S-0250391; 17-NOS-2000; 20000S-0259391; 17-NOS-2000; 20000S-0259391; 17-NOS-2000S-02500S-02
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AAGGAGTCGATACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGT 813

754

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qq δλ pp

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the invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of andiogenesis associated genes (II) having sequences (ABQ66971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in anglogenesis-related genes, for diagnosis and treatment of eye diseases proliferative rethiopathy, necular dependence, inflammation, rheumatoid arthritis, diabetic rethiopathy, macular degeneration caused by necvascularisation, crohn's disease, unflammatory bowel diseases, ulcers and crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                   Human; anglogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; mancalar degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiarteriosclerotic; ds.
814 GGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGA-TGAACAAAGAGTAAGTTTT 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer
                                                                          Human angiogenesis associated polynucleotide SEQ ID NO 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7857 BP; 2110 A; 218 C; 2100 G; 3429 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 105; 41pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                         ABQ67075 standard; DNA; 7857 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-2000; 2000DE-1061338.
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                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                             873 TGAAAATTCTAAAAT 888
                                                                                                                                                (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200246454-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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The present sequence is the genome sequence of Listeria monocytogenes EGD-e. This sequence and fragments of this sequence are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and to study genetic polymorphisms and other genomes. Proteins (ABB47297-ABB50149) expressed from the present sequence are monocytogenes and related organisms, and for biosynthesis and biodegradation, especific antibodies, identification of L. biotegradation, especially biosynthesis of Vitamin B12. This sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, this sequence and proteins encoded by it are useful in pharmacentical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organisms or detailed this patent did not form part of the printed Note: The sequence data for this patent did not sepecification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Goebel W, Kreft J, Kuhn M, Ng E, Varquez-Boland JA; Sernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; T, Domann E, Hain T, Berroe P, Charbit A, Durant L; J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                     Sequence 2944528 BP; 914202 A; 563301 C; 555061 G; 911964 T; 0 other;
889 AGAAATGCATTTGTGTCGAGCTAAAGCTTGCTTCTCTTTATTTTCCTTTTGTAGAATGAT 948
                                                                                                                                                                                                                                                                                                                                                                                   Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                  Listeria monocytogenes EGD-e genome sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 1; 192pp; French.
                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                             ABA03041 standard; DNA; 2944528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dussurget o, Chetouani F, 1
Daniels J, Goebel W, Kreft
Dominguez-Bernal G, Garrido
Chakraborty T, Domann E, Hi
Perez-Diaz J, Baquero F, Gs
Maduenio E, De Pablos B, W
Rose M, Voss H;
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                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                          3627 AAGGTAGGTGGATTAT 3642
                                                                                    949 TCGGTAGTAGGAATAT 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200177335-A2.
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                                                                                                                                                                                                                                                                                                             05-FEB-2002
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                                                                                                                                                                                                                                                                     ABA03041;
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Length 2944528;

DB 24;

3.4%; Score 36.8;

Query Match

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829 ITGATICITIGATAATGACAGAGATGAACAAAGAGTAAGTITITGAAAAATTCTAAAAT 888

; 0

0; Gaps

Indels

62;

3.4%; Score 36.8; D 54.4%; Pred. No. 16; tive 0; Mismatches

Local Similarity 54.4

Query Match Matches

DB 24; Length 7857;

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2501177 AAAAGGACACTGTGGGGGGAATTATGAACAAATAACTATATTGATGTTAAGTATA 2501118
                                                                                                                                                                                                                                                                                                                                                         2501117 ACAGCCGCACTACTTGCATCGT-GTGGAAATGATACGACAACTGATATGAATAATGA 2501059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bb 2501058 AACAACAAAAAACGGAAAATAAATCGCAAGCGCTCTAACGATTACAGATATGGCCGGGCG 2500999
                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                           479 AAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAATTATCTTTATCGAGAGTTCGCATT 538
                                                                                                                                                                                                                                                                                                   539 ACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGGAGCTACA 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           599 AATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCT 658
                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto J;
Best Local Similarity 51.4%; Pred. No. 1.3e+02;
Matches 109; Conservative 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito K, Ya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 2500998 TGATGTTTTTTGATAAAAACCAGAACGAA 2500967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ogai T, Nishikawa T, Hayashi K, S.
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA clone (5'-primer) SEQ ID NO:4186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         659 TGATGGTCTAAGAAATCAGAAAGGAGACCGAA 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 48
AAH07351,C
ID AAH07351 standard; CDNA; 771 BP.
XX
CAH07351;
XX
Human CDNA Clone (5'-primer) SEQ III
WAY
Human; primer; detection; diagnosis
XX
Homo sapiens.
XX
Homo sapiens.
XX
CAC-1999; 99JP-0248036
PR 29-JUL-1999; 99JP-0248036
PR 29-JUL-1999; 99JP-0248036
PR 29-JUL-1999; 99JP-0248036
PR 29-JUL-1999; 99JP-024899.
XX
XX
CB-100; 2000JP-0118176.
PR 09-JUN-2000; 2000JP-018376.
PR 11-JAN-2000; 2000JP-018376.
PR 09-JUN-2000; 2000JP-018376.
PR 11-ANN-2000; 2000JP-018376.
PR 11-ANN-2000; 2000JP-018376.
PR 11-ANN-2000; 2000JP-018376.
PR 11-Length CDNA-018376.
PT THELIX RES INST.
XX
WPI; 201-318749/34.
PT Full-length CDNAs defined in the symmetry full-length CONAs defined in the symmetry full
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in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-iength cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13631 to AAH1842 represent human cDNA sequences; AAB92446 to AAH13633 represent human amino acid sequences; and AAH13629 to AAH13632 represent of the present of sequences; and AAH13629 to AAH13632 for the present consequences; and AAH13639 to AAH13632 for the present consequences.
                                                                                                                                                                                                                                          816 AGCAACCTTCCCTTTGATTCTTTGATAATGACAAAGATGAACAAAGAGTAAGTTTTTGA 875
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New KUZ polypeptides, members of the ADAM family of metalloprotease - useful in neural partitioning and development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kuzbanian; kuz; neurogenic; KUZ protein; neuronal partitioning;
development; WOTCH protein processing; regulation; cell function;
signal transduction pathways; screening; receptor binding;
metalloprotease; soluble; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of the human soluble (lacking a transmembrane domain) Kuzbanian gene, a neurogenic gene. The KUZ protein that it encodes is involved in neuronal partitioning and development. It is also involved in processing
                                                                                                                                                                                                              0
                                                                                                                                                                                DB 22; Length 771;
                                                                                                                                                                                                              Indels
                                                                                                                                                    Sequence 771 BP; 246 A; 131 C; 124 G; 264 T; 6 other;
                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yavari R;
                                                                                                                                                                                Score 36.6; DE
Pred. No. 7.5;
                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens soluble kuzbanian (kuz) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= KU2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Pages 37-38; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xu T,
                                                                                                                                                                                                                                                                                                                     876 AAAATTCTAAAATAGAAATGCAT 898
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                                                                                                                                                                                                                                                                                                                                                                                                       AAV22649 standard; cDNA; 2098
                                                                                                                                                                                 3.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                 Local Similarity 65.19
les 54; Conservative
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29-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                      816 AGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGA 875
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                                                                                                                                                     Ouery Match 3.4%; Score 36.6; DB 19; Length 2098; Best Local Similarity 65.1%; Pred. No. 11; Matches 54; Conservative 0; Mismatches 29; Indels 0;
of the NOTCH protein by cleaving the C-terminal portion. The KUZ protein can be used to screen for compounds that alter binding of KUZ to its receptor or the cleavage of the NOTCH protein, hence acting to regulate NOTCH signal transduction pathways and regulate cell functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito K, Y. Otsuki T;
                                                                                                                   Sequence 2098 BP; 655 A; 353 C; 380 G; 710 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 17797; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA sequence SEQ ID NO:17797
                                                                                                                                                                                                                                                                                                                                       1076 AGGCTACTGAAATATTATTAT 1054
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AAH17997 standard; cDNA; 2333 BP.
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0283776.
09-JUN-2000; 2000JP-02418999.
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the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length coMas. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length coMas. The primers allow obtaining of the full-length coMas easily without any specialised methods. AAH03166 to AAH13628 and AAH3842 represent human coMas sequences, AAB2446 to AAH3622 represent human anno acid sequences; and AAH3629 to AAH3632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                        816 AGCAACCTTCCCTTTGATTGATAATGACAGAAGATGAACAAAGATAAGTTTTTGA 875
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Pred. No. 11;
0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                    Sequence 2333 BP; 699 A; 427 C; 416 G; 791 T; 0 other;
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em\_htg.hum:\*
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Sequence
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| AC119741<br>AC010640<br>AC008517<br>AF206951<br>AC104182<br>AC114497<br>AC113169<br>AC013169<br>AC099770<br>AY040092<br>AF361209  | AX356482<br>AX45861<br>AX458610<br>AX1355610<br>AC107505<br>AC107505<br>AC107505<br>AC107627<br>AC0079761<br>AC012013<br>AC0123864<br>AC0123864<br>AC0123864<br>AC025164<br>AC025164<br>AC025164<br>AC025164<br>AC03364<br>AC03364   | HSDJ495K2<br>HSSD16960<br>AC069321<br>AL840625<br>AL840625<br>AL96252<br>AC050133<br>AC050133<br>AC050133<br>AC1050133<br>AC11524<br>AC116313<br>AC116313<br>AC116313<br>AC116313<br>AC116313<br>AC116313<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699<br>AC10699   |

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Ralman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.

Direct Submission
Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
Location/Qualifiers
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Chlamydophila pneumoniae CWL029
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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Glimmer2; putative"
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1911.
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2816. 3811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CP0806"
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Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J. Umayam, L.A., Utterback, T., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dascon, R., Gwinn, M., Nelson, W., Deboy, R., Kolonay, J., Direct Submission

Submitted (01-MAR-2000) The Institute for Genomic Research, 9712 submitted (01-MAR-2000) The Institute for Genomic Research, 9712 on or before Jun 1, 2000 this sequence version replaced gi:7189730, gi:7189720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE002240 22589 bp DNA linear BCT 30-MAY-2000 Chlamydophila pneumoniae AR39, section 68 of 94 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bomman, C., Bodson, R., Guinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1846 TIGICICAGCITITAGAGCAATCTICAGAATATACTTTGGGTCCAGGGTTCTCTGCAGAA 1905
                                                                                                                            961 ATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGA 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1021 TIGICICAGCITTAGAGCAATCTTCAGAATATACTTTGGGTCCAGGGTTCTCTCGCAGTA 1080
                                                                                                                                                                                                                                                              841 TAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                 901 GIGTCGAGCIAAAGCIIGCIICTCTIIAITTICCIITIGIAGAAIGAIICGGIAGIAGGA 960
                                                                                 781 AAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGA
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Chlamydophila pneumoniae AR39
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
1 (bases 1 to 22589)
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complement(161. .955)
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Nucleic Acids Res. 28 (6), 1397-1406 (2000)
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AE002240.2 GI:8163502
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AE002240/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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us-09-438-185a-1\_1199590\_1200675.rge

gene

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identified by match to PFAM protein family HMM PF00275"
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6766. .7437
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CVFFKEITVTGSSOLORRPMAPLLQALRNFGASFHFSSDKSVLPFTMSCPLRSAYSDV
EGSDOGGASALAVAKCSLARGPCSFTIEBKERRWDISLAMLEKHLHJYSCSOTYTYSF
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GDSRTHYTACVRTFPNFYQTIAIMERRIEDCHDNYSMMSTHKRKYFARGSFG
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                                                                                                                                   Length 22589;
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                                                                                                                                 100.0%; Score 1086; DB 1;
100.0%; Pred. No. 3.7e-244;
Live 0; Mismatches 0;
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Matches 1086; Conservative
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP002548 325865 bp DNA linear BCT 25-MAY-2002
Chlamydophila pneumoniae J138 genomic DNA, complete sequence,
section 4/4.
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Shiral, M. Direct Submission
Submitted (04-JUL-2000) Mutsunori Shiral, Yamaguchi University School of Medicine, Department of Microbiology; 1-1-1
Minamikogushi, Ube, Yamaguchi 75-8505, Japan (E-mail:mshiral@po.cc.yamaguchi-u.ac.jp, Tel:81-836-22-2227, Fax:81-836-22-2415)
On or before Sep 15, 2000 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                AP002548 AB033789 AB033789 AB033790 AB033791 AB033818 AB036083 AB036084 AB036085 AB036086 AB036088 AB036089 AB038350 AB038351 AB038352 BA000008 AB038351 AB038352 BA000008 AB003548.2 GI:10176694
                                                                                                                        /note="synonym:Chlamydia pneumoniae (strain J138)"
221. .1318
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                                                                                       Chlamydophila pneumoniae J138 (strain:J138) DNA.
Chlamydophila pneumoniae J138
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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1. .325865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D 295893 TCCTGRAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTG 295952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295953 ATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGG 296012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296013 ACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGACTCGATACCATAAATTCCGATT 296072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 295653 TATGCGTTGTTTTTTACTAGGAAGACCTTGTACTTTTTCTATGACTTTAGGGAAGAGTCT 295712
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                                                                                                                                                                                                                                                                                    121 AFGFCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGATTGAAGGGAAGACGAATAAT 180
                                                                                                                                                                                                                                                                                                                                                                              181 CTGATCCAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 TATGCGTTGTTTTTACTAGGAAGAGCTTGTACTTTTTCTATGACTTTAGTGAAGAGTCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 TCCCATGTTTATGAAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACGTGCCCTAA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781 AAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGA 840
                                                                                                                                                                                          61 TAACAGACCTTGGTCGAGCATCCATTCTAATTTTGAAGTGAGTTCTACCAGTTCAAA 120
                                                                                               1 TTGGCAAAGTACCTCAAAACCAGAAAGATATTTCTCTTGATTGTAAAGGGGAATTGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 AAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGGTTCGCATTAC
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  Length 325865;
                                                  0; Indels
Ouery Match 100.0%; Score 1086; DB 1; Best Local Similarity 100.0%; Pred. No. 2.7e-244; Matches 1086; Conservative 0; Mismatches 0;
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us-09-438-185a-1\_1199590\_1200675.rge

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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-21M15 Unpublished to 151120)
                                                                                                                                               AC015814
AC015814 6 GI:13940724
HTG; HTGS_PHASE1; HTGS_FULLTOP HOMO sapiens.
1012 GGAAAG 1017
                            848 GTGAGG 843
                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                   TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                       DEFINITION
                                                                                                                                                     ACCESSION
                                                                         RESULT 6
AC015814
                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                 KEYWORDS
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                                                                                                                                                                   PAT 28-DEC-1997
                   1088 RRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCAAGCTCGGAATT 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               952 GTAGTAGGAATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTGTTCTGGAAGAACAG 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908 TAAAACTAACTGCTGTGTATAGAATGCTTTAAGGAGGCTTCCTTTTCTAAACGATTGG 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        832 ATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1028 AATTCTGTGAGCGTATGGCAAACGAAGGAAAAATAGTTATAGTAGCCGCACTCGATGGGA 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATITCAACGIAAACGIITAAIAAIAIITIGAAICTIAIICCAIIAICIGAAAIGGIGG 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                592 AGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAAAT 651
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   1021 ITGICICAGCITIAGAGGAAICTICAGAAIATACTITGGGICCAGGGTICICICGCAGIA 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 TCGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 GAAGAGTCTTCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCAC 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                      6.7%; Score 72.4; DB 6; Length 7218;
illarity 16.0%; Pred. No. 1.1e-06;
Conservative 234; Mismatches 275; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                   1929 t 368 others
                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                            1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fourox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
                                                                                                                                                                        DNA
                                                                                                                                                             7218 bp L
Sequence 14 from patent US 5670367.
166494.1 GI:2724471
                                                                                                                                                                                                                                                                                                                                                                                    /organism="unknown"
1491 c 1486 g
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 16.0%; es 97; Conservation
                                                                                                                                                                                                                                                                                                                                                                     7218
                                                                                                                                                                                                                                                                               Unclassified.
                                                                                                Db 296373 GTGCAC 296378
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                                                                    Qy 1081 GTGCAC 1086
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                                                                                                                                                                                          DEFINITION
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TITLE
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                                                                                                                                              RESULT 5
166494/c
                                                                                                                                                                                                                      VERSION
KEYWORDS
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Expenses 1 to 191120)

Righton L. Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baltren, B., Linton L., Nusbaum, C., Lander, E., Rollander, B., Baldwin, J., Barna, N., Beckerly, R., Boquslavkly, L., Boukhgalter, B., Browh, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewark, K., Domino, M., Donelan, L., Doyle, M., Colerta, P., FitzHugh, W., Porrest, C., Funke, R., Cage, D., L., Leo, C., Locke, K., Machano, M., Bortcon, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Kartas, A., Klein, J., McEwan, P., McGurk, M., McKenth, R., McCandal, P., Marquis, N., McEwan, P., McGurk, J., Norman, C., Kann, L., Kartas, A., Klein, J., McEwan, P., McGurk, J., Norman, C., Kann, L., Kartas, A., Klein, J., Peterson, K., Pollara, V., Kliey, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Stojanovic, N., Subramanian, A., Talamas, J., Wwan, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct, Submission

All repeats were identified using RepeatMasker: html

Lepter, Mitchebead Institute/ MIT Center for Genome Research

Center code: WIBR

Whe site: http://www.seq.wi.mit.edu

Center code: WIBR

Whe site: http://www.seq.wi.mit.edu

Center project information

Center project information

Center project information
AC015814 151120 bp DNA linear HTG 09-MAY-2001
Homo sapiens clone RP11-21M15, WORKING DRAFT SEQUENCE, 5 unordered
                                                                                                                                                                                                                                                                                                                                                       numo verteno
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 151120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 5.9 in 020 bases; agarose-fp Quality coverage: 6.1 in 020 bases; agarose-fp Quality coverage: 6.1 in 020 bases; according to a working draft, sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary caps between the contigs are represented as runitary caps between the contigs are represented as runitary caps between the contigs are represented as this of a sequence as soon as it is available and the accession number will be preserved.
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Center clone name: 21_M15
Center clone name: 21_M15
Sequencing vector: M13: M7815; 2% of reads
Sequencing vector: Plasmid: n/a; 38% of reads
Sequencing vector: Plasmid: n/a; 38% of reads
Chemistry: Dye-terminator H1g Dye: 100% of reads
Assembly program: Phrap; version 0,960731
Consensus quality: 146254 bases at least 040
Consensus quality: 148194 bases at least 030
Consensus quality: 148194 bases at least 020
Insert size: 156000; sqarose-fp
Insert size: 150720; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4930: contig of 4930 bp in length
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1. 193804
/Organism=Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
/map="15621.1"
/clone="RP11-40816"
/clone="RP11-40816"
/clone="RP11-100816"
/note="This clone overlaps RP11-90419 AC066615,
RP11-691D11 AC064813, RP11-313A9 AC025843 and CTD-2150N2
AC023905. Data from overlapping BACs were added and the consensus sequence was determined from RP11-408J6 to the extent possible"
                                     2 (bases I to 193804)

Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,
Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A.,
Nesbitt, R., Traicoff, R. and Hood, L.
Direct Submission
Submitted (28-NOV-2000) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A., Nesbitt, R., Traicoff, R. and Hood, L. Direct Submission

Direct Submission

Submitted (22-MAR-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: Data from AC066615 [Drafting center: UWMSC], AC064813 [Drafting center: WIBR], AC025843 [Drafting center: WIBR] and AC023905 [Drafting center: UWMSC] were added for finishing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98105, USA
On Mar 22, 2001 this sequence version replaced gi:11386266.
Center: Multimegabase Sequencing Center
Center code: UNMSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen6systemsbiology.org
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10350. .104040
113560. .13700
/note="low quality data"
/note="low quality data"
/note="overlap with RP11-313A9, AC025843"
/note="low quality data"
/note="low quality data"
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1 (Dases 1 to 193804)

Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Madan,A., Sequencing of human chromosome 15 D15S146-D15S117 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACUS4882 193804 bp DNA linear PRI 22-MAR-2001
Homo sapiens chromosome 15 clone RP11-40836 map 15q21.1, complete
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13505 TGACACATCTTTTAGCTACACTAAGAAAAAAGAGAGAAGACTCAAATTTACAAAATTAA 13564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13565 AGGTGAAAAAGGAAACATTAAAACTGACACCACAGTAATACAACGATCACAAGAGACTAT 13624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               658 ITGAIGGICTAAGAAATCAGAAAGGAGACCGAAAGCITCTAAGTAATCAAGAAAAATCI 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   778 ATTAAAAAAGGGAGTGCTTACAACAGCCAFATCAGTGGAGCAACCTTCCCTTTGATTCTT 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     598 AAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGC 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.3%; Score 46.8; DB 2; Length 151120; Best Local Similarity 47.9%; Pred. No. 0.8; Matches 135; Conservative 0; Mismatches 147; Indels 0;
4931 5030: gap of 100 bp 5031 89503: contig of 80373 bp in length 85904 86003: gap of 100 bp 86004 97975: contig of 11073 bp in length 9797 98077 147748: contig of 49672 bp in length 147749 14748: contig of 49672 bp in length 147749 14748: contig of 3272 bp in length 1500 bp 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="RR11-21M15"
/clone="RP11-21M15"
1. 4930
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5031. 85903
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86004. 97976
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98077. 147748
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147849. 151120
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ACO84882.2 GI:13430989
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AF119388 1531 bp mRNA linear INV 23-MAY-1999
Caenorhabditis elegans phenylalanine hydroxylase (KO8F8.4) mRNA,
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Submitted (12-7AN-1999) Dept. of Biology, University of San Diego,
5998 Alcala Park, San Diego, CA 92110, USA
Location/Qualifiers
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Loer C.M., Davidson, B. and McKerrow, J.
A phenylalanine hydroxylase gene from the nematode Caenorhabditis elegans is expressed in the hypodermis
J. Neurogenet. (1999) In press
2 (bases 1 to 1531)
                                                                                                     1225 AAAGAAGTAGAGGTTGCAAGCTTCTTCAAA-----TCTTCCTCTGATGCTCCAAGA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473 TGCCCTAAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTT 532
1464 TCTTCAAAATTCTAGTATAGAAATACGCTGACTGGAAAGTAGTAATGAGACATTCTTGC 1405
                                                                                                                                                                                 233 AGTICCIGAGGAGAACTGATAAGAACGGCICCATAIGCTTTICITCCTTCATGGTTTTCA 292
                                                                                                                                                                                                                                                                                                     293 ATAAGTCCGCTTTCAACAGTAAACCAAAAGCAGCGTACAATAGCGATCAGATTGCTTTGT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                993 GATAAGTATCCGGCGACTGGGCGAACACGGAATCCAGTTTTTGCTTTCAAAAACTTGCAG 934
                                                             1053 CGAACGTATTGAGTGCAGAAGAAGACACGATATGCAAGACCTGCCAAGAAATCACGAGCT
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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/strain="Bristol N2"
/db_xref="taxon:6239"
/chromosome="I1"
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/hote="KO8F8.4/bas-2"
90. .1463
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1. .1531
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Caenorhabditis elegans
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AF119388.1 GI:4883766
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FELLERHCGYSRNNIPOLEDICKFIRAKTGFRVRYAGYZARDFLAGLAYRVFCTO
YVRHHADPPYTPEDTVHVELMGHMATFADDPFAQFSQEIGLASIGASEBLKKLATLY
FFSIEFGLSSDDAADSPYKENGSNHERFKYVGAGLLSSAGELQHAVEGSATIIRRDPI
RVVEQECLITTGOSAYFYTRNFEEAQOKLRMFTNNMKRPFIVRYNPYTESVEVLNNSR
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RRSGSLGTPFPVEEDVGCIFFPFWYRREASIREDGEBEGVOILTIVEKSSRVSEDIS
KMIANLPDHTRIEDHERSPSQDGSSKTWDVLLEIELFHYGKGEAMCLMELNGLDVHEV
SSTIRFTAIKEQYTEFGSDDATTGSEWFRSIYDLOICAKRVIMYGAGLDADHFGFKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF135186 1642 bp mRNA linear INV 13-MAY-1999 Caenorhabditis elegans tryptophan hydroxylase (tph-1) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission Subm
                                                                                                                                                                                                                                                                                                                                                    Db 104432 AGGTGAAAAAGGAAACATTAAAACTGACACCACAGTAATACAACGATCACAAGAGACTAT 104373
                                                                                   Db 104492 TGACACATCTTTAGCTACACTAAGAAAAAAGAGAGAGAGCTCAAATTTACAAAATAA 104433
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                                                                                                                                                                      718 TGGACAATAGCTTTTCCATAGAGAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCG 777
                                                                                                                                                                                                                                                                                             778 ATTAAAAAAGGGAGTGCTTACAACAGCCATAICAGTGGAGCAACCTICCCTTIGAITCTI 837
                                               658 TIGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCITCTAAGTAATCAAGAAAAATCT 717
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis,
I chases 1 to 1642)
Sze, J. Y. and Ruvkun, G.
tph-1 encodes a C. elegans tryptophan hydroxylase
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/db_xref="taxon:6239"
/chromosome="II"
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/protein_id="AAD50115.1"
/db_xref="G1:4809153"
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/note="TPH-1"
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Caenorhabditis elegans
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unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone KOBFB. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone KOBFB is at 26081 in sequence 26449.

The true right end of clone KOBFB is at 101 in sequence 26449.

The start of this sequence (1. .100) overlaps with the end of sequence 26449.

The end of this sequence (1. .100) overlaps with the start of sequence 268314.

For a graphical representation of this sequence and its analysis see:— http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
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15707. 15805,15894. 16013)
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15707. .15805,15894. .16013)
/gene="K08F8.2"
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Location/Qualifiers
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/db_xref="cA91283.1"
/db_xref="SPTREMBL:Q1360"
/db_xref
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RLTTHEAAAFLVTGEFYPGKHITTALAIPCADESSCGGGYFDGCFIVBEEFPDTV
AEILDVPKSVRFSTERDGVKAPRLHSIQEEVGRAMEINRMGTDQVYIKNPTASCNNLFER
RRAVHLSIPRVYC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choice—Cootains similarity to Pfam domain: PP00069 (ENkaryotic protein kinase domain), Score=215.4, E-value-2.8e-61, N=1 comes from this gene CDNA EST EMBL:M88996 comes from this gene CDNA EST ykil867.3 comes from this gene CDNA EST ykil867.5 comes from this gene CDNA EST ykil867.5 comes from this gene CDNA EST ykil3612.5 comes from this gene CDNA EST ykil3612.5 comes from this gene CDNA EST ykil363.3 comes from this gene CDNA EST ykil307.3 comes from this gene CDNA EST ykil307.3 comes from this gene CDNA EST ykil307.5 comes from this gene CDNA EST ykil307.5 comes from this gene CDNA EST ykil4079.5 comes from this gene
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8333. .8410,8631. .8755,8864. .9078,9128. .9346)
/gene="KO8F8.1"
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Corganism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="11"
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                                                                                                                                                  /note="similar to sequences presented in GenBank Accession
Numbers C65545 and C55069; phenylalanine-4-hydroxylase;
phe-4-monooxygenase; PAH; PheH"
                                                                                                                                                                                                                                                           Caenorhabditis elegans cosmid KOBF8, complete sequence. 266497
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Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1132 AAAAGTCCGGCTCCGTAAGCTTTTTTCTCCCCATCTTGTTGACAGATTCCAATT 1073
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                                                                           /function="biopterin-dependent aromatic amino acid
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59.1%; Pred. No. 2.5;
iive 0; Mismatches 54; Indels 0;
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                              /EC_number="1.14.16.1"
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                                                                                                                     hydroxylase"
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Best Local Similarity 59.19
Matches 78; Conservative
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AC121238 HG 23-AUG-2002 DNA linear HTG 23-AUG-2002 ordered pieces.

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae, eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Shaull.S., Lin.S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (23-AUG-2002) Department Of Chemistry And Biochemistry,
The University Of Collahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
Uppublished
Cooklob., Kim, D. and Roe, B.A.
Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cooklob., Kim,D. and Roe,B.A.
Direct Submission
Submission
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Db 25366 AAAAGTCCGGCTCCGTAAGCTTTTTTTCTCCCCATCTTGACAGATTCCAAATTCGATT 25425
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Shallis, Lin,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roo-B.A.
Medicago truncatula BAC Clone mth2-34p9
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9.1%; Pred. No. 1.8;
ve 0; Mismatches 54; Indels 0;
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Best Local Similarity 59.1%;
Matches 78; Conservative
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30946. 31051,31100. 31190,31450. 31580)
4000=**(80818.5b**
join(29693. 29728,30107. 30376,30419. 30588,30762. 30896,
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ETIALLGAGABUNULSHIESPERYMENGCYEVLYEPEABAEDIRKIEG LEHOORARKY
ETIALLGAGABUNULSHIESPERYMENGCYEVLYEPEABAEDIRKIEG LEHOORARKY
IVODWNTYNKOWENDSYPEPOKTINDOFANRILGYGAELDABHGGEKOMYYERRKE
FADJAFNEKHORKITYTYTOBELAWRTYVNELTYWYKRACOGFNYTPPLLGONC
FYPERIFOLONDVADPELKOCTGYTIRRYAGLLSSROFLAGLAGAFNYFHSYOYIRHISABK
YPERPIGGHELLGHYPLFADVERAGENGSROFLAGLAGAFNYFHSYOYIRHISABK
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complement(join(24990. .25164,25210. .25439,25484. .25610,
25786. .25921,25972. .26168,26281. .26443,26496. .26688,
27097. .272213,47309. .27344))

/gene="KO8F84" | Foreign Complement 
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ASAKNKLKSWAATINRPFQIRYNAYTQRVEILDKVAALQRLARDIRSDISTLEBALGK
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/LTAGISLACHONKEGELESCHORHEELDVPLICAKEELKFOORPSFEEDHVYKKKTFNFN
PVGKEPFDVEEVLTSDIKLEERWTATVIFGOKRILLSWNAGHSODNIGGCPDWNCEF
TQVRRARPDDAJAULIAHMDNDFVPKPNOYVYFSOESPANSGIOIPRPDYINWTLGFR
TQVRRARPDAJAULIAHMDNDFVPKPNOYVYFSOESPANSGIOIPRPDYINWTLGFR
QKHQIDIYGGGGPWKCARGDSKRYFGOKTOVANLVNKKAKAAAMPYSHCOTNSKREDFVKKL
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/db_xref="SPIREMBE.CQ21361"
/db_xref="SPIREMBE.CQ21361"
/db_xref="SPIREMBE.CA1391"
/db_xref="S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(18851. 19061,19149. 19267,19316. 19421, 19473. 19561,19609. 19713,19799. 19939,19989. 20176, 20245. 20485. 20530. 20599,20934. 21022))
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25786. .25921,25972. .26168,26281. .26443,26496. .26688,
27097. .27213,27309. .27344))
cDNA EST yk273b10.5 comes from this gene"
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/db_xref="G1:3979833"
/db_xref="SWISS-PROT:P90925"
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/db_xref="GI:3878362"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **Consists of Scontigs. Gaps between the contigs are represented as runs of N. The order of the pieces are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

***State of the gaps of unknown length is former to the state of the sequence as soon as it is available and the accession number will be preserved.

***State of the gaps of unknown length is former to the state of the sequence o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              691 AGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGA 750
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/clone=lb="mth6dicago truncatula BAC library H2"
37237 a 17162 c 18248 g 36159 t 400 others
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.llarity 46.1%; Pred. No. 1.6;
Conservative 0; Mismatches 179;
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/db_xref="taxon:3880"
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Sequence 22 from Patent W00111061.
AX083744 1G1:13185472
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1. .109206
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synthetic construct
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/note="consensus sequence of A.t., L.a., and B.n. FAE1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 NNNNNAKAMCKRAKYWGWNRABVNSTCTTWKSKTTKVRTSCWANNCRAGDANKDHKWWKW 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 ATTCTAATTTTGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAGTCT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 CATATGCTTTTCTTCCTTCATGGTTTTCAATAAGTCCGCTTTCAACAGTAAACCAAAAGC 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 NNNGTTMWKRMWAWYWKMDMDWBGTYNNNNNGGRTYYGWTKNKKMWTYYKWKANNCKWRA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  384 GAGCTTGTACTTTTTCTATGACTTTAGTGAAGAGTCTTCCCATGTTTATGAAAATTCAG 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            743 KAAKKHWRWANKWAMRGWHADAAABTTDKRNNGAYTKYTTTNNNNTYRGVVTNTAARDGW 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               744 ACCGTGAGGAAGGAGTCGATACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAG 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANNNNNNNNNNNNNGWSDMWVTWWAYANYGTNNNNNNNNNNNAYAWWTNKWYYTTDDRWR 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      804 CCATATCAGTGGAGCAACCTTCCCTTTGATTTTTTGATAATGACAGAAGATGACAAAGA 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 AAAGATATTTCTCTTGATTGTAAAGGGGAATTGATTCTAACAGACCTTGGTCGAGCATCC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTGCAACAGAGACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 CTTGTGGAGTTGATGTATTGAAGGGAAGACGAATAATCTGGTCCAATTCTAAAGGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 SYDVTYYWWWDDMCKRKVRRWVRTRGRMRNYMVAWBTAHRRYNNGWTBAMAYRRWTMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 CACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAACGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 WDHKTCTHNNTTWWKMKTY-------WNNCYWKSMTNGKSHRBAAAVYTWYMWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               627 YKAKKYAGAGGSNNNNNNNNNNNNNNNATC----ARDDYYAASRWYAMANAKWYYYKBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 11.0%; Pred. No. 3.6;
Matches 114; Conservative 369; Mismatches 541; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1%; Score 45; DB 6; Length 1141; 11.0%; Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 g 112 t 832 others
1 (bases 1 to 1141)
Kunst.L. and Clemens.S.
Regulation of embryonic transcription in plants
Patent: WO 0111061-A 22 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
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1. .1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 c
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RESULT 13 AC024941

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VERSION KEYWORDS

AUTHORS

REFERENCE

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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANNOTATION OF FEATURES:
STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts:
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons EInhked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttctagacag(c)aatgacaata
ctctttgaaa(c)tattatattg
ggcatggtg(c)aacaggcccc
gcatgggtg(c)acaggcccca
aaagactgga(a)caggattgg
tatattacct(t)ttaaaaattt
atattacct(t)taaaaattt
                                                                                                                                                                                                                                                                                                                                                         Submitted (11-JUL-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2001 this sequence version replaced gi:13492990.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                            Direct Submission Submission Submission Submission Submission Submission Submission Submission Submission MARR-2000) Human Generics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA (bases 1 to 172246)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171130
2.13165e-05
0.00600713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Summary Statistics ----
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Fraction of Phrap values less than 40 :
Number of consensus changing edits:
Number of N's in consensus :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggcatggtg(n)nacaggcccc
gcatggtgn(n)acaggcccca
aaagactgga(n)caggattgg
tatattacct(a)ataaaaatnt
atattaccta(a)taaaaatnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Original+Context
ttctagacag(n)aatgacaata
ctctttgaaa(n)tattatattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phrap values in estimate:
                                                            1 to 172246)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                         Worley, K.C.
Direct Submission
Direct Submission
Unpublished
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                                                                                                Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Position
67598
99512
                                                                        (bases
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103636
103660
106704
106705
                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
TITLE
JOURNAL
                                                                                                        AUTHORS
                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                             REFERENCE
                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
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Bukaryota: Metazoa; Chordata; Cranlata; Vertebrata; Buteleostomi;

Mammalia; Butheraia; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheraia; Primates; Catarrhini; Hominidae; Homo.

Manmalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.

Margy, D.M., Adams, C., Adio-Oduola, B., Ali-Caron, T., Buther, E., Benten, D., Buck, J.,

Benton, J., Birteva, M., Brawher, E., Brown, M., Bryant, N.P., Buthey, C.,

Burch, P., Buttera, M., Brawher, E., Brown, M., Bryant, N.P., Buthey, C.,

Burch, C., Coyle, M.D., Dathorne, S. R., Olave, J., Chen, C., Cherland, C.D.,

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Davy-Carrol, L., Dederich, D.A., Delaney, K. R., David, M. L., Davis, C.,

Davy-Carrol, L., Daderich, D.A., Delaney, K. R., David, M. L., Davis, C.,

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Elhaj, C., Emariling, S., Esrotto, M., Falls, T., Berrade, C., Braris, C.,

Ractis, A., Garner, T., Garza, N., Gill, R., Hernandez, J., Hernandez, D.,

Hart, M., Haviak, P., Hawes, A., Hernandez, J., Hernandez, D.,

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Hodgson, A., Hogues, M., Hollvey, C., Hollins, B., Homs, R.,

Louisegd, H., Locado, R.J., Luk, M., Lea, B., Lee, E., Lewis, L.C.,

Leatis, L., Li, J. Li, Z., Lichtarge, O., Lieu, C., Litu, J., Liu, M.,

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Martindale, M., Matthell, T., Wohabbak, K., Mondel, M., Miller, M., Mareria, M., Rein, S., Masser, M., Mollyen, N., Nickerson, R., Walth, M., Okunoun, G., Oraque, P., Morden, S., Marindale, M., Rang, S., Usang, M., Peters, L., Pickens, R., Peters, S., Pater, M., Peters, S., Scort, G., Shoothar, N., Wall, M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC024941 172246 bp DNA linear PRI 11-JUL-2001
Homo sapiens 12 BAC RPI1-900F13 (Roswell Park Cancer Institute
Hunan BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                             983 WMTTTRITWYAATRWKTNNATGSMTRCNATGWKNNNYWTGWKTRWTAYRWATRWKAWWK 1042
                                                                                                                                                                                                                                                                                                                                                     984 GGAGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGATTGTCTCAGCTTTAGAGCAATCT 1043
                                                                                                                                            923 NMTMKTKYYBHAAWNNNNNGKMCTAHTWWVCKATKTTKGCWMNCTTTCRKYKNNCTWYT 982
                                                                                                                                                                                                            924 CITTATTITCCTITIGIAGAATGATICGTAGTAGGAATATGGGGGTCGAGTATGCACGTT 983
    863 BAYTINININRMAYYGAYADDYAYYMSDTCDAWMKWDATKMINATTYNRGTAWRTININNN 922
                                                                        AC024941.30 GI:14669928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1044 TCAGAATATACTTTGGGTCCA 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1103 KYNWHMCKCNNNNNNNNTMMR 1123
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AC034170 180563 bp DNA linear HTG 20-APR-2000 HOMO sapiens chromosome 12 clone RP11-674J5, *** SEQUENCING IN PROCRESS ***, 89 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outpublished to 180563)

2 (bases 1 to 180563)

Biract Submission

Submitted (04-APR-2000) Genome Sequencing Center, Washington

Noiversity School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

On Apr 20, 2000 this sequence version replaced gi:7579885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180563)
Waterston, R.H.
                                                                                                                                                  618 AGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAG 677
                                                                                                                                                                                                 678 AAAGGAGCCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
                                                                                                                                                                                                                                                                       738 GAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTA 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 89 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                         DB 9; Length 172246;
                                                                                                                                                                                                                                                                                                                                         Ouery Match
4 1%; Score 45; DB 9; Length 172;
Best Local Similarity 49:8%; Pred. No. 2.1; Indels
Matches 114; Conservative 0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 699 bp in length ig ap of unknown length or contig of 713 bp in length ig ap of unknown length is contig of 617 bp in length ig ap of unknown length
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HTG; HTGS_PHASE1.
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7999:
1512:
1612:
2229:
2329:
2944:
3044:
4053:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
AC034170
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AUTHORS
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KEYWORDS
SOURCE
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TITLE
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                                                                                                                                                                                                                                                                                                        qq
                                                                                          agactgaatt(c). .
      ttttaaaaat(t)tatgcttagt
ctctgactcc(t)tagcttagtg
cttaacttat(a)aatgctgtag
                                                       acactctgct(c)atctgcctgg
                                                                                                                                                                                                                                                                                                                                                                                               30 35
                                                                                                                                              ----- Distribution of Quality < 40 Bases ---
                                                                                                                                                                                                                                                                                                                                                                                             15 20 25 3
Phrap Value Range
taataaaaat(n)tatgcttagt
ctctgactcoc(c)tagcttagty
cttaacttat(n)aatgctgtag
acactctgct(n)atctgcctgg
cagactgaa(a)t....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="L2"
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complement(13240, .13408)
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6004 .6045
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9713...10458
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complement(674. .798)
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complement(799. .835)
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complement(836, .852)
/rpt. famil
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| 45842: gap of unknown<br>46799: contig of 977 b<br>46899: gap of unknown<br>48409: gap of unknown<br>49768: contig of 1359<br>49868: gap of unknown<br>51672: contig of 1864<br>51772: gap of unknown<br>53070: contig of 1208<br>53170: gap of unknown<br>53070: contig of 1208<br>53170: gap of unknown<br>55990: contig of 2720   | of 2550 unknown unknown unknown of 1710 unknown of 1721 unknown of 1721 unknown of 2075 unknown unknown unknown unknown unknown unknown unknown   | 74764: contig of 2049 74864: gap of uknown 77074: contig of 2210 77174: gap of uknown 79340: gap of uknown 7940: gap of uknown 80990: contig of 1885 81090: gap of uknown 81090: gap of uknown 82075: contig of 1885 83075: gap of uknown 8755: contig of 1881 8756: contig of 1851 8756: contig of 2528 87554: contig of 2528 87652: contig of 2528 87652: contig of 2528 87652: contig of 2528 87653: contig of 1851 87554: contig of 1851 | unknown of 2169 unknown of 2169 unknown of 2068 unknown of 2945 unknown of 2945 unknown of 2772 unknown of 2773 unknown of 2633 unknown of 2633 unknown of 2633 unknown of 2633  |
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ITNYYPFKEQNNPFIKOAOYSSWYVLDDIINNLDYSIDNIHAIDMLYEHILNLL
EEERKNEILEEILKNILKIILCDVETTVRRSAQKVLQNAEGDTNLMLKRAKGLQSLGKM
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                                                                                                                                                                                                                                                                                                        complement (4238. .4798)
/gene="PFB0985c"
/note="predicted by GlimmerM"
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complement(4238. .4798)
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

(bases 1 to 12029)

Cardone, M. J., Tettelin, H., Carucci, D. J., Cummings, L. M., Aravind, L., Koonin, E. V., Shallom, S., Mason, T., Yu, K., Frijii, C., Pederson, J., Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D. C., Pertea, M., Sanzberg, S., Zhou, L., Sutton, G. G., Clayton, R., Whitte, O., Smith, H.O., Fraser, C. M., Adams, M.D., Venter, J. C. and Hoffman, S. L., Chromosome 2 sequence of the human malaria parasite Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 114475 AAAGTATTCAAGTAAAAATTAGATAATCATGAAATAACTTTCTACCCAGTGTGAAATG 114534
                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 114415 AGGAAAAAAGCTTTTCAAAATTGGATTAATCAATAATAGCATGAGTGACGAATAGTATTG 114474
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Gardner, M.J.
Direct Submission
Submission
Submitted (02-NOV-1998) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20814, USA
Location/Qualifiers
1. 12029
1. 12029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    678 AAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
                                                                                                                                                                                                                                                                                                                                                                            618 AGGAAAAATGTTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAG 677
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contig of 3222 bp in length gap of unknown length contig of 3286 bp in length gap of unknown length contig of 3201 bp in length contig of 4290 bp in length contig of 4290 bp in length
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Mismatches 115; Indels
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Science 282 (5391), 1126-1132 (1998)
99021743
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2754. 3603
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/gene="PFB0980w"
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cal Similarity 49.8%;
114; Conservative
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Direct Submission
Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinkton, Cambridge CB10 1SA, UK
On Dec 12, 1999 this sequence version replaced 91:5731898.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P.falciparum. IMPORFANT: This sequence is not the entire insert of clone MALAP2. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5644. .6063
/gene="MALAP2.02"
/note="WALAP2.02, very hypothetical protein, len: 139 aa"
                                                                                                                                                                                             Plasmodium:

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium:

1 (bases 1 to 234112)

Devlin,K., Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D.,
Quali,M. and Barrell,B.

Direct Submission
                             INV 31-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="MALAP2.01"
/noce="MALAP2.01" hypothetical protein, partial orf, len:
> 1130 aa, contains NKSKPDD repeat sequence"
          PFNAL4P2
Plasmodium falciparum MAL4P2, complete sequence.
AL035475 G1:6562702
AL035475 G1:6562702
Prosenal protein: replication A protein; ribosomal processing protein: ribosomal protein: rifin; transcription factor; var.
Plasmodium falciparum 3D7
Elekarvorta Almana 3D7
                                                                                                                                                                                           Apicomplexa; Haemosporida; Plasmodium:
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/protein_id="CAB62842.1"
/db_xref="G1:6562703"
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/note="G(7)-tract upstream of MAL4P2.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Plasmodium falciparum 3D7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="3D7"
/db_xref="taxon:36329"
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/gene="MAL4P2.02"
5644. .606?
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                                                                                                                                                                      HSA343706 783 bp DNA linear PRI 18-JUL-2002
Homo sapiens genomic sequence surrounding NotI site, clone
NR5-FITR.
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Zabarovsky, E.R.
Direct Submissary (5.R.
Submitted (16.MAY-2001) Microbiology and Tumorbiology Centre,
Rarolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 783)
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      276 CIGCATIGITGTTABAGAAAAAGACIATAGAGAGCICACAIGAAAATAAAGTAAAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 ACAACCCCATGAAAAAGGAAGGGCTATAGAATACCCATCTATTAACCAATAAATGGTTAC
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                                                                                5486 TGTATTATATATGTTATTATTATCCTATTATACAACTATT 5527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the human genome
Nucleic Acids Res. 30 (14), 3163-3170 (2002)
                                                             908 GCTAAAGCTTGCTTCTCTTTTTTCCTTTTGTAGAATGATT 949
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Pred. No. 5.8;
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1.783
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NRS-FI7R"
a 154.c 141 g 202
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4.1%;
Best Local Similarity 48.7%;
Matches 149; Conservative
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576 GGGAAT 581
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9747. .9756
/gene="MAL4P2.03"
/note="alternative splice acceptor sequence for exon 9 of
MAL4P2.03"
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9730. .9739
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/gene="kML4P2.03"
/note="predicted splice acceptor sequence for exon 11 of
MAL4P2.03"
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                                                                                                                                                                                                                                      /note="predicted splice acceptor sequence for exon 6 of MAL4P2.03"
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                                                                                                                                                                                                                                                                                                                          /note="potential splice donor sequence, cag/gtagga, for exon 6 of MAL4P2.03"
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                                                                                    for
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/gene="MAL4P2.03"
/note="predicted splice acceptor sequence for exon 9 f 9747. 9756
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exon 5 of MAL4P2.03"
8141. *8150
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/gene="MALAP2.03"
Anote="predicted splice donor sequence, acc/gtaaat, exon 8 of MALAP2.03"
9645. 9650
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4.1%; Score 44.2; DB 3; Length 234112;
Best Local Similarity 50.2%; Pred No. 3.1;
Matches 109; Conservative 0; Mismatches 108; Indels 0;
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/gene="MAL4P2.03"
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/gene="MAL4P2.03"
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/gene="MAL4P2.03"
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                                                                                                                                                                                                                                                                 6787. 6792
/note="alternative donor sequence (att/gtatga) for alternative 5'-exon for MAL4P2.03"
join(6794. 6857,6942. 7075,7272. 7383,7566. 7663,7926. 10170. 10250,10340. 10370,10551. 10706,10776. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706,10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706. 10706
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6787..6792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Mal4p2.03"
/Gene="mal4p2.03"
//note="predicted splice acceptor sequence for exon 3 of
Mal4p2.03"
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(6932. 6941)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="predicted splice donor sequence, aac/gtttgt, exon 4 of MAL4P2.03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6858. .6863
/gene="MAL4P2.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7076. .7081
/gene="MAL4P2.03"
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/gene="MAL4P2.03"
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ACO08008 167257 bp DNA linear PRI 16-MAY-2002 Homo sapiens Xp22 PAC RPCI6-102 (Roswell Park Cancer Institute Human PAC Library) complete sequence.
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Direct Submissor, Su
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INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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Worlby,K.C.

Boinett Submission

Submitted (31-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

5 (bases 1 to 167257)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muzny, D., Arenson, D.D., Bouck, J., Brundage, E., Bunac, C., Chen, Z., Di, W., Dugan, S., Durbin, J., Forcum, J., Garcia, C., Chen, Z., Di, W., Ding, Y., Duran, J., Forcum, J., Garcia, C., Correll, J.H., Gorrell, L.L., Hernandez, J., Jackson, L., Kondejewski, N., Leal, B., Lichtarge, O., Liu, W., Logan, O., Lu, J., Marthac, C., Oswal, G., Pampell, L.R., Parish, B., Perez, L., Rashid, N.D., Rives, C., Scherer, S.E., Shen, H., Simon, M., VO, O., Millamson, A., Worley, K.C., Yu, W., Zhou, X., Nelson, D. and
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Direct Submission
Submitted (09-OCT-1999) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

6 (bases 1 to 167257)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                 Db 222544 ATAAAAATTTTAATTAAATAACAAAAAAAAAAAA 222508
750 AGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAA 786
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Unpublished
2 (bases 1 to 167257)
Worley, K.C.
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Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences. Genes and Region of sequence similarity are identified by BLAST GNUC. Acids Res. 25:3387-3402) similarity (expect < 1e-34) to the EST and CONA sequences. Genes demonstrate at least two excns flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum sequenced of double strand coverage with a minimum of 2 clones and 3 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region dose not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

QUALSTAT-REPORT--

atgacgattg(c)acatgaaatc tgacgattg(a)catgaaatca tgattactag(t)gataactact aaagggtcag(g)agatgcagtt acttgcatc(c)tcaatcccag tgagcattt(a)caggtatatt tttctttcc(t)ttttttt cccaccagtg(t)gccatgtcag atggagctgt(a)acactgctgc caccagatta(a)ttgaaatgaa aattaccaaa(t)gtgggggggt ccaaatgtgg(g)ggggtcagga tgtggggggg(t)caggatttga caacacttag(t)gggtttaaaa tgtggttctg(t)ggatggacta aattcaccca(a)aaaaagtagac attcacccaa(a)aaagtagaca agaaaatgga(a)aaaaaaattt aataagtgat(c)tgatttcatt ttattctgat(t)tgcctcctct ctgaggacta(g)ctaaaaacag tcttacatca(a)ataaataaag aaataccttt(c)cataagacat ttgtgatgac(g)attgcacatg gatgacgatt(g)cacatgaaat 167257 166248 0.000259222 0.0376546 phrap values in estimate:
Average error rate (BCM-Phrap estimate):
Fraction of Phrap values less than 40:
Number of consensus changing edits:
Number of N's in consensus: caccagatta(n)ttgaaatgaa aattaccaaa(n)gtggnggggn ccaaangtg(n)ggggcagga ngtggnggg (n)caggattga caaccctta(n)gggtttaaaa tgtggttctg(n)ggatgacta aattaacca(n)maaagtagac attaaccan(n)aaaagtagaca agaaaatga(n)aaaaaattt aataagtga(n)tgattcatt ttattctgat(n)tgattcatc ctgaggacta(n)ctaaaaacag atgacnatth(n)ncatgaaatc tgacnatth(n)catgaaatca tgattactag(n)gataactact aaagggtcag(n)agatgcagtt acttgcatct(t)tcaatccag tgagcattt(n)caggtatatt ttttcttcc(n)ttttttttt atggagcígí(n)ácacigcígc cgittiggcic(t)innaggagat titiggcicit(n)naggagatta aaataccttt(n)cataagacat cccaccagtg(n)gccatgtcag ttgtgatgac(n)attnnncatggatggatggatg ttggctcttn(n)aggāgāttag Summary Statistics Consensus changing Original+Context Contig length: Position 11124 19982 124786 150222 150332 150332 150354 150594 160400 160400 119977 21880 11130 11660 32920 32998 21881

Distribution of Quality < 40 Bases -

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Peatures listing.

ANNOTATION OF FEATURES:
STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

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71348 AAGTTTTCTATAAAGAGGGCATTATGCGACTCAATGACAATTGAAAAGCGAAAGTATTA 71407

698 AAGTAATCAAGAAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGG 757

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578 AAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAAT 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1%; Score 44; DB 9; Length 167257; 46.9%; Pred. No. 3.6;
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0; Mismatches 155; Indels
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                                                                                                                  15 20 25 Phrap Value Range
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complement(8394 . 8628)
/rpt_famlly="Alusg"
complement(9633 . 9771)
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9907 . 11222
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/rpt_family="AluJb"
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/rpt_family="LlMA7"
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complement(11720. .11846)
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    .167257
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    /db_xref="taxon:9606"

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complement/sia"
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1531. .1578
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3178
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Location/Qualifiers
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Matches 137; Conservative
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198230 bp DNA linear PRI 01-MAR-2002 AC092862 AC028678 AC092662.2 GI:16303564 HTG.
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Submitted (20-OCT-2001) Genome Sequencing Center, Washington
Noriersity School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 198230)
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                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 198230)
Sulston,J.E. and Waterston,R.
                      758 AGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAG 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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Harris,A., Abbott,A., Dixon,R., Dignan,G. and Phillips,A.

The sequence of Homo sapiens BAC clone RP11-510H11

Upublished (2001)

A bases 1 to 198230)

Waterston,R.H.
                                                                                                    818 CAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGT 869
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Waterston, R. H.
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Waterston, R.
Direct Submission
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DB 9; Length 198230; 3.5;
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(NID:q10323061)"
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(NID:912763443)"
7683. .7975
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46.4%; Pred. No.
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7008. .17085
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7092. .17417
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9860. .19901
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23469. 2365
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6936. .17007
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6603. .16761
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/1775. .12096
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8846. 9142
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24567. .25448
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5797. .16899
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0016. .20038
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8268. .19599
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9660. .19697
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7423. .17913
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6587, 16210
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2152. .1236?
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12528.
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6770. 1601.
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22060.
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                                                                                                                                                                                                  MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The clone sequenced to the left is RP11-569P21, 2000 bp overlap; the clone sequenced to the right is RP11-727011. Actual start of this clone is at base position 1 of RP11-510H11; actual end is at base position 198230 of RP11-510H11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence of AC026578 has been incorporated into AC092662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //oce="similar to Homo sapiens EST BE907740 (NID:910401605)"
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**Mote="similar to Homo sapiens EST BE874285"
|NID:q10313061)"
:805. .6607
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755. 7549
7655. 7649
700te="similar to Homo sapiens EST BE907740
ND:910401605)"
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NID:910323061)"
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/db_xref="taxon:9606"
/chromosome="2"
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3782. .4214
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/clone_lib="RPCI-11"
151. .265
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1. .198230
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4246. .4282
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288. .328
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rpt_family="L1"
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rpt_family="L1"
076. .7108
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8654. .3683
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AX344846/c
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                                                                                                                                                                       Db 102509 ACCATATTTTATAATCATAACATAAATAATTGAAGTCATGCAGTACAACAAAAATCAAT 102568
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/db_xxef="taxon:32630"
1. 1141
/note="consensus sequence of A.t., L.a., and B.n. FAE1
                                                                                                                                                                                                                187 CAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGA 246
                                                                                        67 ACCTTGGTCGAGCATCCTAATTTTGAAGTGAGGTTCTACCAGTTCATCAAAATGTCT 126
                                                                                                                                                     127 TATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATAATCTGATC 186
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                            7 AAGTACCTCAAAAACCAGAAAGATATTTCTCTTGATTGTAAAGGGGAATTGATTCTAACAG 66
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4.0%; Score 43.8; DB 6; Length 1141;
Best Local Similarity 11.6%; Pred. No. 6.9;
Matches 86; Conservative 248; Mismatches 405; Indels 1;
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0; Mismatches 165; Indels
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Regulation of embryonic transcription in plants
Patent: WO 0111061-A 22 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
Location/Qualifiers
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Sequence 22 from Patent WO0111061.
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PAT 01-FEB-2002
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/organism="synthetic construct"
/db_xref="texaon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
a 219 c 1585 g 3023 t
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                                                                                                                     708 GAAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACC 767
                                                                                                                                                                                                                                                                       696 CWWNNTDARRINNTTVMRRRWMTNTKTRWYSTTRRHHYTGATNNNNNNNNNNNNNSC 637
                                                                                                                                                                                                                                                                                                                                  768 ATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCC 827
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816 NNNNNNNNNNNNNNTWCHYTTANABBCYRANNNNAAARMARTCNNYMHAAVTTTHTDWCYK 757
                                                                                      648 TAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGGGAAAGCTTCTAAGTAATCAA 707
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Diagnosis of diseases associated with development genes
Patent: WO 0200927-A 271 03-JAN-2002;
Epigenomics AG (DE)
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Sequence 271 from Patent WO0200927.
AX348846 AX344846.1 GI:18492732
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate
                                                                                                                            678 AAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
618 AGGAAAAATGTGTTTCTAATICGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAG 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Waterston, R.H.
Direct Submission
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Submitted (28-APR-2000) Shih-Feng Tsai, National Yang-Ming
Submitted (28-APR-2000) Shih-Feng Tsai, National Yang-Ming
University, Institute of Genetics; 155 Li Rong St. Section 2,
Peritou, Talipei, Talianan 11221, Republic of China
(E-mail:Wmpetsal@ym.edu.tw. URL:http://genome.ym.edu.tw/,
These sequences are draft human sequences, not finished sequences
These sequences are draft human sequences, not finished sequences of the same clone are represented as 100 N.

* NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is
a ribit rary. Gaps between the contigs are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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*** SEQUENCING
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 88966)
                                                                                                                Gaps
                                                                              801 CAGCCATATCAGTGGAGCAACCTTCCTTTGATTGATAATGACAGAAGATGAACAA 860
                                                                                                                                                                                                       861 AGAGTAAGITITIGAAAAATICIAAAATAGAAATGCATTIGIGTGGAGCTAAAAGCTTGCI 920
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Pred. No. 5.9;
0; Mismatches 88; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP001943 88966 bp DNA linear H'
Homo sapiens chromosome 4 clone 2185F9 map 4q22-q24, '
IN PROGRESS ***, 7 unordered pieces.
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/db_xref="taxon:9606"
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HTG; HTGS_PHASE1.
Homo sapiens DNA, clone:2185P9.
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Matches 96; Conservative
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Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 3, 2002 this sequence version replaced 91:16077045.
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1 (bases 1 to 14667).
Sulston, J. E. and Waterston, R.
                      738 GAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTA 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
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                                                                                                                                                                                                                                                                           ACUY3810 146671 bp DNA linear PRI 01-MA Homo sapiens BAC clone RPl1-354024 from 4, complete sequence.
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Kalicki,7. and Hagjund,K.
Kalicki,7. and Hagjund, K.
The sequence of Homo sapiens BAC clone RP11-354024
Unpublished (2001)
3 (bases 1 to 146671)
Waterston,R.H.
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repeat\_region

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chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RECI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 511-8. The clone may be obtained either from and coworkers at http://www.chori.org
and coworkers at http://www.chori.org
wcron: pBACc3.

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is ACO87607; the clone sequenced to the left is ACO87607; the clone sequenced to the left is ACO87607; the clone sequenced to clone is at base position 1 of RPII-354024; actual end is at base position 34976 of RPII-48483.

There is an ambiguous at base position 5636.

/rpt\_family="ERV1" /rpt\_family="L1" /rpt\_family="L1" 1644 .1728 ... /rpt\_family="MIR" /rpt\_family="MIR" /rpt\_family="MIR" /rpt\_family="MIR" /rpt\_family="MIR" The sequence of AC023636 has been incorporated into AC093810. Location/Oualifiers

Location/Oualifiers

Location-Refort

/organism="Homo sapiens"
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24359. .24406
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33937. .33971
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18782. .18840
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0271. 20072
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6136. .16229
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
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Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Respon of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:389-3402) similarity (expect < le-34) to the EST and CDMA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                         Submitted (18-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 158066)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 (bases 1 to 158066)
Worley, K.C.
Direct Submission
Submitted (28-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 158066)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (22-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (31-JUL-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Mar 28, 2002 this sequence version replaced gi:18449849. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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Submitted (OZ-MAY-2002) Human Genome Sequencing Center, Departmen
Submitted (OZ-MAY-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 158066)
Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y.,
Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANNOTATION OF FEATURES:
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Direct Submission
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12. (Dasea: 1 to 158066)

13. Muzny, D.M., Adams.C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alabrocks, S.L., Amaratunge, H.C., Arel., R., Ayele, M., Banks, T., Barbaroks, S.L., Amaratunge, H.C., Arel., R., Metel., M.; Banks, T., Barbaria, J.; Benton, J.; Bimage, K., Blankenburg, K., Bonnin, D., Bowk, J.; Bowie, S. Brieva, M.; Brown, E.; Brown, M.; Bryant, N. P., Buhay, C., Burch, P., Burket, C., Burrell, K.L., Byrd, N. P., Carron, T.F., Carter, M., Cavazos, S.R.; Chacke, J., Chen, R., Chen, Z., Chowdhry, I., Othistopoulos, C., Clarch, C., Cox, C., Coyle, M.D.; Dathorne, S. R., David, R., Delaney, K.R., Deladeo, D., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Dubbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.; Falls, T., Ferraguto, D., Pangan-Rocha, S., Dubbin, K.J., Gorlell, J.H., Clevara, W., Gunerathe, P., Hale, S., Hamilton, K., Harris, C., Liu, W., J., Martinez, E., Massey, E., Martin, R., Lucier, A., Lucier, R., Lucier, M., Moore, S., Worgan, M., Moore, S., Warth, M., Moore, S., Worgan, M., Moore, S., Okumon, G., Octubo, C., Harris, C., Marris, S., Morgan, R., Paneshari, M., Sparks, A., Solubokan, T., Rohfe, M., Marthera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC107307 158066 bp DNA linear PRI 31-JUL-2002
Homo sapiens 3 BAC RP11-657G2 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                            42648 CCAAGCTAAAAGGTAGGTTTTTTGAAAAGATCAACAAAACTAACAGACATTTATCTATATG 42589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42708 AGAATAATGAAGATTAGAATTAAAAGCAGTGAAATAGAAATTACAATTTTAAAGAATCAA 42649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    738 GAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTA 797
                                                                                                                                                                                                                                                                                                                                        678 AAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
                                                                                                                                                                                             618 AGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAG 677
                                                                                                                              Gaps
                                              Score 43.2; DB 9; Length 146671;
Pred. No. 5.6;
0; Mismatches 88; Indels 0;
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                                                      4.0%;
                                                               Query Match 4.0%;
Best Local Similarity 52.2%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42528 CAAC 42525
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AC107307/c
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/note-"overlaps bases 17989. .19988 of clone AC117506"
*Inction="clone overlap"
136. .686.
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1042. .11070
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20605. .22071
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omplement'107
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/rpt_family="MER52A"
complement(23423...23578)
                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                     complement(958. .1128)
/rpt_family="MER53"
1252. .1799
                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="AT_rich"
1951. .4985
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5079. .5504
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complement(10229. .109
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16709. 17324
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/rpt_family="AT_rich"
19658. .19680
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3519. .3940
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421. .4479
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rpt_family="AT_rich"
.0136. .10175
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/rpt_family="Af_rich"
complement(19837. .200
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19258. .19280
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complement(4514. .47
                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AluSx"
4895. .4924
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020. .5041
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686. 8997
rpt_family="Aluy"
            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             rpt_family="HERVL"
180. .4513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family-"L1MA4"
8140. .8445
                                                                                /clone-"RP11-657G2"
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8446. .8679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_family="L1M2"
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374. .6818
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3330. 3367
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QUALSTAT-REPORT
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            FEATURES
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UnderSon,S., Baldwin,J., Bastian,V., Bastian,V., Beda,F.,
Baddwin,J., Baura,N., Bastian,V., Beda,F.,
Campoplano,A., Castler,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,R., Diaz,J.S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,R., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Howland,J.C., Tiley,T., Johnson,R., Jones,C., Kann,L.,
Klein,J., LaRcoque,K., Lamazares,R., Landers,T., Lehoczky,J.,
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Murphy,T., Naylor,J., Norman,C., Miranda,C., Mienga,V., Morrow,J.,
Wurphy,T., Naylor,J., Norman,C., Riley,R., Rogov,P., Rothman,D.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfeye,S., Theodorea,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viell,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Yeung,G., Zainoun,J., Zimmer,A. and Zody,M.
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HOMO saplens clone RPll-657G2, WORKING DRAFT SEQUENCE, 15 unordered
pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159716)
Birren,B., Linton,L., Nusbaum,C. and Lander.E.
                                                                                                                                                                                                                                                                                           79221 ACTTTCAGATCTAATGCCATTTATTTTCATTTGTCAGTGGAGATAAAAGGTAACATTGTA 79162
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                                                                                                                                                                                                                                                          607 AACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTC 666
                                                                                                                                                       Score 42.8; DB 9; Length 158066; Pred. No. 6.8;
                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 187;
                                                                             .27211)
                                                                                                  /rpt_family="LTR16B"
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AC025807 2 GI:7342200
HTG: HTGS_PHASE1: HTGS_DRAFT.
HOMO sapiens
HOMO sapiens
/rpt_family="MIR"
25577. .25684
/rpt_family="L2"
complement(27105.
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                                                                                                                                                       3.9%;
ilarity 45.3%;
Conservative (
                                                                                                                                                       Query Match
Best Local Similarity
Matches 155; Conserv
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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AC025807
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KEYWORDS
SOURCE
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Human chromosome 14 DNA sequence BAC R-603H7 of library RPCI-11 from chromosome 14 Of Homo sapiens (Human), complete sequence. Al109847 AL109847.5 GI:13160357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 125201 AAATGGAACATATGAAAACATTAAAAGGAATCCAAATAATGGAATTAGGGCTGTGGGCAG 125260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 125261 ACTITCAGAICTAAIGCCATITAITITCAITIGICAGIGGAGAIAAAAAGIAACAIIGIA 125320
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3.9%; Score 42.8; DB 2; Length 159716;
Best Local Similarity 45.3%; Pred. No. 6.8;
Matches 155; Conservative 0; Mismatches 187; Indels 0;
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/note="assembly_fragment"
BASE COUNT 53196 a 26713 c 26963 g 51443 t 1401 others
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vector_side.right"
51458. .72400
72501. 90337
/note="assembly_fragment"
/note="assembly_fragment"
    /note="assembly_fragment"
22560. 30751
/note="assembly_fragment"
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40620 .51357
/note="assembly_fragment
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/note="assembly_fragment"
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/note="assembly_fragment"
10516. .14122
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/note="assembly_fragment"
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vector_side:left"
16505. 22459
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            Direct Submission
Submitted (14-MAR-2000) Whitehead Institute/MIT Center for Genome Submitted (14-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAT 30, 2000 this sequence Version replaced 9:7239693.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                       Center code: WIBR
Web Site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@enome.wi.mit.edu
Contact: sequence_submissions@enome.wi.mit.edu
Contact: sequence_submissions@enome.wi.mit.edu
Center project Information
Consensus quality: 157485 bases at least Q40
Consensus quality: 157717 bases at least Q30
Consensus quality: 157717 bases; at least Q30
Consensus quality: 157717 bases; at least Q30
Consensus quality: 157717 bases; an least Q30
Consensus quality: 157717 bases; sum-of-contigs
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1120. .2370
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                    Db 61470 AAAAGACATATACAGATGACAAATAAGCACATGAAAAATGTTAAAAAATCATTAGTTATT 61529
                                                                                                                                                                                                                                                                                                         61590 AAAATGCCAAGAATGTGGAACAACCAGCTCTTTCATGCATTGCTTATGAGAATGTAAAAT 61649
                                                                                                                                                                   678 AAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
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                                                               DB 9; Length 186158;
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                                                            Score 42.8; DB 9; I pred. No. 6.7; 0; Mismatches 102;
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                                                               3.9%;
                                                            Query Match 3.99
Best Local Similarity 50.59
Matches 104; Conservative
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Rattus norvegicus
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AC112384/c
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                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (26-APR-2001) Genoscope - Centre National de Sequencage :
Br 191 91006 EVR cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Feb 28, 2001 this sequence version replaced gi:11611112.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 186158)

Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Bertifer, P., Cattolico, L., Barbe, V., Pelletier, E., Artiquenave, F., Levy, M., Eckenberg, R., Bruls, T., Geberardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Weissenbach, J.

Uppublished

C. (bases 1 to 186158)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end): R-66E7 Downstream BAC (overlapping the SP6 end): R-423117 (AC=AL513142)
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146274. .146413
/note="matching EMBL:F01603
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/note="matching EMBL:T16335
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Location/Qualifiers
1.1.186158
/ Organism="Homo sapiens"
/ db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: Phrap; version 2.0
Quality coverage: 7.54x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Genoscope / Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
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NOTE: This is a "working draft" sequence. It currently consists of 65 configs. The true order of the pleces is not known and their order in this sequence record is arbitrary, gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                               2 (bases 1 to 188385)
Worley, K.C.
Bubmission
Submitted (22-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 188385)
                                                                                                                                                                                                                                                                                                 Direct, Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department Submitted (13-JUL-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 7030, USA
On Jul 12, 2002 this sequence version replaced gi:20303170.
    Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
Unpublished
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Whe balter: http://www.hgsc.bom.tmc.edu/
Contact: hgsc.help@bom.tmc.edu/
Contact: hgsc.help@bom.tmc.edu

Contact: project Information
Center project name: GRA30-3014
Center clone name: GRA30-3014
Center clone name: GRA30-3014
Center clone name: Plasmid:
Grenter clone name: Plasmid:
Consensus quality: 129147 bases at least Q40
Consensus quality: 139955 bases at least Q30
Consensus quality: 139955 bases at least Q20
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gap of unknown length
contig of 1659 bp in length
contig of 1133 bp in length
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Center code: BCM
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AUTHORS
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Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Oct 20, 2001 this sequence version replaced gi:14916169.
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Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Homo sapiens.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia: Eutheria, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159035)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                  Db 171535 GGAGATATAACAACAGAATCTAAGGAACTTCAAAAAAATAATCAGATCCCTCTTCAAAATC 171476
                                                                                                                                                                                                                                                                                          728 CTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAG 787
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                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159035 bp DNA linear PRI 01-
HOMO Sapiens BAC clone RP11-20H7 from 2, complete sequence.
AC092584 AC015490
HUMO SI:16303525
                                                                                                                                       DB 2; Length 188385;
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3 (bases 1 to 159035)
Waterston, R. H.
: gap of unknown length
: contig of 5552 bp in length
: gap of unknown length
: contig of 3454 bp in length
: gap of unknown length
: contig of 3807 bp in length
                                                                                                                                                                           0; Mismatches 112; Indels
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Genome Res. 8 (11), 1097-1108 (1998)
99063792
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                                                                                                                                       Score 42.8;
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Waterston, R.H.
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Matches 110; Conservative
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Submitted (20-OCT-
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Direct Submission
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Louis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Data from AC068537, AC073994, and AC016827 was used to finish this clone, AC092584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa. K., woon.p.Y., 2hoo.B., Frengen.E. Tatenc.M., Catenese,J.G. and de Jong.P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong WECTOR: pBACe3.6
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The clone sequenced to the left is RPI1-138Cl3, 2000 bp overlap: the clone sequenced to the right is RPI1-2IL7. Actual start of this clone is at base position 1 of RPI1-2OH7; actual end is at base position 159035 of RPI1-2OH7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. 3MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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Location/Qualifiers
1. .159035
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
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1. .108
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3780. .4131
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4308. .4401
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/rpt_family="L1"
148. 550
/rpt_family="L1"
344. 387
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/codon_start=2
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ILIDEIKSLCFDIIVI"
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                                                                                                               /rpC_family="r-rich"
/rpC_family="r-rich"
32226. 33096
//note="similar to Sus scrofa EST BI184750 (NID:914659159)"
32227. 32588
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Thao, M.L., Clark, M.A., Burckhardt, D.H., Moran, N.A. and Baumann, P. Direct Submission
Direct Submission
Submitted (16 MAY-2000) Microbiology Section, University of Submitted (16 MAY-2000) Microbiology Section, University of California, Davis, One Shields Avenue, Davis, CA 95616-8665, USA 1. 2706
                                                                                                                                                                                                                                                                                21687 GCCAGACAAAAAAAAAAAGGTCCAAATAAATAAATAAATCAGAAATGAAAATGGAG 21628
                                                                                                                                                                                                                                                                                                                                                                                                               21627 ACGITACAACTGCTATCCCAGAAATTCAAAGATTATTTGTGGCCTCTATGAGCAAACTA 21568
                                                                                                                                                                                                                                                                                                                                                                                            792 IGCITACAACAGCCATATCAGIGGAGCAACCTICCCTITGATTCITIGATAAIGACAGAA 851
                                                                                                                                                                                                                                                                                                                            732 TCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAGGGAG 791
                                                                                                                                                                                                                                                            672 AATCAGAAAGGAGCGGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTT 731
                                                                                                                                                                                                                                 Gaps
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Best Local Similarity 52.8%; Pred. No. 8.5;
Matches 114; Conservative 0; Mismatches 101; Indels 1;
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/specific_host="Aphalaroida inermis"
/db_xref="taxon:114186"
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                 /rpt_family="L1"
29568. .29848
/rpt_family="Alu"
29849. .32251
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31201. .31310
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<1. .184
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'rpt_family - Ar_rich"

4492 . 15506

'rpt_family = "11"

5546 . 15895

NID:99808862)"

NID:99808862)"
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9948 9990
/rpt_family="(TCCA)n"
10104 10426
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4. 10605
family="(TTTTA)n"
1. 11026
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9069. 1015.
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/rpt_family="(GAAA)n"
21727. .21845
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3365. .13877
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2799. .13336
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987. .12289
.512. .5561
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545. .5567
                                                                                                                           /rpt_family-"(TCTA)n"
                                                       /rpt_family="AT_rich"
6515. .7739
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8684 ;
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/rpt_family="L1"
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.085. .18013
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8027
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.8381. .18406
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632. .9817
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family="L1"
6. .10564
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2777. .12812
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1879. .14061
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|231. .14412
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|391. .14436
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1062. .11958
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7582, 7622
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26258. .266
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AC108007/c
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                                                                                         COMMENT
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//LEASTACTOR WAS CONTRIBUTED OF WAS CONTRIBUTED.
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Homo sapiens chromosome 5 clone CTD-2015B23, complete sequence.
ACO10342
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2 (Dases I to 126010)

DOE Joint Genome Institute.

Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (Dases I to 126010)

3 (Dases I to 126010)

DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (28-APR-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 126010)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 950 CGGTAGTAGGAATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTGTTCTGGAAGAAC 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     830 TGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATA 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 2706;
                                                                                                         /product="RNA polymerase beta-prime subunit"
/protein_id="AAK55949.1"
/db_xref="GI:14193387"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
3.9%; Score 42.2; DB 1; Length 2;
Best Local Similarity 50.2%; Pred. No. 15;
Matches 104; Conservative 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1010 AGGGAAAGTGATTGTCTCAGCTTTAGA 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2304 AAAAGGATTAACTGATACTTCTTTAAA 2330
                                                                 /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC010342.5 GI:13876487
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Homo sapiens
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AC010342/c
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VERSION
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TITLE
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ACLOBOO SAPIENS CHROMOSOME 11 clone CTD-3038L12 map 11, *** SEQUENCING IN PROGRESS ***, 8 ordered pieces.
Direct Submission
Submitted (01-MAY-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Apr 28, 2001 this sequence version replaced gi:13699503.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 141635)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56662 AAGAAATTTGCATAACATAAACATGTTTGACATGATGAATTATGTTGCACTCTGCCCTCA 56603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56602 AAAAGATAACAGGAAATAAGAATTTAAAATATAGCGGCACATCTACAGAAGCAACAACT 56543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56482 AAGTCAATTGTATTAGAAATTGTAAAGATAGTGTTATATATCACCAATAAATTTGGAAAT 56423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525 CGAGAGTTCGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATT 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      645 ATTIAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAAT 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          765 ACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTT 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             825 CCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTA 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       585 GATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      705 CAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42.2; DB 9; Length 126010;
                                                                                                                                                                  www.jgi.doe.gov
Writshing Completed at Stanford Human Genome Center
Www.sigc.stanford.edu
Quality: Phrap Quality >-40 99.9% of Sequence;
StStinnted Total Number of Errors is 0.1.
SHS Content:
SHGC-104285 G58244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 9.7; . . 0; Mismatches 243; Indels
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="CTD-2015B23"
41323 a 21680 c 22194 g 40813 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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AUTHORS TITLE JOURNAL REFERENCE AUTHORS

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192168 bp DNA linear HTG 17-JUL-2002 Usus musculus chromosome X clone RP23-247H23, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.
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Db 118892 CACATGGAGGTATTATTACAGCCTAAACCTTCAGAAAAGGTTTGAAAATCACT 118833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 119072 AAGTCAATTGTATTAGAAATTGTAAAGATAGTGTTATATATCACCAATAAATTTGGAAAT 119013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 119012 TTAATAAAAGCCCTACTAAATAACTTTTGGTTTAAAGAATATGTTACAAAGGAAATATGG 118953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 119252 AAGAAATTIGCATAACATAAACATGTTIGACAIGAIGAATTAIGTIGCACICTGCCCTCA 119193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525 CGAGAGTICGCATIACAGAGGCAATGGGAAAGIAACGGTCCTGCAACAGAGACAAGTAIT 584
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                                                                                                                                             120535 120534: gap of 100 bp 120535 126202: contig of 5668 bp in length 126203 126302: gap of 100 bp 129159 129259: gap of 100 bp 129159 129259 131961: contig of 2856 bp in length 131962 132061: gap of 100 bp 131962 135061: gap of 100 bp 135740 138839: gap of 100 bp 135740 138839: gap of 100 bp 135840 141655: contig of 5796 bp in length 135840 141655: contig of 5796 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 243; Indels
1 92004: contig of 92004 bp in length

92005 92104: gap of 100 bp

92105 117227: contig of 25123 bp in length

117228 117327: gap of 100 bp

117328 1220434: contig of 3107 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="11"
/clone="CID-3038L12"
/clone_llb="CITD2 Human BAC"
42227 a 27391 c 27480 g 43740 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .141635
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
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HTG: HTGS_PHASE1.
Mus musculus.
Mus musculus
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Best Local Similarity
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AL807375/c
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                                                                                                                 Bitten, B., Lintcon, L. Bondan, C., Lander, E., All, A., Allen, N., Anderson, S., Barra, N., Bastlen, V., Bogoslawky, L., Boukhaalter, B., Anderson, S., Barra, N., Bastlen, V., Bogoslawky, L., Boukhaalter, B., Cincase, J., Camperlano, A., Cohang, J., Cadago, J., Carden, J., Cockep, P., Cockep, J., Colangelo, M., Colling, S., Collymore, A., Cook, A., Cook, B., Cooke, P., DeArellano, K., Dewar, K., Diaz, J., S., Dodge, S., Faro, S., Gord, S., Gord, S., Goyette, M., Carad, J., Gardoy, J., Gardoy, S., Farreta, P., Fitzhudp, W., Colling, J., Cander, Pierre, N., Indoce, B., Gord, S., Goyette, M., Carad, J., Gardoy, J., Margus, S., Hagos, B., Horton, L., Hulme, W., Illevy, I., Johnson, R., Jones, C., Landers, T., Landers, T., Landers, T., Landers, T., Landers, T., Landers, P., Margus, D., Margus, C., Macch, R., Norbus, C., Macch, R., Margus, P., Margus, D., Margus, C., Macch, R., Norbus, C., Macch, R., Marga, P., Margus, D., Margus, C., Micol, R., Norbus, C., Marga, P., Margus, P., Margus, D., Margus, C., Micol, R., Norbus, C., Retta, R., Misheck, M., Rilley, R., Rise, C., Rood, R., Phunkhang, P., Pitzre, N., Pollara, V., Roman, J., Reserty, R., Subramanian, A., Sancos, R., Schupback, R., Schupback, R., Seerry, R., Subramanian, A., Margus, T., Subramanian, A., Tavars, M., Tava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome Research
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This sequence will be replaced
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                 Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone CTD-3038L12
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Web site: http://www-seq.wi.mit.edu
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                                                                                                      2 (bases 1 to 141635)
Birren, B., Linton, L.,
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REFERENCE

Gaps

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus.
1 (bases 1 to 192168)
Plumb, B.
                                                                                                                                                                               Direct Submission
Submitted (14-7UL-2002) Wellcome Trust Sanger Institute, Hinxton,
Submitted (14-7UL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 12, 2002 this sequence Version replaced gi:21727570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 19080 bases at least Q30 consensus quality: 19080 bases at least Q40 consensus quality: 19080 bases at least Q40 consensus quality: 19080 bases at least Q30 consensus quality: 19081 bases at least Q30 consensus quality: 19081 bases at least Q30 lnsert size: 191468; sum-of-contigs at least Q20 lnsert size: 192804; 3.1% error; agarose-fp coverage: 6.94x in Q20 bases; sum-of-contigs Quality coverage: 6.89x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
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/clone="RP23-247H23"
/clone_lib="RPCI-23"
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AL831718 202801 bp DNA linear HTG 12-AUG-2002 Mus musculus chromosome X clone RP23-146020, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 202801)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 155143 AATGTTGAAAGCAGAAAATCTCAATAACATTAAAAGCCAGGTCAAAGTCTCGAGAAGAA 155084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D 155083 CACATAGTTACTTCAGGAAATCAATTTTTTTTTTTTTCATGGAAATAAGGGGATATGCTTTAA 155024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBHO 185A, UK. E-mail enquirise: hunquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk on Aug 13, 2002 this sequence version replaced gi:21953128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 AATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 CTGATAAGAACGCTCCATATGCTTTTCTTCCTTCATGGTTTTCAATAAGTCCGCTTTCA 307
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Content project name: bhild6020

Assembly program: XGAP4; version 4.5

Chamistry: Dye-terminator; 100% of reads

Consensus quality: 202322 bases at least Q40

Consensus quality: 202337 bases at least Q30

Consensus quality: 202377 bases at least Q20

Insert size: 202401; sum-of-contigs

Insert size: 202401; sum-of-contigs

Ouality coverage: 13.08x in Q20 bases; sum-of-contigs Quality

coverage: 13.69x in Q20 bases; agarose-fp
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HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 42.2; DB 2; Length 192168; Pred. No. 9.3;
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                        130257. 135973.
// Once-assembly_fragment:01769
fragment_chain:1"
136074. 138937.
// Once-assembly_fragment:01554
fragment_chain:1"
139038. 192168
// Once-assembly_fragment:02173
fragment_chain:1
chain:1"
cone_chain:1"
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57525 a 37280 c 37166 g 59494 t
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
fragment_chain:1"
130257. .135973
                                                                                                                                                                                                                                                                                                                                                                                                              3.98;
55.08;
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Best Local Similarity
Matches 83; Conserv
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                               misc_feature
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ORIGIN
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AL831718
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PKLNYTITANYPGGICLIMNINIDGPDAYPASAPLMEISNGWHFFLNSSQIAND
TVKIIQAPWNANKSDSYNWYSGIVUILGSEGGPHLLIKGLHLSPGKXEVKLYTPAISS
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/gene-"ST1855"
/note-"OW1.AADOXP24H2 percent identity: 68.590 in 156aa."
                                                                                                                                                               Technology and Example 1.0 of 100 of 
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Complete genome sequence of an aerobic thermoacidophilic cronarchaeon, Sulfolobus tokodail strain7
DNA Res. 8 (4), 123-140 (2001)
21456156
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288. 830
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                           TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266050 bp DNA linear BCT 11-OCT-2001 STG109088 BCT 00023 AP000988.1 GI:15622946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus tokodaii (strain:7) DNA.
Sulfolobus tokodaii
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD 190083 AATGTTGAAAGCAGAAAATCTCAATAACATTAAAAGCAAGGTCAAAGTCTCGAGAAGAA 190142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawarabayasi,Y., Hino,Y., Horikawa,H., Jin-no,K., Takahashi,M., Sekine,M., Baba,S., Ankai,A., Kosugi,H., Hosoyama,A., Fukui,S., Nagai,Y., Nishijima,K., Orsuka,R., Nakazawa,H., Takamiya,M., Kato,Y., Yoshizawa,T., Tanaka,T., Kudoh,Y., Yamazaki,J., Kushida,M., Oguchi,A., Aoki,K., Masuda,S., Yanagii,M., Nishimura,M., Yamagishi,A., Oshima,T. and Kikuchi,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 AATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCCAAGTTCCTGAGGAGAA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 CIGATAAGAACGGCTCCATAIGCTITICTICCTICAIGGITITCAATAAGTCCGCTITCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
             runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 202801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                      92825 92924: gap of 100 bp in length 102535 102534: contig of 9610 bp in length 102535 102534: contig of 9610 bp in length 102535 102546: gap of 100 bp in length 109247 110046: gap of 100 bp in length 112096: length 112096: contig of 7312 bp in length 112096 112155; gap of 100 bp in length 112196 202801: contig of 90606 bp in length. Location/Qualifiers
                                                                                                                                                                                          92824: contig of 92824 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110047. .112095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38425 g 61192 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 190203 AATGAACCTTAGCCTGGCCTTCATTAGAGA 190233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42.2; DE Pred. No. 9.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 ACAGTAAACCAAAAGCAGCGTACAATAGCGA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragment_chain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38445 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 55.03
nes 83; Conservative
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ORIGIN
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Matches
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AP000988/c
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AUTHORS
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KWNTAGIPVIISLIGFARPPVATVDTTVYFFUGSARFALSKROHT
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4578 6440
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GETYFLIPESLTYVEVSAILLANGESSLSLAPHTANIUGIDTUVGSILGSTREITHENEF
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EREALEFRAINMLYSSLENYYYNLGFESOALENKRMIELEKDIJOISSHKDKILELLE
EREALELEKDISKESKONVLYPLLINLYDVASGSLKYDIAVTVWDKFLSLKDYCPDVIR
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IVGEOKREKLSYTYQHLYEELVERKRYEDVIOCLKVARKYWIEDPNNLLSQIKRNYR
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/gene="sn1859"
/note="swiss_Prot:046819 percent identity: 32.759 in 58aa.
motif=prokaryotic membrane lipoprotein lipid attachment
site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Swiss_Prot:P26235 percent identity: 25.946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ST1859"
4578. . 6440
                                                                                                                  RKRQLVSLINKYLS"
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                                                                                                                                                                                                              2952. .4544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ST1860"
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FAIFSRFQILDIIISILLVVLFFLEGGGKIAKLLELIRGYVKYREIEFATIISVIFIIG
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complement(10828..12117)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC004854 98697 bp DNA linear PRI 04-JUN-2002 Homo sapiens PAC clone RP4-673M15 from 7pl3-pl1.2, complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 98697)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   575 GACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           635 AATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCT 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       695 TCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAA 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.9%; Score 42.2; DB 1; Length 266050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="239aa long hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMKISQIMETKNRTS"

complement (10064. .10783)

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complement (10064. .10783)

/gene="ST1863"

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Best Local Similarity 51.39
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||| |||
|11935 TAAAGTTAATA ||1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         755 AGGAGTCGATA 765
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AC004854.3
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VERSION
KEYWORDS
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COMMENT

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EST AA057332 (NID:g1550170) zf56all.rl"
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                                                                                                                                                                           Actual start
                                                                                                                                                                                                                                Base positions 19689 to 19719 of the submitted sequence is represented by single chemistry only.

Location/Qualifiers
1. 98697
/organism="Homo sapiens"
/db xxef="taxon:9606"
/map="7plis-pliz"
/clone="RR4-673M15"
/clone="RR4-673M15"
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The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
VECTOR: pcYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NID:98424032)"
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                                                                                                                                                                      The clone sequenced to the right is DJ0647J21. this clone is at base position 1 of DJ0673M15.
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/note="similar to 886. 922
/note="similar to 1381. 166?
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1663. .1954
/rpt_family="Alu"
1673. .1727
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/note="similar to
554. .857
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886. .1080
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/note="similar to
886. .1080
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886. .1075
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/note="similar to
177. .568
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/note="similar to
254. .568
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3239. .3404
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/rpt_family="Alu"
862. .1003
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|468. .2522
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Direct Submission
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Direct Submission
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jun 4, 2002 this sequence version replaced g1:4827328.
                                                                                                                                                                                                                                                                                     Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA 4 (bases 1 to 98697)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-MAY-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at http://www.chori.org using the method described by loannou et al., Nature Genetics 6:84-9 (1994).
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mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
University, Afforest Park Avenue, St. Louis, Missouri 63108,
7 (bases 1 to 98697)
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Missouri 63108,
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Center code: WUGSC
                                                                                                                         2 (bases 1 to 98697)
Ozanich,A. and Mead,K.
The sequence of Homo sapiens PAC clone RP4-673M15
Unpublished (2001)
3 (bases 1 to 98697)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (22-COT-1999) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
6 (bases 1 to 98697)
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Contact: sagiens@wastl.edu
contact: sagiens@wastl.edu
contact summary Statistics
Center project name: H_DJ0673M15
                                            Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                      Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 98697)
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0; Mismatches 160; Indels
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                              4241. .4542
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|11903. .???^
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/rpt_family="Alu"
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LOCUS AC108637 124767 bp DNA linear HTG 13-JUL-2002 DEFINITION Rattus norvegicus clone CH230-276G19, \*\*\* SEQUENCING IN PROGRESS

RESULT 36 AC108637/c LOCUS

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REFERENCE
MCGLOBG673 GT.1137753
MCGLOBGE TO COURT AND ADDRESS AND
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843 ATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGT 902
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                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
             Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 59885 bases at least Q40
Consensus quality: 65135 bases at least Q40
Consensus quality: 65093 bases at least Q20
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Lough Streen, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Andersen, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Andersen, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Chocken, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearchlano, K., Dewar, J. S., Dodge, S., Conko, M., Doyle, M., Ferreira, P., Felzelugh, W., Forrest, C., Gage, D., Fenestor, J., Ferreira, P., Filzelugh, W., Forrest, C., Gage, D., Gaddyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, M., Riein, J., Landers, T., Largocque, K., Lehczky, J., Levine, R., Klein, J., Landers, T., Largocque, K., Lehczky, J., Levine, R., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Norman, C., Hino, G., Connor, T., O'Donnell, P., O'Nell, D., Ollvar, T. M., Newans, L., Mihova, T., Miranda, C., Pollara, V., Raymon, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Subrerson, K., Pierreson, K., Lender, S., Theodocor, J., Tirrell, A., Travers, M., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
/protein_id="CaA83842.1"
/db_xref="G1:530493"
/db_xref="SPTREMBL:0A9087"
/translation="YFNWWNSCKTNSKVIGIVKAYNTRVGSGAMPTEIKTELANKLR
FKTRSCGSNTGRPRETGWLDLVALKYAIRVGGIDQLFLTLFDVLDTEEKIKICTAYKL
DNOIIHSIPANENDFKDV"
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Homo sapiens chromosome 1 clone RP11-711C8 map 1, LOW-PASS SEQUENCE
SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       666 CTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAAATCTTGGACAAT 725
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                                                                                                                                                                                                                                                                                                                                                          9:
                                                                                                                                                                                                                                                                                   Score 41.8; DB 1; Length 363;
Pred. No. 23;
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1 (bases 1 to 7641)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 1, clone RP11-711C8
Unpublished
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HOMO SADiens.
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Matches 146; Conservative
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Direct Submission
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EMBL, Meyerhofstr.1, 69012 Heidelberg, Germany
E-mail borkeembl-heidelberg, de
More than 870,477 bases have been sequenced by the genomic walking technique and assembled into 372 non-overlapping contigs (Accession numbers 233005 to 23336) covering 214,528 base pairs. The length of the contigs varies from 63 base pairs to 2049 base pairs with an average length of 58 base pairs. The length of the contigs varies from 63 base pairs to 2049 base pairs with an average length of 58 base pairs. The length of the contigs varies from 63 base pairs to 2049 base pairs with an average length of 58 base pairs. The length of the contigs varies from 64 base pairs and 204,437 bases (94%) produced by genomic walking. Of the latter 155,805 bases (77%) have multiple covered on both strands. There is a total of 968 ambiguous nucleotide assignments in the data set (65%) are covered on both strands. There is a total of 968 ambiguous rucleotide assignments in the data set (65%) are compared 8,868 bases of our data with Mycoplasma capricolum sequences already stored in the public databases and note less than 0.7% difference between the two data sets (77%) including ambiguous calls, insertions, deletions and mismatches).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 363)
Gillevet, P., Ally, A., Barton, F., Brenner, S.E., Clark-Whitehead, R., Bollan, M., Douglas, N., Hsu, E., Purzcki, M.S., Richter, B., Russo, S., Sartell, J., Smith, S.W., Wang, C., Williams, J. and Gilbert, W.
Direct Submission
Submitted (13-UUL-1994) Mycoplasma caprincolum Genome Project, Harvard University, Cambridge, MA 02138 Prokaryotic Genomes Project Institute for Computational Sciences and Informatics George Mason Gillevet(wranus.nchgr.nih.gov
3 (bases 1 to 363)
BOTK, P., Ouzounis, C. Casari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bork,P., Ouzounis,C., Casari,G., Schneider,R., Sander,C., Dolan,M.,
Gilbert,W. and Gillevet,P.M.
Exploring the Mycoplasma capricolum genome: a minimal cell reveals
                                                                                                                                                                                                                                BCT 10-AUG-1994
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/strain='ATCC 27347(kid)"
/db_xref="taxon:2095"
complement(<1...556)
/note="emptrified by homology to SwissProt entry swiss|P30520|PURA_HUMAN: Probablity 3.8-33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bork, P., Ouzounis, C., Casari, G., Sander, C., Dolan, M. and Gillevet, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
Entomoplasmataceae.
                                                                                                                                                                                                                                   linear
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/product="adenylosuccinate synthetase"
                                                                                                                                                                                                                                   DNA
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/transl_table=4
                                                                                                                                                                                                                         363 bp
M.capricolum DNA for CONTIG MC445.
233336
                                                  Db 95237 CCCAAAATACAGCTTGCTTTAGTTGA 95212
                                                                                                                                                                                                                                                                                                                                                adenylosuccinate synthetase.
Mycoplasma capricolum.
Mycoplasma capricolum
                       903 GTCGAGCTAAAGCTTGCTTCTTTA 928
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AUTHORS
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AUTHORS
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34108: contig of 774 bp in length 14982: contig of 774 bp in length 14982: contig of 774 bp in length 14982: contig of 781 bp in length 14983: gap of 100 bp in length 14971: gap of 100 bp in length 17691: gap of 100 bp in length 17692: gap of 100 bp in length 17692: gap of 100 bp in length 17692: gap of 100 bp in length 17680: gap of 100 bp in length 17691: gap of 100 bp in length 17651: gap of 100 bp in length 17691: gap of 100 bp in length 17691: gap of 100 bp in length 17691: gap of 1765 bp in length 17691: gap of 1765 bp in length 17691: gap of 1760 bp in length 176000 bp in length 176000 bp in leng
                                                                                         22762 22761: gap of 100 bp 100 bp 22562 22761: gap of 1782 bp in length 23644 23642: contig of 783 bp in length 23644 23642: contig of 783 bp in length 23644 2426: contig of 783 bp in length 2427 24257 contig of 771 bp 2427 25297: contig of 771 bp 25297: contig of 771 bp 25297 25297: contig of 799 bp in length 26197 26296: gap of 100 bp 26197 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 27187 271
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21785: cont., 100 cr
22661: contig of 776 bp in leny.
22651: contig of 776 bp in leny.
100 bp ... of 782 bp in length
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19032 49812: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36817 37591: contig of 37592 37691: gap of 137692 38467: contig of
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40185 40284:
40286 41912
41192 41191:
41194 42042:
4284 42924 42924
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44581 44681:
44581 44681
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38568 3933
39337 39436:
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                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                for
                        Submitted (28-FEB-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, Ma 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This record contains 87 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. Will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * 13890 13889; contig of 756 bp in length

* 13890 13889; contig of 756 bp in length

* 13990 14814; contig of 825 bp in length

14815 14914; gap of 100 bp

15683 15782; contig of 778 bp in length

15783 16561; contig of 779 bp

16562 16661; qan of
                                                                                                                                                                                                                                       Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
Contact: project Information
Center project name: L6722
Center clone name: 711_C_8
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100 bp
of 792 bp in length
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12249 13033: contig of 785 bp in length
13034 13133: gap of 100 bp
13134 131893: contig of 756 bp in length
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764 bp in length
100 bp
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f 803 bp in length
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f 776 bp in length
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if 783 bp in length
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[766 bp in length
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01 7000: gap of 100
11 7784: contig of 78
5 7884: gap of 100
7 8766: contig of 76
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1856 2461; contig of 70.
2462 2561; gap of 6.
3365 3464; gap of 100.
3465 4249; contig of 70.
3465 4249; contig of 70.
3465 4249; contig of 70.
3465 1429; contig of 70.
3485 1480; contig of 70.
3486 117; gap of 100.
3486 117; gap of 100.
3486 118; contig of 70.
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41: gap of 7
6017:
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17: gap of 7
6900:
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20919: cont
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17553 18316: con
18317 18416: gap of
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19193 19292: gap of
19293 20055: con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be preserved.
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AL391883 126371 bp DNA linear PRI 15-NOV-2001
Human DNA sequence from clone RP11-91K11 on chromosome 1, complete
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* consists of 8 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 18478 18577: contig of 18477 bp in length
* 18578 20885: contig of 2308 bp in length
* 20886 20985: gap of unknown length
* 20886 20985: gap of unknown length
* 25967 26066; gap of unknown length
* 25967 26066; gap of unknown length
* 25967 26066; gap of unknown length
* 25969 20001; gap of unknown length
* 25060 22759: gap of unknown length
* 3560 22759: gap of unknown length
* 35862 82961: gap of unknown length
* 3682 82961: gap of unknown length
* 3682 30821: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 562 GTCCTGCAACAGAGACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   622 AAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAG 681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.8%; Score 41.8; DB 2; Length 115666; 12.3%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="053NBb0009c07"
/note="japonica cultivar-group"
24957 c 25425 g 31751 t 1043 others
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC105744 115666 bp DNA linear HTG 25-APR-2002 Oryza sativa chromosome 10 clone OSJNBb0009C07, *** SEQUENCING IN PROGRES ***, 8 ordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-JAN-2002) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA 3 (bases 1 to 115666) Buell, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-APR-2002) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, M D 20850, USA
00 Apr 25, 2002 this sequence version replaced gi:20153307.
* NOTE: This is a "working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 656 GCTTGATGGTCTAAGAAATCAGAAAGGAGCCGAAAGCTTCTAAGTAATCAAGAAAAAT 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                716 CTTGGACAATAGCTTTTCCATAGAGAAACCGTGAGGAAAGGAGTCGATAACTTC 775
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3.8%; Score 41.8; DB 2; Length 76
al Similarity 46.3%; Pred. No. 13;
100; Conservative 0; Mismatches 116; Indels
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         100 bp
f 780 bp in length
100 bp
f 763 bp in length
f 776 bp in length
                                                                                                                                                                                                                                                       83: gap of 100 bp 56757: contig of 774 bp in length
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54244: gap of
55007: conti
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Submitted (25-APR-
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Oryza sativa.
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AC004153 156060 bp DNA linear HTG 12-AUG-2000 Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 110223 CAAAAAAAAAAAATAATAATGATGATAATTCAGATATGGAATGGGAAAATTTCAATCCAC 110282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              748 TGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAAGGGAGTGCTTACAACAGCCAT 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   808 ATCAGIGGAGCAACCIICCCITIGAITCIITGATAAAGACAAGAAGAAGAAGAAAA 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           628 TGITICTAATICGAAGAATITAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACC 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568 CAACAGAGACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATG 627
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 156060)
Manan, R.W., Fung, E.L., Qin, F., Rowley, D., Mao, J., Tamaki, T., Kurdi, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the daps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Aug 12, 2000 this sequence version replaced gi:8810454.
** NOTE: This is a "working draft' sequence. It currently ** consists of 2 contigs. The true order of the pieces ** is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2." (bases 1 to 156060)
Hyman, R.W., Oln, F., Fung, E.L., Conway, A.B. and Davis, R.W.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 156060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102169: contig of 102169 bp in length 102369: gap of unknown length 156060: contig of 53691 bp in length.
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/db_xref="taxon:5833"
/chromosome="12"
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ilarity 45.3%; Pred. No. 12
Conservative 0; Mismatche
                                                                                                                                                                                                                                   PROGRESS ***, 2 unordered pieces
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1. .156060
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Plasmodium falciparum
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Db 45252 TACACAGTCTTGC 45264
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                                                                                                                                      Direct Submission

Direct Submission

Submitted (15*NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. F-mail enquiries.

Cambridgeshire, CB10 18A, UK. P-mail enquiries.

Runduery@aanger.ac.uk Clone requests: clonerequest@anger.ac.uk

Our Nov 16, 2001 this sequence version replaced gi:15131273.

During sequence assembly data is compered from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-

10); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw; SWISSERF; T:. TREMBL; We: WoRNPEP! Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Porojects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group Further information can be found at

REIL-/www.sanger.ac.uk/Porojects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group Further information can be found at

REIL-/www.sanger.ac.uk/Porojects/Celegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1 of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone strings be shorter because we sequence overlapping sections only once, except for a short overlap.
The true right end of clone RPI1-91KII is at 126371 in this sequence. The true left end of clone RPI1-460G22 is at 31870 in this sequence. The true left end of clone RPI1-460G22 is at 31870 in this sequence.
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      Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 132;
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/clone_lib="RPCI-11.1"
_27351 c 28154 g 35512 t
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47.8%; Pred. No. 12
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      Bukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 126371)
Ellington, A.
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                            63911: contig of 6774 bp in length 64011: gap of 100 bp
54822 54921: gap of 100 bp
54922 57037: contig of 2116 bp in length
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/note="assembly_fragment:00785
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2247. 5841:
7.note="assembly_fragment:00201
fragment_chain:1"
5942. 8400
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/note="assembly_fragment:00968
fragment_chain:4"
47741. .52469

    .157515
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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/clone="RP11-97J18"
/clone_lib="RPCI-11.1"
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151873 151972: gap of
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57138 63911: conf
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Direct Submission

Submitted (21-0CT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest(sanger.ac.uk)

On Oct 26, 2000 this sequence version replaced gi:10716373.
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Sequencing vector: plasmid; L08722; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 141371 bases at least Q40
Consensus quality: 151757 bases at least Q20
Insert size: 154715; sum-of-contigs
Insert size: 174718; sum-of-contigs
Coulty coverage: 3.16x in Q20 bases; sum-of-contigs Quality
Coverage: 3.01x in Q20 bases; agarose-fp
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40092: contig of 2452 bp in length
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52469: contig of 4729 bp in length
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contig of 2252 bp in length
Db 110523 ACAAAAATAAAAATATGAATCATACATCTT 110555
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AL391598.3 GI:11023953
HTG; HTGS_PHASE1; HTGS_DRAFT.
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47741 52
52470 52565
52570 54
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                                                                                                                                                               RESULT 42
AL391598/c
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VERSION
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SOURCE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 194247)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 13143 AAGGAAATATAAACAAATATTGTATAATAGGTATTGACACACATACTAAAGAATTTAAGG 13202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 0% of reads
Chemistry: Dye-terminator; 0% of reads
Chemistry: Dye-terminator ET-amersham; 3% of reads
Chemistry: Dye-terminator ET-amersham; 3% of reads
Chemistry: Dye-terminator ET-amersham; 3% of reads
Chemistry: Dye-terminator Big Dye: 0% 0% of reads
Consensus quality: 194218 bases at least Q40
Consensus quality: 194247 bases at least Q40
Consensus quality: 194247 bases at least Q20
Insert size: 194247; sum-of-contigs
Insert size: 194347; sum-of-contigs
Coulity coverage: 10.76x in Q20 bases; sum-of-contigs Quality
coverage: 12.13x in Q20 bases; sum-of-contigs Quality
                                                                HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment:05625"
52994 a 42433 c 43263 g 55557 t
                                                                                                                                                                                                                                                                                                                                                                                      Contact: humquery@sanger.ac.uk
------ Project Information
Center project name: bA460G22
                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Statistics
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/db_xref="taxon:9606"
PROGRESS ***, in ordered pieces. AL358253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                AL358253.14 GI:21998163
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Summary
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                                                                                       Homo sapiens.
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3.8%; Score 41.8; DB 2; Length 157515;
Best Local Similarity 47.8%; Pred. No. 12;
Matches 121; Conservative 0; Mismatches 132; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2824 others
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[28401. 133358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="assembly_fragment:00671"
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AL358253
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FEATURES
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15. Upbases 1 to 200279)
15. Birren, B. Lintcon, L. Nusbaum, C., Lander, E., Ali, A., Allen, N.,
15. Anderson, S., Barra, J. Campoplano, A., Chango, J., Chazaro, B.
16. Morderson, S., Barra, J. Campoplano, A., Chango, J., Chazaro, B.
16. Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Caook, A.,
16. Cooker, P., Derkellano, M., Dellins, S., Collymore, A., Cook, A.,
16. Cooker, P., Pritzhugh, W., Gag, D., Galagan, J., Gardon, S.,
16. Tide, S., Gorgette, M., Grehm, L., Cohnson, R., Lones, C.,
16. Lianderson, R., Mells, C., Larcque, K., Lamazares, N.,
16. Mordonald, P., Marquis, N., Matthews, C., McCartty, M.,
16. Mordonald, P., Margor, J., Marquis, N., Matthews, C., McCartty, M.,
16. Mordonald, P., Margor, J., Marquis, N., Matthews, C., McCartty, M.,
16. Mordonald, P., Margor, J., Marquis, N., Matthews, C., McCartty, M.,
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16. Mordonald, P., Margor, J., Marquis, N., Matthews, C., McCartty, M.,
16. Mordonald, P., Margor, J., Margor, M., Margor, P., Spencer, B., Stanger-Thomann, N., Scolanovic, N.,
16. Rettis, R., Rabback, M., Rilley, R., Rise, C., Rogov, P., Roman, J.,
17. Taphan, K., Travers, M., Travers, M., Traylin, J., Ve, M.J., Young, G.,
18. Sepecier, B., Stanger-Thomann, N., Scolanovic, N.,
18. Sepecier, B., Stanger-Thomann, D., Ye, M.J., Young, G.,
19. Lindon, J., Zamber, L., Zimmer, A. and Zody, M.
19. Lindon, J., Zamber, L., Zimmer, A. and Zody, M.
19. Sanderson, S., Barra, N., Bastien, V., Bloom, T., Margor, Dearster, R.,
19. Chases it of 200279)
10. Nusbaum, C., Traylin, M., Margor, D., Candagan, J., Gardor, P.,
10. Gardor, S., Goyette, M., Gardor, Diaza, V.,
10. Mordon, S., Goyette, M., Gardor, J., Onnson, R.,
10. Margor, P., Margor, M., Margor, S., Endocare, S., Schubback, R.,
10. Gardor, S., Goyette, M., Gardor, S., Collymore, A.,
10. Margor, P., Margor, M., Margor, S., Margor, D., Margor, S., Margor, M., Margor, M., Margor, M., Trayler, R., Margor, M., Trayler, R., Margor, J., Margor, P., Margor, R., Trayle
                                                                                                                                                                                       AC109165 200279 bp DNA linear HTG 25-APR-2002
Mus musculus clone RP23-30B3, WORKING DRAFT SEQUENCE, 16 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalli: Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2002/9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-30B3
                                                                                                                                                                                                                                                                              AC109165
AC109165.3 GI:20303726
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus.
Db 13383 TACACAGTCTTGC 13395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                    LOCUS
DEFINITION
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VERSION
KEYWORDS
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AC109165/c
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ityskediiesnyvdssynnnnnnssnynnunisiekkiredikpeptyqpi
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DDEMILEAVQEATINHTIVIKHDANLNAHWSNSFESGNIVITFKSVTNTNDVQTFDFIK
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (31-MAY-2002) Genome Analysis, Institute of Molecular Submitted (31-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany Copy Bredictions from GeneID may contain errors. Further Information is available from TMB Jena, Department of Genome Analysis available from TMB Jena, Opfortellum, of Genome Analysis and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostellum/project.shtml
HTG; HTGS_PHASE2.
Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
Eukaryota (pases 1 to 27785)
Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K.,
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                   Submitted (05-APR-2002) Genome Analysis, Institute of Molecular Submitted (05-APR-2002) Genome Analysis, Institute of Molecular Submitted (05-APR-2002) Genome 3 (bases 1 to 27785)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agency: Deutsche Forschungsgemeinschaft (DFG).
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
                                                                                                                                                                    Sequence and Analysis of Chromosome 2 of Dictyostelium Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(6336, .6630,6711, .11386,11471, .14377)
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/db_xref="GI:21281373"
                                                                                                                                                                                                                            The Dictyostelium Genome Sequencing Consortium 2 (bases 1 to 27785)
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join(2445..2467,2559..3372)
/note="ORF_ID:dd_01250"
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/note="ORF_ID:dd_01248"
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DNLSAVKRALKSSSDWSIDELSLETVPRYADDLKNSFGHIFAGIVEKVAANLARKCA
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CATPOGEVYSWGLSVFGOLGHGNKSYLHPRKIOGPVELBERIAQVOGSNFTWNRS
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HTIVYTDENEVYQWGWGSSGALGLGNKRFQLVPQLITSLSGEEIASITAGEKHTIVVR
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FHSLALPDMGKYSWGRSKGQLGIGGSGLDIGSTNGLIEMPRLSSQRIEG
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                                                                                                              819 AACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(21354 .23054,23166 .23375))
/note="ORF_ID:dd_00710"
/codon_start=1
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0; Mismatches 204; Indels
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/note="ORF_ID:dd_00704"
/codon_start=1
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/protein_id="AAM45266.1"
/db_xref="GI:21281379"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"hypothetical protein"
/protein_id="AAM45265.1"
/db_xref="GI:21281378"
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/note="ORF_ID:dd_00709"
/codon_start=1
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q δ

us-09-438-185a-1\_1199590\_1200675.rge

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note="11PBa repeat: matches -1551, .-1343 of consensus" [9328, .19373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="34_copies 2 mer tt 66% conserved"
32814. 32972
/note="118416 repeat: matches 6010. .6152 of consensus"
complement(34432. .34805)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //note="Natusg repeat: matches 1. .299 of consensus"
22292. .23161
//note="Charlie3 repeat: matches 53. .897 of consensus"
23667. .23603
                                                                             /note="2 copies 40 mer 90% conserved"
4468. .4856
/note="LIMEL repeat: matches 5768. .6163 of consensus"
4891. .5808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 363. .1016 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1292-17592

7note="17 copies 2 mer ta 88% conserved"

13024. 16519

7note="LIPS repeat: matches 1263. 5781 of consensus"

16520. 16796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lips repeat: matches -265. .1263 of consensus" .18819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anote-"WERSA repeat: matches 151. .188 of consensus" 26883. .27175
Anote-"Alusx repeat: matches 1. .295 of consensus"
                                                                                                                                                                  4891. .5809
/notc="LIM4 repeat: matches 4494. .5479 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29184. .29623
//note="11.2 repeat: matches 1472. .1940 of consensus"
29945. .30376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L2 repeat: matches 2271. .2748 of consensus" 31.294. .31361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27691. 28135
/note="12 repeat: matches 2268. .2744 of consensus"
28160. .28329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L2 repeat: matches 1942. .2132 of consensus"
8334. .28945
                                                                                                                                                                                                                                                                                                                                                                                             2 repeat: matches 2341. .2736 of consensus"
12171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2 repeat: matches 2699. .2746 of consensus"
12962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Alusx repeat: matches 1. .289 of consensus"
[6797, .18337
                                                                                                                                                                                                              5894. .6201
/note="AluY repeat: matches 1. .296 of consensus"
6235. .7203
                                                                                                                                                                                                                                                                    5235. ,7203
/note="LTR5 repeat: matches 1. ,969 of consensus"
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/note="MER4D rej
29184.
complement (2145.
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28949. 29170
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18333. 1881
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misc_feature
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Direct Submission

Direct Submission

Submitted (15-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15s, (15-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15s, (15-FEB-2000) Sanger ac.uk

requests: clonerequest@sanger.ac.uk

On Feb 7, 2000 this sequence version replaced gi:678223.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the ortsponding to the overlapping clone, as we submit sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6 constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at thip://www.sanger.ac.uk/HGP/Chr6 RPI-39M18 is from the library RPC1-1 constructed at the Roswell Park Canner Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em.; EMBL; Sw.; SWISSPOTY; Tr.; TREMBL; WP:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                               ALI36130 69674 bp DNA linear PRI 02-MAR-2000 thuman DNA sequence from Clone RPI-39M18 on chromosome 6q26-27. Contains part of the PDB10A gene for phosphodiesterase 10A, ESTS, STS, and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORANT: This sequence is not the entire insert of clone RP1-38MH8 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone RP1-39MH8 is at 1 in this sequence. The true left end of clone RP1-39MH8 is at 69575 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 69674)
Laird, G.
                                              /note="MIR repeat: matches 158. .206 of consensus" 1502. .1595
                              879 ATTCTAAAATAGAAAIGCATTTGTGTCGAGCTAAAGCTTGCTTCTCTTTATTTTCCTTTT
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/note="47 copies 2 mer tt 61% conserved"
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/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                           AL136130
AL136130,7 GI:6911361
HTG; PDE108; phosphodiesterase.
Homo sapiens.
Homo sapiens
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/clone_llb="RPCI-1"
57. .110
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Anote-"Light repeat: matches 2592. 2665 of consensus"

Anote-"12 repeat: matches 2592. 2265 of consensus"

Anote-"12 repeat: matches 2592. 2265 of consensus"

Anote-"12 repeat: matches 2220. 2414 of consensus"

Anote-"12 repeat: matches 3. 300 of consensus"

Anote-"14 repeat: matches 1. 33 of consensus"

Anote-"14 repeat: matches 1. 371 of consensus"

Anote-"14 repeat: matches 1. 372 of consensus"

Anote-"14 repea
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                                                                                                           Joseph 12 repeat: matches 1013. .2076 of consensus. 37262. .37446

Anote-"MSTB repeat: matches 202. .422 of consensus. 37788. .37867. .3788. .37867. .38849. .38849. .38849. .38849
/note-"match: GSS: Em:AQ129042"
34047. .35639
.7hote-"L1 repeat: matches 3078. .3788 of consensus"
35657. .36708
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/note="match: GSS: Em:AQ061408"
51996. .52051
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                                                                                                                                                                                                                                                                                                                                   68183 GCTCTACTACTGTATAAATATATAAAAACTTTAATTAGGACAAGCATCTTTTAGAGGCTA 68124
                                         68243 TACAATATCAAATTTATCTATAATATCCAGTGTTGAACTGAGTCTCTAAGATTAATTCCT 68184
658 TTGATGGTCTAAGAAATCAGAAAGGAGCCGAAAGCTTCTAAGTAATCAAGAAAAAATCT 717
                                                                                                                                        718 TGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCG 777
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Mammalia; Eutheria;
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AC115405
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COMMENT

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6560 others
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/db_xref="taxon:10116"
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NOTE: This is a 'working draft' sequence. It currently consists of 50 configs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:19549112.

Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center cales ECM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: GN2A
Center clone name: CH230-74P14
                                                                                                                                                       Submitted (13-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 103337)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid;
Sequencing vector: plasmid;
Assembly program: Phrap; version 0.990329
Consensus quality: 50186 bases at least Q40
Consensus quality: 53149 bases at least Q30
Consensus quality: 55140 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1068: contig of 1068 bp in length
1168: gap of unknown length
2333: gap of unknown length
2433: gap of unknown length
3343: gap of unknown length
3543: gap of unknown length
4555: contig of 1012 bp in length
4555: contig of 1012 bp in length
4555: contig of 1012 bp in length
4554: gap of unknown length
7409: contig of 102 bp in length
7409: contig of 102 bp in length
7509: gap of unknown length
7509: gap of unknown length
1789: gap of unknown length
1789: gap of unknown length
1189: gap of unknown length
1189: qap of unknown length
1185: contig of 1075 bp in length
1185: contig of 131 bp in length
1455: contig of 1831 bp in length
1455: contig of 1889 bp in length
16183: contig of 1889 bp in length
16183: contig of 1889 bp in length
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Worley, K.C.
Direct Submission
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site: http://www.sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 13 clone RP11-78L16, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.

AL334818
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 148549)
Burton,J.
                                                                                                                                       57537 TAAAAGGTCCAGAGGAAATTTCCCAAATTCAGAAAATCAGATATGAAAAGGTAGACGTAG 57596
                                                                                                                                                                                                                                                                                                91774 TTAGCCAGACCAAAAAAGAGAGAGAGAGACCCAAATAAACAAAACCAGAGATAAAAAAG 91833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91714 ACAAAACATCAATGAAACAAAAATTGGTTTTTTTAGAAGATAAATTATGGACAAACCA 91773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquirles: humquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk
On Sep 9, 2000 this sequence version replaced gi:9581627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   729 TITICCATAGAGAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAGG 788
                                                                                                             678 AAAGGAGCCCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
                                                                                                                                                                                           738 GAGAAAACCGTGAGGAAAGGAGTCGATACCATAAAATTCCGATTAAAAAAGGGGAGTGCTTA 797
                                                                                                                                                                                                                                                                         798 CAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTTTTGATAATGACAGAAGATGAA 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       669 AGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGC 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                           Gaps
                                  DB 2; Length 103337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS AL353694 Accession AL353694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41.6; DB 2; Length 110000;
Pred. No. 14;
0; Mismatches 69; Indels 0;
                                  Score 41.6; DB 2; Length 1
Pred. No. 14;
0; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91834 GAGACATTACAACTGATACCACAGAAATTCAA 91865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 789 GAGTGCTTACAACAGCCATATCAGTGGAGCAA 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL354818.3 GI:10039795
HTG; HTGS_PHASE1; HTGS_CANCELLED.
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310000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence split into 4 fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.8%;
                                Query Match 3.89
Best Local Similarity 51.69
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.89
Best Local Similarity 54.69
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Begin
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                                                                                                                                                                                                                                                                                                                                                                                           57657 CAAA 57660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fragment Name
AL353694_0
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AL353694_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 48
AL353694_1
WPCOMMENT
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AL354818/c
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DEFINITION
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Center code: SC

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Assembly program: X6744; version 4.5

Assembly program: X6744; version 4.5

Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consenus quality: 133724 bases at least Q40

Consenus quality: 133724 bases at least Q30

Consenus quality: 142544 bases at least Q30

Insert size: 146149; sum-of-contigs

Insert size: 153445; S.9% error; agarose-fp

Quality coverage: 3.00x in Q20 bases; sum-of-contigs Quality

coverage: 3.00x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will.
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contig of 22568 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4894: contig of 4894 bp in length
4895 4994: gap of
4995 16378: contig of 11384 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18590; gap of 1900 bp 212846; contig of 3256 bp in length 21946; gap of 100 bp 25998; contig of 5052 bp in length 27098; gap of 100 bp 29374; contig of 2276 bp in length
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3127 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oontig of 8803 bp in length contig of 6456 bp in length
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5661 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72: gap of 100 bp
52389: contig of 4017 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of 100 bp 96: contig of 9907 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196: gap of 100 bp 107828: contig of 5332 bp in length
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contig of 4979 bp in Length
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70819: contig of
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32601: contig of
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Contact: humquery@sanger.ac.uk
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.o: gap of
148549: ^^
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118187: ~
287
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130709: c...
1800
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143470: cc
3570
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112698: cont
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38362: con+
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139531; cont
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FEATURES

| BASE COU<br>ORIGIN<br>Query<br>Best L   | Matche<br>Qy 59   | Db 3108      | 31  | 2y 71   |              | 060 qq  | Db 3084   | RESULT S<br>AC046180<br>LOCUS  | DEFINIT   | VERSION<br>KEYWORDS<br>SOURCE<br>ORGAN | REFERENC<br>AUTHOI  | AUTILE<br>JOURNI<br>REFEREN<br>AUTHOI  |  |   |  |   |  |   |  | TITLE   | COMMENT   |
|---|---|--------------|---|---|--------------|---|---|--|---|--|---|--|--|---|--|---|--|---|--|---|---|
|   |   |              |   |   |              |   |   |  |   |  |   |  |  |   |  |   |  |   |  |   |   |
| Location/Qualifiers 1148549 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome=113" /clone="RP11-78L16" | /clone_lib="RPCI-11.1" 1. 4894 /note="assembly_fragment:01091 |              | _ragumin_cnain:1<br>16490<br>/note="assembly_fragment:00411 | Iragment_chain:1" IRS9121846 Fines21846 fines21846 fines21846 |              | rragment_cnain:1<br>2709929374<br>/note="assembly_fragment:00091<br>fragment_chain:2" | 2947532601<br>/note="assembly_fragment:00282<br>fragment_chain:2" | 3270238362<br>/note="assembly_fragment:00258<br>fragment_chain:3"<br>39463 A9777 | /note="assembly_fragment:00607<br>fragment_chain:3" | 40.7                                   | 62497. 67828<br>/note="assembly_fragment:01219<br>fragment_chain:5" | 6/329/0819<br>./note="assembly_fragment:00679<br>fragment_chain:5"<br>7092079571 | /note="assembly_tragment:00075"<br>7967283474<br>/note="assembly_fragment:00377" | 8357590030<br>7.hoto-massembly_fragment:00645"<br>90131112698 | /note="assembly_tragment:00b85"<br>112799. 118187<br>/note="assembly fragment:00757" | 118288. 122327<br>/note="assembly_fragment:00791" | 122428. 130709<br>//note="assembly_fragment:00937"<br>130810. 132827 | /note="assembly_fragment:01022"<br>132928 .136248 | /note="assembly_iragment:011b0"<br> 136349139531<br> /note="assembly fragment:01267" | 139632143476<br>/note="assembly_fragment:00779<br>frammont chain.6" | 1139ment_chain;<br>113571148549<br>/note="assembly_fragment:00210<br>fragment_chain:6<br>clone_end:T7 |
| JRES<br>SOUTCE  | misc_feature  | misc_feature | misc_feature  | misc_feature  | misc_feature | misc_feature  | misc_feature  | misc_feature   |   | misc_feature                           |   | misc_feature<br>misc_feature   | misc_feature   | misc_feature<br>misc_feature                                  | misc_feature   |   | misc_feature   |   | misc_feature   | misc_feature  | misc_feature  |

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Updates 1 to 215896)

Birren, L. Intron, L. Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Birren, B., Lintcon, L.,
Barnán, J., Bastien, V., Beda, F.,
Boguslavkíy, L., Baldwin, J., Barnán, N., Bastien, V., Beda, F.,
Boguslavkíy, L., Baldwin, J., Barnán, N., Burkett, G.,
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Itevine, R., Lieu, G., Locke, K., Mandcand, P., Marquis, N.,
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Stange-Thomann, M., Schauer, S., Severy, P., Spencer, B.,
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Trastesye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J.,
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Homo sapiens chromosome 15 clone RP11-465J17 map 15, WORKING DRAFT
SEQUENCE, 27 unordered pieces.
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 AGGATGAATGGAAACACCAGACATTATTTTAAGAAGTATTAAGGCTCTTATACATAGTT 30965
                                                                                                                                                                                                                                                                                                                                                                      717
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                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 TTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 148549; Score 41.6; DB 2; Length 148549; Local Similarity 48.6%; Pred. No. 13; Local Similarity 60; Mismatches 149; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 T-GATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAAT 888
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43637 a 27779 c 27991 g 46687 t 2455 others
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1 (bases 1 to 215896)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone RP11-465JI?
Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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115010 115099: gap of 100 bp 111 rengum 115010 115099: gap of 100 bp 115010 115032 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115010 115
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NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1012 1111: qap of 1011 bp in length 1012 1111: qap of 100 bp 2013 2033: contig of 10152 bp in length 2033 2033: contig of 1360 bp in length 4193; qap of 100 bp 2033: contig of 1360 bp in length 4194 392 qap of 100 bp p in length 7089 7088: contig of 100 bp in length 7089 7088: contig of 100 bp in length 7089 7088: contig of 2315 bp in length 7080 7089: qap of 100 bp p in length 7080 7089: qap of 100 bp p in length 7080 7089: qap of 100 bp p in length 7080 7089: qap of 100 bp p in length 10305 10404: qap of 100 bp p in length 10305 10404: qap of 100 bp p in length 10305 10404: qap of 100 bp p in length 10305 10404: qap of 100 bp p in length 10305 10405: qap of 100 bp p in length 10305 10405: qap of 100 bp p in length 10379 23519: contig of 2334 bp in length 10379 23519: contig of 4231 bp in length 10379 2352 23519: contig of 4333 bp in length 10393 3132: qap of 100 bp 200 bp 100 bp 200 700 pp 200
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54497: contig of
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77167: contig of
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77168 77267:
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| quence 366, App<br>quence 13312, A<br>quence 1, Appi;<br>quence 244, Appi;<br>quence 244, Appi;<br>quence 246, Appi;<br>quence 26, Appi;<br>quence 26, Appi;<br>quence 526, App;<br>quence 526, App;<br>quence 526, App;<br>quence 526, App;<br>quence 526, App;<br>quence 626, App;<br>quence 626, App;<br>quence 626, App;<br>quence 626, App;<br>quence 626, App;<br>quence 634, Appi;<br>quence 84, Appi; | Sequence 84, Appl Sequence 115, Appl Sequence 115, Appl Sequence 1234, Appl Sequence 1, Appl Sequence 2, Appl Sequence 1, Appl Sequence 2, Appl Sequence 3, Appl Sequence 3, Appl Sequence 5, Appl Sequence 333, Appl Sequen  |
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| 9-813-790-36<br>9-815-242-12<br>9-84-0-242-12<br>9-84-0-242-12<br>9-861-36-38<br>9-765-9-37-6<br>9-768-9-37-6<br>9-768-9-37-6<br>9-768-9-37-6<br>9-768-9-37-6<br>9-78-9-85-9-85<br>9-78-9-85-9<br>9-818-6-5<br>9-818-6-5<br>9-818-6-5<br>9-818-6-5<br>9-818-6-5<br>9-818-6-5<br>9-818-6-5<br>9-818-6-5<br>9-818-6-5<br>9-818-6-5<br>9-91-818-84<br>9-991-818-84<br>9-991-818-84<br>9-991-818-84<br>9-991-818-84<br>9-991-818-84   | US-00-980-722-84 US-09-980-722-84 US-09-980-722-84 US-09-980-727-84 US-09-980-732-84 US-09-980-732-84 US-09-980-732-84 US-09-990-442-84 US-09-990-442-84 US-09-990-442-84 US-09-990-456-84 US-09-990-456-84 US-09-990-752-84 US-09-990-752-84 US-09-990-725-84 US-09-990-725-84 US-09-980-725-691-35 US-09-9815-242-1304 US-09-9815-242-1304 US-09-815-242-12209 US-10-072-903-410-41 US-09-817-512-88 US-09-817-512-88 US-09-817-512-88 US-09-817-512-88 US-09-817-512-88 US-09-817-512-88 US-09-817-512-88 US-09-817-88-304 US-10-007-270-28  |
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RESULT 1
US-10-154-674-8
Sequence 8, Application US/10154674
Publication No. US20020192694A1
GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: LIVENTION: No. US20020192694A1el Human Hydroxylases and Polynucleotides
FILE REFERENCE: LEX-0352-USA
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OUS-09-815-242-1143
OUS-09-815-242-1145
OUS-09-815-242-11753
OUS-09-815-242-11753
OUS-10-013-297-6
OUS-10-033-297-6
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OUS-10-033-297-6
OUS-10-033-297-102
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OUS-10-033-297-102
OUS-10-033-297-1132
OUS-10-06-867-1132
OUS-10-06-867-1132
OUS-10-078-99-115-242-1132
OUS-10-078-99-115-242-1132
OUS-10-078-99-116-132
OUS-09-735-705-369
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OUS-09-735-705-369
OUS-09-815-242-11522
OUS-10-078-99-117
OUS-09-815-242-11522
OUS-09-735-705-369
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OUS-09-815-242-11522
OUS-09-735-705-369
OUS-09-735-705-369
OUS-09-815-242-11522
OUS-09-735-705-369
OUS-09-735-75-879-17
OUS-09-735-73-13345
OUS-09-735-73-13345
OUS-09-735-73-13345
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Sequence 12620, A
Sequence 169, Appl
Sequence 9, Appli
Sequence 55, Appl
Sequence 55, Appl
Sequence 1345, A
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Sequence 2, Appli
Sequence 113, App
Sequence 113, App
Sequence 10490, A
Sequence 145
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Sequence 39, Appl
Sequence 39, Appl
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PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 485
TYPE: PRT
ORGANISM: homo sapiens
US-10-154-674-6
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US-10-154-674-6
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                                                                                                                                                        Query Match
Best Local S
Matches 67
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Publication No. US20020192694A1
GENERAL INFORMATION
APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Hu, Yi
TITLE OF INVENTION: No. US20020192694A1el Human Hydroxylases and Polynucleotides
FILE REFERENCE: LEX-0352-USA
CURRENT APPLICANTION NUMBER: US/10/154,674
CURRENT FILING DATE: 2002-05-23
CURRENT FILING DATE: 2002-05-23
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CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/294,076
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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Best Local S
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229 IEKVQALPSKKQRIQTIQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHA
                                        282 FLAGLAYRVFHCTQYIRHGSDFLYTPEPDTCHELLGHVPLLADPKFAQFSQEIG-----
                                                           169 YLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKV 228
                                                                                              222 LSKLYPTHACREYLKNFPLLTKYCGYREDNVPQLEDVSMFLKERSGFTVRPVAGYLSPRD
                                                                                                                           117 LWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYYPVSGFVAPHQ 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 FLAGLAYRVFHCTQYIRHGSDPLYTPEPDTCHELLGHVPLLADPKFAQFSQEIG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 LSKLYPTHACREYLKNFPLLTKYCGYREDNVPQLEDVSMFLKERSGFTVRPVAGYLSPRD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 IEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHA
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al Similarity 26.2%;
67; Conservative 4
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Similarity 26.2%; Pred. No. 5.4e-13;
67; Conservative 42; Mismatches 104;
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; Pred. No. 5.4e-13;
42; Mismatches 104;
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                                                                                                                                                                               Length
                                                                                                                                                        Indels 43;
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104 RNLW---YRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHF 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 RVRPVAGYLSARDFLAGLAYRVFFCTQXVRHHADPFYTPEPDTVHELMGHMALFADPDFA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLI------ 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 LSDKACVKAFDPKTTCLQECLITIFQEAYFVSESFEEAKEKMRDFAKSITRPFSVYFNPY 450
                                                                                                                                                                                                                                                      117 LWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYYPVSGFVAPHQ 168
                                                                                                                                                                                                                                                                                                227 LSKLYPTHACREYLKNFPLLTKYCGYREDNVPQLEDVSMFLKERSGFTVRPVAGYLSFRD 286
                                                                                                                                                                                                                                                                                                                                                                                           229 IEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHA 288
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                                                                                                                                                                                                           43;
                                                                                                                                                        Match 11.5%; Score 216.5; DB 9; Length 490; Local Similarity 26.2%; Pred. No. 5.5e-13; les 67; Conservative 42; Mismatches 104; Indels 43
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TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REPERRENCE: 00786/351004
CURRENT PAPLICATION WUMBER: U8/09/205,658
CURRENT FILING DATE: 1990-12-03
EARLIER APPLICATION NUMBER: 08/857,076
EARLIER APPLICATION NUMBER: 08/88534
EARLIER FILING DATE: 1997-07
EARLIER FILING DATE: 1997-07
EARLIER FILING DATE: 1997-07
EARLIER FILING DATE: 1998-05-15
NUMBER: 0F SEQ ID NOS: 328
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 313
LENGTH: 532
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Caenorhabditis elegans
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Best Local Similarity 25.2%
Matches 70; Conservative
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                                                                   TYPE: PRT
CRGANISM: homo sapiens
US-10-154-674-2
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Sequence 2, Application US/10154674
Sequence 2, Application Wo. US20020192694A1
GENERAL INFORMATION:
APPLICANT: Wiranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Hu, YI,
APPLICANT: Hu, YI,
TITLE OF INVENTION: NO. US20020192694A1e1 Human Hydroxylases and Polynucleotides Encery TITLE REPRENCE: LEX.0152-105A
CURRENT APPLICATION NUMBER: US/10/154,674
CURRENT FILING DATE: 2002-05-23
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yu. Xuanchuan
APPLICANT: Yu. Xuanchuan
APPLICANT: Miranda, Maricar
TITLE OF INVENTION: No. US20020192694Alel Human Hydroxylases and Polynucleotides Ence
FILE REPERBUCS: LEX-0152-USA
CURRENT APPLICATION NUMBER: US 10/154,674
CURRENT FILING DATE: 2002-05-23
PRIOR PLILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 FLAGLAYRVFHCTQYIRHGSDPLYTPEPDTCHELLGHVPLLADPKFAQFSQEIG----- 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 IEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 FIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE-------- 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 LWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYYPVSGFVAPHQ 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.5%; Score 216.5; DB 9; Length 486; 26.2%; Pred. No. 5.4e-13; tive 42; Mismatches 104; Indels 43; Gaps
        336 ---LASLGASDEDVQKLAT-----CYFFTIEFGLCKQEGQLRAYGAGLLSSIGELKHA 385
                                                        289 FIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE------L 329
                                                                                             386 LSDKACVKAPDPKTTCLQECLITTPQBAYFVSESFEEAKEKMRDFAKSITRPFSVYFNPY 445
                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10154674 Publication No. US20020192694A1 GENERAL INFORMATION:
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                                                                                                                                                                                                      446 TOSIEILKDTRSIENV 461
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Matches 67; Conserve
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US-10-154-674-2
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US-10-154-674-4
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US-09-801-368-354
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APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 99/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SEQ ID NO 354
LENGTH: 1427
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Best Local :
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  264 LIENHEGRK--
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                                                                                                                                   438 DFQLTIVTCKQFFKLSCIQLNCIDTQFTKLLD-DNPTEFDWPTYVDQNPLTMHKIIQLIL 496
                                                                                                                                                                             167 HOYLSLLODRYFPIASVM------RTLDKDN-----FSLTPDLIHDLLGHVP
                                                                                                                                                                                                                                                                                                                 327 YYIVSSSKSMINDENYIINDIKKNNKIKLNILKILSSLILKIFQEQSLEVFIFPTSNWEI 386
                                                                                                                                                                                                                                                                                                                                                                                                         267 EFINKMENFEFLPLSLHILMIFWNDICQIDTNAPVAATITSSQKEPFFLVTKITDMLLHK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 YILE---KLIFDMTNHYNDSQQL-RTWKRQISYFLKLLGNCYSLRLINKE---IFHHWLV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 SILEFEKNLLF----VHLLSLSKNQREGCSTDMAVVST-----PFF------- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 YILKIALKLRQSLSLFFQNSQSLQRAYSTFYSYYRII-----LQKENKEKQALARHKCI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                           WSIHPSRQFDHYESN-----QLVAKLLLL-----RINSTDEDLHEFQIEDAIWSLVFQ-
                                                                                     WLLHPS--FSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNL--IAIVRCFWFTVESG
                                                                                                                                                                                                                           YKPLLFEIVSNADTNQNSDMKKKLELISYRNESLKNNSSIR------NVIMSASNAN
                                                                                                                                                                                                                                                                  YCPRFF-----LDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP 166
                                                                                                                                                                                                                                                                                                                                                               -----WKS 120
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Holtzman, Kevin
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Salama, Sofie
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  --AYGAV--
  ---LISSP----QELGHAFID--
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TITLE OF INVENTION: Dwf5 MUTANTS
FILE REFERENCE: 2225-0020 / 91020.002
CURRENT APPLICATION NUMBER: US/09/817,774
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/192,202
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 45
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO.23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-817-774-23
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  RESULT 8
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Patent No. US2002201211A1
GENERAL INFORMATION:
APPLICANT: CHOE, Sunghwa
APPLICANT: FELDMANN A., Kenneth
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4.9%; Score 92; DB 10; Length 427;

Best Local Similarity 20.4%; Prod. No. 0.41;

Matches 87; Conservative 53; Mismatches 138; Indels 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 GTAVFWDIELYYLYTHFLQFALAAIV----FSVVLSVYLYARSLKVPRDELSPASSGNA 176
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                                                                   411 WEKYCQ 416
                                                                                                            357 FEVLCQ 362
                                                                                                                                                           351 WWGFVRHPNYLGDLIMALAWSLPCGFNHILPYFYVIYFTALLIHREARDEHQCRRKYGLA 410
                                                                                                                                                                                                    320 ----IRHFDELVELTSKLEWMLDQGLLESIPLYN--------QEKYLSG 356
                                                                                                                                                                                                                                                   293 DLSWPLTSVIIALKLCGYVIFRCANSQKNAFRKNPTDPKLAHLKTIP--TSTWKSLLVSG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                177 VYDFF--IGRELNPRIGAFDLKFFCELRPGLIGWVVINLVMLLAEMKVQERSAPSLAMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 -----IKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTFDL 198
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                                                                                                                                                                                                                                                                                            284 ELGHAFIDNVRVLPL-----------ELDQIIRLPFNTSTPQETLFS- 319
                                                                                                                                                                                                                                                                                                                                        235 VNSFQLLYVVDALWF--EEALLTTMDIIHDGFGFMLAFGDLVWVPFTYSLQAFYLVNHPQ
                                                                                                                                                                                                                                                                                                                                                                                 248 ----NLIAIVRCFWFTVESGLIEN----HEG---RKAYGAV------LISSPQ
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Gaps

19;

us-09-438-185a-1047.rapb

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APPLICANT: Burgees, Catherine E.

APPLICANT: Burgees, Viscous 1120 Catherine E.

TITE OF INVENTION: No. US20020137202Alel Proteins and Nucleic Acids Encoding Same
TITE OF INVENTION: No. US200210132041

CURRENT APPLICATION NUMBER: US/09/746,491

CURRENT FILING DATE: 1090-12-20

PRIOR FILING DATE: 1999-12-21

SOFTWARE: Patentin Ver. 2.0

SEQ. ID NO 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 NFREVLEKLESDPVCQRLSLKSFLILPPQRITRLKLLLQNILK----RTQPGSSEBABAT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 NOREGCSTD----MAVVSTPFFNRNLWYRLLSSRFSLW-------KS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 21.9%; Pred. No. 1.2;
Matches 84; Conservative 59; Mismatches 109; Indels 131; Gaps
                                                                                                                                                                                                                                                                                                                                                        272 KAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTS 331
                                                                                                                                                                                                                                                                                                                                                                                         9 SKLINSSQLLYQEYSD-----VVLNKEIQSQQRLE------SL 40
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                                                                                                   178 PPIASVMRTLDK--DNFSLTPDLIHDLLGH------VPWLLHPSFSE----FFINMGR 223
                                                                                                                                                                                               224 LFTKVIEKVQALP----SKK-----QRIQTLQSNLIAIVRCFWFTVESGLIENHEGR 271
                                                                                                                                                                                                                                                                                                      204 NFREVLEKLESDPVCQRLSLKSFLILPFQRITRLKLLLQNILK----RTQPGSSEEAEAT 259
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                                                                     121 YCPRFFLDYLEAFGL--LSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYL-SLLQDRY 177
36 SETPGPSSPRQPRKALVSSESYLORL---SWASSGELWQELPVVRNSTVLLSMTHEDQKL 92
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Patent No. US20020137202A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 KLEWMLDQGLLESIPLYNQEKYL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-09-746-491-40
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US-09-746-491-40
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THE REFERENCE: 15966-621

FILE REFERENCE: 15966-621

CURRENT APPLICATION NUMBER: US/09/746,491

CURRENT FILING DATE: 2000-12-20

RIOR APPLICATION NUMBER: US/09/746,491

CURRENT FILING DATE: 199-11-21

NUMBER OF SEQ ID NOS: 72

SOFTWARE: Patentin Ver. 2.0
                                                                                                               APPLICANT: TERMAN, David S
TITLE OF INVESTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
TITLE OF INVESTION: UNCHOREN: 18/09/870,759
CURRENT APPLICATION WUMBER: 18/09/870,759
CURRENT APPLICATION NUMBER: 18/09/870,759
PRIOR APPLICATION NUMBER: 18/09/08,128
PRIOR PILING DATE: 2000-05-30
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PATENTIN VETSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4211 YTREELCTMFIREVGTVLSQVXSKVHNGSEIL------FSYFQDLVITLPFE------ 4257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4258 RKHKLIDVISMYREL-----LKDLSKEAQEVFKALQSLKTTEVL-RNLQDLLQFIFQLIED 4312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 ARHKCISILEFFKNLLFVHLLSLSKNOREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP---- 166
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4.9%; Score 92; DB 9; Length 4563;
Best Local Similarity 20.7%; Pred. No. 10;
Matches 61; Conservative 48; Mismatches 118; Indels 68; Gaps
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                                         Sequence 128, Application US/09870759
Patent No. US20020177551A1
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Sequence 37, Application US/09746491
Patent No. US20020137202A1
GENERAL INFORMATION:
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US-09-746-491-37
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US-09-870-759-128
                                                                                              GENERAL INFORMATION:
                           -09-870-759-128
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RESULT 12
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US-09-746-491-39
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US-09-746-491-39
               Sequence 4, Application US/09981421
Patent No. US202098185A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Mohler, Kendall M.
APPLICANT: Mohler, Kendall M.
APPLICANT: Mohler, Kendall M.
APPLICANT: Mohler, Teresa L.
TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEDIATED DISORDERS
FILE REFERENCE: 3086-A
CURRENT APPLICATION NUMBER: US/09/981,421
CURRENT APPLICATION NUMBER: US 60/241,408
PRIOR FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 60/241,408
PRIOR FILING DATE: 2000-10-18
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Patent No. US20020137202A1

GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: No. US20020137202A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 39
LENGTH: SEO
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SOFTWARE: PatentIn version 3.1
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296 KIEFE----CKIFPLISQSRWL 313
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59; Mismatches 109; Indels 131;
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US-10-157-447-2
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LENGTH: 541
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Patent No. US20020143155A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/578,178

FILING DATE: CUNADOWN:
APPLICATION UNMBER: 09/110,618

FILING DATE: CUNADOWN:
APPLICATION UNMBER: 09/110,618

ATTORNEY/ACENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION UNMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619

TELEPHONE: (206) 587-0430

TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 TPEGKWHA----SKVLRIE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 CENSYYQTLVNSTSLYKN-CKKLLLENNK------NPTIKKNAEFEDQ-GYYSCVH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 SPOELGHAFIDNVRVLPLE 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 RLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFW-FTVESGLIEN-HEGRKAYGAVLIS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 FVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 -RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 --VLEFWPVELNDTGSYFFOMKNYTOKWKLNVIRRNKHSCFTEROVTSKIVEVKKFFQIT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 ISILEFF------KNLLFVHLLSLSKNQREGCSTDMAVVS-----TPFFN-- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 EPFYLKHCSCSLAHEIETTTKSWYKSSGSQEHVELNPRSSSRIAL------HDC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 DPKYI----LKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKC 64
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTMARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,447
FILING DATE: 28-May-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Kathryn A. Anderson, STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T: Parnet, Patricia et al.
INVENTION: Receptor Designated 2F1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   792 G------ELESSSYSYPQADNI-------IRNVLNIITKDSHALPPY 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

4.4%; Score 84; DB 10; Length 978;
Best Local Similarity 17.9%; Pred. No. 7.4;
Matches 53; Conservative 42; Mismatches 77; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       639 UDQTYKLKAIDPKQRELSFIVNSSVFLEEVISELLCKILYAFSHNMLVTENPDRVKLKLT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LDPKYILKIALKIRSLSLFFQNSQSLQRAYST-----PYSYYRIILQKENKEKQALA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 R-----ILEFFKNLLFV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             759 HRVIQS-----DTICFGRKIYYLLLEBIY------DY-QVQSLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 ------DLIHDLLGHVPWLLH------PSFSEFFINMGRLFTKVIEKV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     826 ITVLPHSLLEDMVYRLLGHVFPSTHTBNELKEKKFPPDDEFVEAASKLTDEIIKEI 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: MAP TO AC008174.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
CTHER INFORMATION: EXPRESSED IN BRAIN, 5.00e-03
US-09-664-761-43207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Forsyth, R. Allyn
APPLICANT: Porsyth, Rari L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli FILE OF INVENTION WHERE: US/09/741,669
CURRENT FILIG DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR PLING DATE: 1999-12-23
                          FastSEQ for Windows Version 4.0
        APPLICATION NUMBER: PCT/US01/00663
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; TYPB: PRT
; ORGANISM: Escherichia coli
US-09-741-669-385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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SOFTWARE: FastSEQ for
SEQ ID NO 385
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US-09-741-
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CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR PELING DATE: 2000-02-04

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,356

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-10-04

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
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                                                                                                                                                                                                               Query Match
4.6%; Score 87.5; DB 12; Length 541;
Best Local Similarity 21.3%; Pred. No. 1.5;
Matches 68; Conservative 50; Mismatches 106; Indels 95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        65 ISILEFF-----TPPFN------KNLLFVHLLSLSKNQREGCSTDMAVVS-----TPFFN-- 103
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                                                                                                                                                                                                                                                                                                                                                          34 EPFYLKHCSCSLAHEIETTTKSWYKSSGSQEHVELNPRSSSRIAL------HDC 81
                                                                                                                                                                                                                                                                                                                    9 DPKYI----LKIALKIRQSLSIFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKC 64
SEQUENCE CHARACTERISTICS:

LENGTH: 541 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: Thear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-157-447-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parame 43207, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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APPLICANT: Wang, Peijing Jeremy
APPLICANT: Page, David C.
APPLICANT: Page, David C.
FILE REFERENCE: 0399.2007-002
CURRENT APPLICATION NUMBER: US/09/801,574
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 60/187,518
PRIOR APPLICATION NUMBER: 60/261,557
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH. 835
TYPE: DET
RESULT 17
US-09-864-761-49017
; Sequence 49017, Application US/09864761
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; ORGANISM: Mus musculus
US-09-801-574-22
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US-09-801-574-22
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9.44; Score 83.5; DB 10; Length 835;
Best Local Similarity 24.44; Prod. No.6.7;

Matches 47; Conservative 26; Mismatches 47; Indels 73
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Patent No. US20020081592A1
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Best Local
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                                                                                                                                                           307 İPLFINDLENÇĞE 319
                                                                                                                                                                                                                                                                                                                                        324 DELVE-----LTSKLEW------MLDQGL-----LES 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 LHPSFSEFFINMGRLFTKVIEKVQALP--SKKQRIQTLQSNLIAIVRCFWFTVESGL--- 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 RHFDELVELTSKLEWMLDQ-GLL 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 PHOYLSLLODRYFP---IASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 LFIGIIRGWIŚLW------MLAAAGVL-----GIVGMFWLALKRYGMNVSGDEA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 LWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVA 165
                                                                                                                                                                                                                   IPLYNOEKYLSGF 357
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                                                                                                                                                                                                                                                                               NDLITKLFSPVLLETHCIENGLEWHEYMKTYLLYPEKLWQGLPNVGNTCYINVVLQSLCS 306
                                                                                                                                                                                                                                                                                                                                                                                                       ISNEKGKERNVREVDISKP---GFGF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IENHEGR-KAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLPSSSTFLHNVGLLENQFIKRKRFFSDLAKNEK----QSNLKDSIRDF----EANLVVC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FYTFLYLTRDTFSPWENLALLLQNYDNIDFQGLAPIVRDFYVFIPSWLWPGRPSMVLNSA 317
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                                                                                                                                                                                                                                                                                                                                                                                                   -----PFETNYPEDSGVDVRDL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SRVVFFI 413
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                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 995

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

FEATURE:

OTHER INFORMATION: MAP TO AC007282.2

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.6

OTHER INFORMATION: EST HUMAN HIT: AI023682.1, EVALUE 8.00e-72

OTHER INFORMATION: SWISSPROT HIT: P30622, EVALUE 1.00e-06

US-09-864-761-49017
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PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR APPLICATION NUMBER: US 60/23,366

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2000-00-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00663

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PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2000-01-29
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 70
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SEQ ID NO 49017
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OP INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OP INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                   170
                                                                                                                           112
                                                                                                                                                                                       110
   162 GFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINM 221
                                                                                                                                                                                                                                               HLISEVPNSKSGSSGTVHDYIMRQIFTAPIFSELEIEVKEPSETPMNLENQLPTPWKRSL 169
                                                           SSHILFHEENADEIELPQPRSATSQIIQAFPI--DTLLESGIKVIELDKEHHKSSLLGT 227
                                                                                                                    SSRFSLWKSYCPRFFL------DYLEAFGLLSDFLDHQAVIKFFEL--ETHFSYYPVS 161
                                                                                                                                                                                                                                                                                                        ch 4.4%; Score 82.5; DB 10; Similarity 20.9%; Pred. No. 11; 70; Conservative 45; Mismatches 117;
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Indels 103; Gaps Length 995;

15;

us-09-438-185a-1047.rapb

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435 GITSPKGNLKDSQEYYSEİRSETEPLSEQSIPIIPKDTTSV------SRAEFIQED 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 GRLFTK------VIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 AVLISSPQELGHAFIDNV------RVLP-LELDQIIRLPFNTSTPQETLFSIRH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 HILLSLSKNOREGCSTDM-----AVVSTPFFNR-------NL------WYRLL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 HLISEVPNSKSGSSGTVHDYIMRQIFTAPIFSELEIEVKEPSETPMNLENQLPTPWKRSL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 SSRFSLWKSYCPRFFL------DYLEAFGLLSDFLDHQAVIKFFEL--ETHFSYYPVS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 SSHILFHEENADEIELPQPRSATSQIIQAFPI--DTLLESGIIKVIELDKEHHKSSLLGT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 GFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINM 221
                                                                                                                                                                                                                                                                                                                                                                          4.4%; Score 82.5; DB 10; Length 1202;
20.9%; Pred. No. 14; No. 14; Style 45; Mismatches 117; Indels 103; Gaps
         OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.81
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.73
OTHER INFORMATION: EXT HUMAN HIT: A1023682.1, EVALUE 1.00e-71
OTHER INFORMATION: ST_HUMAN HIT: A1023682.1, EVALUE 1.00e-71
US-09-864-761-43061
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APPLICANT: Oblean, Kari L.
APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Taxick, John D.
APPLICANT: Taxick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Vamanoto, Robert T.
APPLICANTON: PCARTYON: 10611,096
FILIS REPRENCE: ELITRA, 0114
FRIOR PELICATION NUMBER: 60/201,727
FRIOR PELICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR PELING DATE: 2000-05-26
FRIOR PELING DATE: 2000-05-26
FRIOR PELING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR PELING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: 60/253,939
FRIOR FILING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR APPLICATION NUMBER: 60/267,931
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR APPLICATION NUMBER: 60/267,931
FRIOR APPLICATION NUMBER: 60/267,931
FRIOR FILING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: 60/269,008
FRIOR APPLICATION NUMBER: 60/269,008
FRIOR FILING DATE: 2000-01-27
FRIOR PRIOR FILING DATE: 2000-01-27
FRIOR FILING D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 20.9% es 70; Conservative
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APPLICANT: Harzel, David R.
APPLICANT: ON THE EXPRESSION ANALYSIS BY HIGROARRAY
FILTE OF INVENTION: HARBER: US 60/2064,761
PRIOR FILMOR DATE: 2000-02-46
PRIOR PLING TAING NATE: 2000-05-56
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
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PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                      276 AVLISSPQELGHAFIDNV-----RVLP-LELDQIIRLPFNTSTPQETLFSIRH 322
228 GITSPKGNLKDSQEYYSEIRSETEPLSEQSIPIIPKDTTSV-----SRAEFIQED 277
                                                                                                                 222 GRLFTK-----VIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                323 FDELVE-----LISKLEWMLDQGLLES 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 LEELQEDFDKADKLDRKPILSPKLRVFLEE-LSES 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43061, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
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Sequence 366, Application US/09833790

Patent No. US20020068288A1

GENERAL INPORMATION:

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Wang, Tongtong

APPLICANT: Wang, Tongtong

APPLICANT: Mohamath, Raodoh

APPLICANT: Mohamath, Raodoh

APPLICANT: Mohamath, Raodoh

APPLICANT: Fan, Liqun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: A
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                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT; ORGANISM: Homo sapiens US-09-833-790-366
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US-09-833-790-366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 12990
LENGTH: 909
                                                                                                                                                                                                                                        Query Match 4.3%; Score 81.5; D
Best Local Similarity 19.8%; Pred. No. 10;
Matches 57; Conservative 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Query Match
Similarity 22.4%; Pred. No. 10;
Matches 87; Conservative 66; Mismatches 144; Indels 92; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
TYPE: PI
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140 LDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRT--LDKDNFSLTPD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      829 FA----VIDEG--PGISLEEQQKIFEPF 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 LTSKLEWMLDOGLLESIPLYNOEKYLSGF 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 FTKVIEKVQALP---SKKQRIQTLQSNLIAIVRCFWFTVE-----SGLIEN----HE 269
                                                                                                         27
                                                                                                                                                                       95 AVVSTPF-----FURNLWYRLLSSRFSLWKS-YCPRFFLDYLEAFGLLSDF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 LARHKCISILEFFKULLFVHLLSLS---KNORE-GCSTDMAVVSTPFFNRNLWYRLLSSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 KYILKIALKLRQSLSLFFQNSQSLQRAYSTP----YSYYRI--ILQKE-----NKEKQA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSPIK-----GILA--IDYQSSQVINPYDASILESMLNELSLA-----VEN 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KFQYSITKKQLYRTDLLFQFNDSIKQTYTVENLLINAGYQINQLLQQSITIYVINQSKVI 571
                                                                                                     AFVTTPMCCPSRSSMLTGKYVHNHNVYTNNENCSSPSWQAMHEPRTFAVYLNNTGYRTAF 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFD-ELVE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTLLKQTRESMLQAERQLTHSNFLRSISHDIRTPLTTIMGNLDILVSHSKD----- 709
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                                                                                                                                                                                                                                                                                                                 DB 10; Length 818;
                                                                                                                                                                                                                                            93; Indels 99; Gaps
                                                                                                                                                                                                                                                    12;
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; ORGANISM: Streptococcus pneumoniae US-09-815-242-13312
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US-09-815-242-13312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 13312
LENGTH: 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PPIICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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134 GLLSDFLDHQAVIKFFELETHFSYYFVSGFVAPHQYLSLLQ---DRYFFIASVMRTLDKD 190
                                                                                          676 NAQKWASSQKGLIHTALAEKLKQFMDILASWRLYAKTHSLYDLIWKIYNDRFYYDYV--- 732
                                                                                                                                                                                                                                                                                                                                                 556 TGEMRLVIKEILKLHQEKGVAFKEIALLTSSRSRNDQILLALSEYGIPVKTDGEQNNYLQ 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 NYAPNMDKHWIMQYTGPMLPIHMEFTNILQ------RKRLQTLMSVDDSVERLYNMLV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 YFTDLITNESINYFKMSKRMYPHRPVMMVISHAAPHGPEDSAPQFSKLYPNASQHITPSY 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 LIHDLL-----
                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                           7 TLDPKYILKIALKLRQSLSLFFQ-----NSQSLQRAYSTPYSYYRIILQ----KENKEKQ 57
                                                                                                                                                        NQREGCSTDMAVVST-----PFFNRNLWYRLLSSRFSL----WKSYCPRFFLDYLEAF 133
                                                                                                                                                                                                                     SLEVQVMLDTLRVIHNPLQDYALVALMKSPMFGFDEDELARLSLQKAEDKVHENLYEKLV 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETGELEN----TYIIYTADHGYHIGQFGLVKGKSMPYDFD--IRVPF 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPF 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FG-----KYLN-EYNGSYIP-PGW---REWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 4.3%; Score 81.5; DB 10; 
il Similarity 21.6%; Pred. No. 17; 
69; Conservative 46; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Mismatches 123; Indels 81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GHVPWLLHPSFSEFFINMGR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1216;
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Sequence 2, Application US/08984090

Ratent No. US20010021502A1

GENERAL INFORMATION:
APPLICANT: Michael R.
APPLICANT: Athma, Prasanna
APPLICANT: Athma, Prasanna
APPLICANT: Athma, Predisposition to Breast Cancer by
TITLE OF INVENTION: Mutations at the Ataxia-Telangiectasia Genetic Locus
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1475 YINQRPSCIMDVSLRSFSLCCLLLSQVCQTAVTYCKDALENHL--HVIVGTLIFLVYEQV 1532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 WKSYCPRFFLDY-LEAFGLLSDFLDH--QAVIKFFE--LETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 ALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
4.3%; Score 81.5; DB 8; Length 3056;
Best Local Similarity 18.5%; Pred. No. 60;
Matches 61; Conservative 58; Mismatches 114; Indels 97; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 PKYILKIAL------KLRQSLSLFFQNSQSLQRAYSTPYSYYRIIL---QKENKEKQ 57
791 AVELM--TIHKSKGLEFPYV-----FILNMDQDFNKQDSMSEVILSRQ---NGLGVKY 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 ---HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: Rothwell, Figg, Ernst & Kurz, P.C.
P: 555 Thirteenth Street, N.W., Suite 701-E
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/08/984,090 FILING DATE: 03-DEC-1997 CLASSIFCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,435
FILING DATE: 03-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L
REGISTRATION NUMBER: 28,957
TELECOMPUNICATION INFORMATION:
TELEPHONE: 202-783-6046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: ZUUUH
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
.....TIM SCHEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FRINGTH: 3056 maino acids
                                                                250 IAIVRCFWFTVESGLIENH 268
                                                                                                                       839 IA-----KMETGAVEDH 850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                           RESULT 23
US-08-984-090-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          556 TGEMRLVIKEILKLHQEKGVAFKEIALLTSSRSRNDQILLALSEYGIPVKTDGEQNNYLQ 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          616 SLEVQVMLDTLRVIHNPLQDYALVALMKSPMFGFDEDELARLSLQKAEDKVHENLYEKLV 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 NOREGCSTDMAVVST-----PFFNRNLWYRLLSSRFSL----WKSYCPRFFLDYLEAF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.3%; Score 81.5; DB 10; Length 1216;
Best Local Similarity 21.6%; Pred. No. 17;
Matches 69; Conservative 46; Mismatches 123; Indels 81; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       733 GALPNGPARQA--NLYALALRADQFEKSNFKGLSRFIRMIDQVLEAQHDLASVAVAPPKD 790
                                                                       191 NFSLTPDLIHDLIG-HVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKORIQTLOSNL 249
                                                                                                                791 AVELM--TIHKSKGLEFPYV-----FILNMDQDFNKQDSMSEVILSRQ---NGLGVKY 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ITAWALCA, UGIN D.
APPLICANT: ATAMACA, UGIN D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard U.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
TILE REFERENCE: ELITEA 0.11A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PRIOR PRIOR DATE: 2000-05-23
PRIOR PRIOR DATE: 2000-05-23
PRIOR PRIOR DATE: 2000-01-23
PRIOR PRIOR DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-27
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PRIOR PRIOR PRIOR DATE: 2000-11-27
PRIOR PRIOR PRIOR DATE: 2000-11-27
PRIOR PRIOR PRIOR DATE: 2000-11-27
PRIOR PRIOR PRIOR DATE: 2000-01-2-20
PRIOR PRIOR PRIOR DATE: 2000-01-2-20
                                                                                                                                                                                                                                                                                                                                                                               Sequence 13698, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                                                           250 IAIVRCFWFTVESGLIENH 268
                                                                                                                                                                                                                              839 IA-----KMETGAVEDH 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert
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APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCES: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SEQ ID NO 352
TYPE: PAT
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-352
                   RESULT 25
(WS-09-765-272-60
) Sequence 60, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
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US-09-801-368-352
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APPLICANT: Busby, KOLL

APPLICANT: Cali, Brian

APPLICANT: Hecht, Peter

APPLICANT: Holtzman, Doug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1587 PFSLLEEINH-FLSVSVYDALPLTRLEGIKDLRRQLELHKDQMVDIMRASQDNPQDGIMV 1645
                                                                                                                                                                                                             351
                                                                                                                                                                                                                                                      257
                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 YFPIASYMR-----TLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 CPOYIRTLVSEARTLWPEFIPPDPTKVTEFEFYLLEELESY----LIVHHPYOSLKO-- 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 CPRFFLDYL-EAFGLLSDFL--DHQAV--IKFFELETHFSYYPVSGFVAPHQYLSLLQDR 176
                                                                                                                                                                    300 WDKY 303
                                                                                                                                                                                                                                                                                                                                                                               231 KVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.3%; Score 81; DB 10; Length 323; Local Similarity 23.0%; Pred. No. 3.2; les 56; Conservative 31; Mismatches 71; Indels
                                                                                                                                                                                                           -EKY
  APPLICANT: Choi et. al.
                                                                                                                                                                                                                                                                                             DNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQ 350
                                                                                                                                                                                                                                                                                                                                                                                                                         ---IVQVLKQPPFQITLSSDDLQNCWSLINDSYINDVHLLYPPH---------
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Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Royer, John
Salama, Sofie
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                                                                                                                                                                                                                                                      -AIRDPKNSSSPVQIAFNRFMAESLVD----LEEVMDT-IQEQITLYDH 299
                                                                                                                                                                                                                                                                                                                                         -----IAVACLFITI-----SIHGKPTKGSSLASAASE-----
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                                                                                                                                                                                                                                                                                                                                         256
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-765-272-60
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              Sequence 244, Application US/09895913A
Patent No. US20020160456A1
GENERRAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: A1-Garawi, Amal
APPLICANT: M11cr, Charles
APPLICANT: Tomb, Jean François
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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  APPLICANT:
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                                                                                                                                                                                                                                                      286 YOKLKEAVKYLTDLIEETKATILYLESVETVLNOAGLEEIAEIREELIQTGF 337
                                                                                                                                                                                                                                                                                           314 -QETLFSIRHFDELVELT-----SKLEWMLDQGLLESIPLYNQEKYLSGF 357
                                                                                                                                                                                                                                                                                                                                      226 ATDNAEEFRQKGELLTTFLHQVPNDQDQVILDNYYTNQPIMIALDKALTPNQNAQRYFKR 285
                                                                                                                                                                                                                                                                                                                                                                                                                         173 EPFANLSDLLDTYYKDKAERDRVKQQASELIR-----RVENELQKNRHKLKKQEKELL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 LTAKNLQSLFQGLGRDTANELERILVSEKLSAFRNFFNQETKPCLTETSFSPVPFANQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 LLSDFLDHQ--AVIKF--FELETHFSYYPVSGFVAPHQYLSL-----LQDRYFPIASVMR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 LLVDKSSHKILEVIKHVGFSQNSYRTLLPGSTYIAPPSTKSLNPFTIKDEKLFEILQTQE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
PILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
FILING DATE: 17-Drown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BROOKES, A. Anders
REGISTRATION NUMBER: 36,3
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION.
TELEPHONE: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  SSP----QELGHAFIDNVRVLPLELDQIIRLPFNTSTP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLFTKVIEKVQAL---PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 474 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
Al-Garawi, Amal
Miller, Charles
Tomb, Jean Francois
Oomen, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11arity 20.2%; Pred. No. 5.4;
Conservative 44; Mismatches 113; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172
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us-09-438-185a-1047.rapb

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1264 RENRT---DSACSLKQMVHE--GNQRW-------DNLQKRVTSILRRLKHFIGGREE 1308
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                          1154 DACATDAECDSIQQATRNLDRRWRNICAMSMERRLKIEETWRLWQKFLDDYSRFEDWLKS 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1309 FETARDSILV-----WLTEMDLQLTNIEHFSECDVQAKIKQLKAFQQEISLNHNKIEQII 1363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | : : :: :: | : : : | | 10 WSMTPQT-----VNAYYLPTKNEIVFPAGILQAPFYARNHPKALNFGGIGVVMGHELTHA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 DLIHDLLGHVPWLLHP-----SFSEFFINMGRLF---TKVI-EKVQALPSKKQ 240
                                                                                                                                                                                                                                                                                                 182 SVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQR 241
                                                                                                 88 EGCSTDMAVVSTPFFNRNL---WYRL-----LSSRFSLWKSYCPRF--FLDYLEA 132
                                                                                                                                                                                               133 FGLLSDFLDHQAVI-----KF--FELETHFSYYPVSGFVAPHQYLSLLQDRYFPIA 181
                                                                                                                                                                                                                                                                                                                                                                                                        ------VESGLIENH---EGRK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 AYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSI-RHFDELVELTS 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 DAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQ 69
30 NSQSLQRAYSTPYSYYRIILQKENKEKQALARHK--CISILEFFKNLLFVHLLSLSKNQR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.3%; Score 80.5; DB 10; Length 197; 23.8%; Pred. No. 1.8; tive 22; Mismatches 41; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION UNDER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 KLEWMLDQGLLESIPLYNQEKYLSGFEV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 526, Application US/09978295A; Patent No. US20020156006A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           242 IQTLQSNLIAIVRCFWFT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 836, Application US/09764853
Patent No. US2002009672A1
GENERAL INFORMATION:
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 23.8
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 FIDNVR 294
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US-09-764-853-836
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TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456Alel Helicobacter Polypeptides in the
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/043002
CURRENT PEPLICATION NUMBER: US/09/895,913A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 08/881,227
NUMBER OF SEQ ID NOS: 368
SOUTHARE: PSECESC for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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4.3%; Score 81; DB 9; Length 1993;
Best Local Similarity 18.0%; Pred. No. 38;
Matches 70; Conservative 61; Mismatches 121; Indels 136; Gaps
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APPLICANT: Sugiyana, Janice
APPLICANT: Mytiad Genetics, Incorporated
APPLICANT: Sugiyana, Janice
APPLICANT: Gimbora, Janice
APPLICANT: Gimbora, Janice
APPLICANT: Gimbora, Janice
TITLE OF INVENTION: TSG101-INTERACTING PROTEINS AND USE THEREOF
FILE REFERENCE: 1907.06
CURRENT APPLICATION NUMBER: US 60/276,259
PRIOR PILING DATE: 2002-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-07-07
PRIOR APPLICATION NUMBER: to be assigned
PRIOR APPLICATION NUMBER: to be assigned
PRIOR PILING DATE: 2001-07-07
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PRIOR PILING DATE: 2002-01-07
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Patent No. US20020177207A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
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US-09-895-913A-244
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Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
                                                                                 Ferrara, Napoleon
Filvaroff, Ellen
Folgo, Sherman
Gao, Wel-Qiang
Gerber, Hanpeter
Gerritsen, Mary E.
Goddard, Audrey
Botstein, David
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4.3%; Score 80.5; DB 9; Length 736;
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APPLICATION UNMBER: 60/083559
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083500
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APPLICANI: WOOD WILLIAGUS, F. TLANDER APPLICANI: WOOD WILLIAGUS, F. TLANDER APPLICANI: WOOD WILLIAGUS, F. CALGE ENCOCHING the Same FILES OF INVESTIONS: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVESTIONS: Secreted and Transmembrane Polypeptides and Nucleic CURRENT APPLICATION NUMBER: UG/09/978,697

CURRENT APPLICATION NUMBER: UG/09/978,697

REALDS FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: G0/06534

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PRIOR PLING DATE: 1997-11-10-10

PRIOR PLING DATE: 1998-03-12

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PRIOR PLING PATE: 1998-03-12

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PRIOR PLING PATE: 1998-03-20

PRIOR PLING DATE: 1998-03-20
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Sequence 526, Application US/09978697 Patent No. US20020169284A1 GENERAL INFORMATION:

RESULT 30 US-09-978-697-526

289 FIDNVR 294 | | | | 579 FDDQGR 584 APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P.

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RESULT 31
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; APPLICANT: Ashkenazi, Avi

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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
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APPLICANT: Pan, James,
APPLICANT: Pan, James,
APPLICANT: Pan, James,
APPLICANT: Pan, Margaret Ann
APPLICANT: Stelton, David L.
APPLICANT: Stelton, David L.
APPLICANT: Stelton, David L.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, Daniel
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Societed and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Societed and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: PAGS 100-10
FILE REFERENCE: PAGS 100-10
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 06/06220
PRIOR APPLICATION NUMBER: 06/06220
PRIOR FILING DATE: 1997-11-03
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R APPLICATION WINDER: 60/078336
F APPLICATION NUMBER: 60/078316
R APPLICATION NUMBER: 60/078910
R FILING DATE: 1998-03-20
R FILING DATE: 1998-03-20
R FILING DATE: 1998-03-27
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079294
R FILING DATE: 1998-03-25
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kuo, Sophia S.
Napier, Mary A.
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FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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FILING DATE: 1998-03-27
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APPLICATION UNDER: 60/077791
TILING DATE: 1998-03-12
APPLICATION NUMBER: 60/078004
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APPLICATION NUMBER: 60/078886
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FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066364
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TLING DATE: 1998-03-10
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APPLICATION NUMBER: 60/077641
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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              Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
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RESULT 32
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; Sequence 526, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
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Best Local
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DR APPLICATION NUMBER: 60/085580
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085573
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085704
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085697
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OR APPLICATION NUMBER: 60/084640

OR FILING DATE: 1998-05-07

OR APPLICATION NUMBER: 60/084598

OR FILING DATE: 1998-05-07

OR APPLICATION NUMBER: 60/084600

OR FILING DATE: 1998-05-07
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FILING DATE: 1998-05
APPLICATION NUMBER: 6
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085323
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/
FILING DATE: 1998-05-07
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/083500
FILING DATE: 1998-04-29
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FILING DATE: 1998-0
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ilarity 23.8%;
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Pred. No. 11;
2; Mismatches
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CCURRENT FILING DATE: 120-001-10-24
PRIOR APPLICATION NUMBER: 05/05/959,832A
CCURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/06344
PRIOR PILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1997-11-3
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077632
PRIOR PILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/07791
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PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078936
PRIOR PILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079656
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C63
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Baker Kevin P.
Botstein, David
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Shelton, David L.
Trawart, Timothy A.
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Grimaldi, J. C
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Filvaroff, Ellen
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197 DLIHDLIGHVPWLLHP-----SFSEFFINWGRLF---TKVI-EKVQALPSKKQ 240 241 RIQTLOSNLIAIVRCFWFTVESGLI------ENHEGRKAYGAVLISSPQELCHA 288 4.3%; Score 80.5; DB 9; Length 736; 23.8%; Pred. No. 11; tive 22; Mismatches 41; Indels 33; Gaps PRIOR APPLICATION NUMBER: 60/083554
PRIOR APPLICATION NUMBER: 60/08358
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Sequence 526, Application US/09978189 Publication No. US20030004102A1

RESULT 33 US-09-978-189-526

| REPLICANT: Gerber, Hanspeter APPLICANT: Gerber, Hanspeter APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Gurmy, Austin Lyas J. APPLICANT: Gurmy, Austin Lyas J. APPLICANT: Hillan, Kanneth J. APPLICANT: Hillan, Kanneth J. APPLICANT: Hillan, Kanneth J. APPLICANT: Hillan, Kanneth J. APPLICANT: Wayler, Mary A. APPLICANT: Wayler, Wayler, Mary A. APPLICANT: Wayler, Wayler, Mary A. APPLICANT: Wayler, Wayler, Mary A. APPLICANT: Wayler, Wayler, Wayler, Mary A. APPLICANT: Wayler, Wayler, Wayler, Mary A. APPLICANT: Wayler, Wayler, Wayler, Mary A. APPLICANT: Wayler, Wayler, Wayler, Mary A. APPLICANTON WAMBER, GO/062250 ARIOR FILING DATE: 1999-11-13 ARIOR FILING DATE: 1999-11-13 ARIOR FILING DATE: 1999-11-13 ARIOR FILING DATE: 1999-11-13 ARIOR FILING DATE: 1999-11-13 ARIOR FILING DATE: 1999-11-12 ARIOR APPLICATION WAMBER, GO/07632 ARIOR APPLICATION WAMBER, GO/07632 ARIOR APPLICATION WAMBER, GO/07939 ARIOR APPLICATION WAMBER, GO/07636 ARIOR FILING DATE: 1999-03-12 ARIOR APPLICATION WAMBER, GO/07636 ARIOR FILING DATE: 1999-03-25 ARIOR APPLICATION WAMBER, GO/07636 ARIOR FILING DATE: 1999-03-26 ARIOR APPLICATION WAMBER, GO/07636 ARIOR APR | PLICANT: Ashkenazi<br>PLICANT: Ashkenazi<br>PLICANT: Baker K<br>PLICANT: Botseteii<br>PLICANT: Desnoyei<br>PLICANT: Perrara<br>PLICANT: Filvaroi<br>PLICANT: Fong, 81<br>PLICANT: Goo, Wei  |
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APPLICANT: Wood, William I.
APPLICANT: Shang, Zenan,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-01-15
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Gurney, Austin L.
Patent No. US20020127584A1
                                                                                                 Baker, Kevin P.
Chen, Jian
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197 DLIHDLLGHVPWLLHP----SFSEFFINMGRLF---TKVI-EKVQALPSKKQ 240

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Best Local Similarity 23.8% Matches 30; Conservative

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                                                                                                                                                                                                                                                                                                                                                                             DLIHDLLGHVPWLLHP------SFSEFFINMGRLF---TKVI-EKVQALPSKKQ
                                                                                                                                                                                                                                                                       RIQTLQSNLIAIVRCFWFTVESGLI --
                                                                                                                                                              FIDNVR 294
                                                                                                            FDDQGR
                                                                                                                                                                                                                                                                                                                                                                                                                               4.3%; Sc
Similarity 23.8%; Pr
                                                                                                            584
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 80.5; DI
Pred. No. 11;
22; Mismatches
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APPLICATION NUMBER:

---ENHEGRKAYGAVLISSPQELGHA 288

DB 12; 41;

Length 736; Indels

33;

Gaps

ű

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Query Match
4.2%; Score 80; DB 10; Length 560;
Best Local Similarity 20.3%; Pred. No. 8.4;
Matches 60; Conservative 43; Mismatches 109; Indels 84; Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 RELLATDNAEBFRQKGELLTTFLHQVPNDQDQVILDNYYTNQPIMIALDKALTPNQNAQR 367
                                                                                                                                                                                                                                                                                                    135 LLSDFLDHQ--AVIKF--FELETHFSYYPVSGFVAPHQYLSL----LQDRYFPIASVMR 185
                                                                                                                                                                                                                                                                                                                                           186 TLDXDNFSLTPDLIHDLLGHV----- 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 LTAKNIQSLFQGLGRDTANELERILVSEKLSAFRNFFNQETKPCLTETSFSPVPFANQAG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 BFFINMGRLFTKVIEKVQALPSKKQRIQTLOSNLIAIVRCFWFTVESGLIENHEGRKAYG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 -----QETLFSIRHFDELVELT-----SKLEWMLDQGLLESIPLYNQEKYLSGF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 YFKRYQKLKEAVKYLTDLIBETKATILYLESVETVLNQAGLBEIABIREELIQTGF 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 AVLISSP-----QELGHAFIDNVRVLPLELDQIIRLPFNTSTP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: IGENITICACION OF ESSENICATION OF INVENTION: Prockaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-01-23
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR APPLICATION NUMBER: 60/25,578
PRIOR APPLICATION NUMBER: 60/25,578
PRIOR PLING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-21-6
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SOFTWARE: FastSEQ for Windows Version 4.0
ERNGTH: 897
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 13304
LENGTH: 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11609, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                           ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Helicobacter pylori
US-09-815-242-11609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     493 DAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSKDQ 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 DLIHDLIGHVPWLLHP-----SFSEFFINMGRLF---TKVI-EKVQALPSKKQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.3%; Score 80.5; DB 10; Length 765;
23.8%; Pred. No. 11;
tive 22; Mismatches 41; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Onlean, Nail, W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramenco, Robert T.
APPLICANT: Tamenco, Robert T.
APPLICANT: Tamenco, Robert T.
APPLICANT: Wall Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE OF INVENTION: Prokaryotes
FILE OF INVENTION: Prokaryotes
FILE OF INVENTION PROKARYOTES
FILE OF INVENTION NUMBER: 60/991,078
PRIOR APPLICATION NUMBER: 60/201,107
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                           APPLICANT: WHYTE, DAVID
APPLICANT: CAENEREEL, SEAN
APPLICANT: CHARVDCZAK, GLEN
APPLICANT: CHARVDCZAK, GLEN
APPLICANT: SUDARSANAM, SUCHA
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
PRIOR APPLICATION NUMBER: 06/214,047
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR PILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOTTWARE: PATCHING DATE: 2000-06-26
SEQ ID NO 80
SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13304, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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FILING DATE: 2001-02-16
             Sequence 80, Application US/0988615
Patent No. US20020064856A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Best Local Similarity 23.8%
Matches 30; Conservative
                                                                                                    APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-80
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RESULT 38
US-09-731-231A-2
US-09-731-231A-2
Sequence 2, Application US/09731231A
Patent No. US20020082189A1
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/731,231A

CURRENT FILING DATE: 2000-12-07

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 645
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TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GUEGLER, KARI et al TITLE OF INVENTION: ACCLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACCL MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                       177
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                                                               314 AAHIINAMQKRIHLQTLRALSEVQKMTPRERMRLRKLQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 SLEKIYENLDLAKNLLSPKMYQAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 ----CISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 FFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 YCE-RTLDPKYILKIALKLRQSLSLFFQN---SQSLQRAYSTPYSYYRIILQKENKEKQA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGFTCVEVGGFEADDVIASLATLSPYKTRIYSKDKD-----FN-----QLLSDKIALFD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FYKDRKNM-----PFIVFALESQTKTKRAEKLGEYKONRKDAPKEMLLQIPIALEWLQK 107
                                                                                                                           YPKELNAIMESMLNKNPSLRPSAIEIL--KIPYLDEQLQNLMCRYSEMTLEDKNLDCQKE 313
                                                                                                                                                                                                                                                       Y-FPIASVMRTLDKDNFSLTPDLIHDLLGHVPWL-----LHPSFSEFFINMGRL-----
                                                                                                                                                                                                                                                                                                                    IWSLACILYEMCCMNHAFAGSNFL--SIVLKIVEGDT-----
                                                                                                                                                                                                                                                                                                                                                                            LWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                            FLKNNLLKIGDF-
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55; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GVSRLLMGSCDLATTLTGTPHYMSPEALKHQGYDTKSD 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104;
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                                                                                                                                                                                                                                                                                                                    -----PSLPER 255
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR PELICATION NUMBER: 60/049787
PRIOR PELICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065710
PRIOR APPLICATION NUMBER: 60/06770
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/075945
PRIOR PILING DATE: 1997-12-24
PRIOR PILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/07945
PRIOR APPLICATION NUMBER: 60/07945
PRIOR APPLICATION NUMBER: 60/083322
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/087106
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/087607
PRIOR PILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087607
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US-09-992-598-84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 84, Application US/09992598 Patent No. US20020160384A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
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OR FILING DATE: 1998-06-03
OR APPLICATION NUMBER: 60/08021
OR PELICATION NUMBER: 60/08025
OR APPLICATION NUMBER: 60/08025
OR APPLICATION NUMBER: 60/08026
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/08026
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/08028
OR APPLICATION NUMBER: 60/08029
OR APPLICATION NUMBER: 60/08030
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/
FILING DATE: 1998-06-02
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Williams, P. Micke
Wood, William I.
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Kljavin, Ivar J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Margaret Ann
art, Timothy A.
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139 FLDHQAVIKEPELETHFSYYP-----VSGFVAPH------QYLSLLQDRYFFIASVMR 185 195 LITNDSV-SFF--RTSKKMYPHRPVLMVISHAAPHGPEDSAPQY-----SKLFPNAS-QH 245 99 TPFFNRNL------WYRLL-SSRFSLWKSYC----PRFFLDYLEAFGLLSD 138 138 TAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNY-TLCRNGVKEKHGSDYSKDY--LTD 194 85; Indels 70; Gaps Query Match
4.2%; Score 79; DB 9;
Best Local Similarity 23.8%; Pred. No. 19;
Matches 59; Conservative 34; Mismatches 8; PRIOR APPLICATION NUMBER: 60/090429
PRIOR PILLING DATE: 1998-06-24
PRIOR PILLING DATE: 1998-06-24
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PRIOR PILLING DATE: 1998-07-02
PRIOR PILLING DATE: 1998-0 APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 셤 ò q ò

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GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

"""", ICANT: Desnoyers, Luc

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US-09-989-293A-84
CURRENT FILING DATE: 1297-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR TILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065316
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-12
PRIOR PELICATION NUMBER: 60/065311
PRIOR PELICATION NUMBER: 60/075945
PRIOR PELING DATE: 1997-11-24
PRIOR PELICATION NUMBER: 60/075945
PRIOR PELICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/08332
PRIOR PELICATION NUMBER: 60/08332
PRIOR PELICATION NUMBER: 60/087106
PRIOR PELICATION NUMBER: 60/087106
PRIOR APPLICATION NUMBER: 60/087609
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PRIOR APPLICATION NUMBER: 60/087827
PRIOR APPLICATION NUMBER: 60/087827
PRIOR APPLICATION NUMBER: 60/087827
PRIOR APPLICATION NUMBER: 60/080021
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/080021
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PRIOR FILING DATE: 1998-06-04
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5. US20020177164A1
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Gerber, Hanspeter
Gerber, Mary E.
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Kljavin, Ivar J.
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23.8%; Pred. No. 19;
Live 34; Mismatches 85; Indels
                      PRIOR APPLICATION NUMBER: 60/090246
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2730PLG1
CURRENT APPLICATION NUMBER: US/09/989,735
                                       195 LITNDSV-SFF--RTSKKNYPHRPVLMVISHAAPHGPEDSAPQY-----SRLFPNAS-QH 245
                                                                                        186 TLDKDNFSLTPDLIHDLIGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKORIOTL 245
                                                                                                                                      246 ITPSYNYAPNDD------KKHWIMRYTGPMKPIHME--FINMLQ-------RKRLQTL 287
                                                                                                                                                                                      246 OSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIR 305
                                                                                                                                                                                                                                 288 MSVDDSMETIYNMIVETGELDN-----TYIVYTADHGYHIGQFGLVKGKSMPYEFD--IR 340
139 FLDHQAVIKFFELETHFSYYP-----VSGFVAPH------QYLSLLQDRYFPIASVMR 185
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PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/065186
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PRIOR PELING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065710
PRIOR FILING DATE: 1997-11-24
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PRIOR PRIOR PRIORATION NUMBER: 60/083322
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Forno, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Murney, Austin L.
Kljavin, Ivar J.
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APPLICATION NUMBER: 60/087607
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Publication No. US20020193299A1
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Eaton, Dan L.
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APPLICATION NUMBER: 60/089598
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 MSVDDSMETIYNMLVETGELDN-----TYIVYTADHGYHIGQFGLVKGKSMPYEFD--IR 340
                                                                                                                                                                                                                                                                                                                              195 LITNDSV-SFF--RİSKKMYPHRPVLMVISHAAPHGPEDSAPQY----SKLFPNAS-QH 245
                                                                                                                                                               99 TPFFNRNL------WYRLL-SSRFSLWKSYC-----PRFFLDYLEAFGLLSD 138
                                                                                                                                                                                                         138 TAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNY-TLCRNGVKEKHGSDYSKDY--LTD 194
                                                                                                                                                                                                                                                                          139 FLDHQAVIKEFELETHFSYYP-----VSGFVAPH-----QYLSLLQDRXFPIASVMR 185
                                                                                                                                                                                                                                                                                                                                                                                        186 TLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                      246 ITPSYNYARNPD-----RKHLQTL 287
                                                                                                           70; Gaps
                                                Query Match

4.2%; Score 79; DB 9; Length 867;
Best Local Similarity 23.8%; Pred. No. 19;
Matches 59; Conservative 34; Mismatches 85; Indels
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R FILING DATE: 1997-06-16
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R APPLICATION NUMBER: 60/065186
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R APPLICATION NUMBER: 60/065311
DR APPLICATION NUMBER: 60/065311
DR APPLICATION NUMBER: 60/066770
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DR APPLICATION NUMBER: 60/06570
DR APPLICATION NUMBER: 60/075945
PILING DATE: 1998-02-25
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PRIOR FILING DATE: 1997-06-16
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Sequence 84, Application US/09990444
Publication No. US20020193300A1
GENERAL INFORMATION:
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Fong, Sherman
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Paoni, Nicholas F.
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Gerritsen, Mary E.
Goddard, Audrey
, PRIOR FILING DATE: 1998-07-09
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Napier, Mary A.
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Botstein, David
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Eaton, Dan L.
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341 VPFYVRGP 348
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APPLICATION NUMBER: FILING DATE: 1998-00 R FILING DATE: R APPLICATION N R FILING DATE:

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E: 1998-06-17 V NUMBER: 60/0 1998-06-

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RESULT 43
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Best Local S
Matches 59
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 84, Application US/09989730 Publication No. US20020197674A1
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Mood, William I.
APPLICANT: Enang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and I
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PlC69
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
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OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/092182
OR FILING DATE: 1998-07-09
OR APPLICATION NUMBER: 60/092182
OR FILING DATE: 1998-07-09
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59; Conserv
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Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Roy, Margaret Ann
Stewart, Timothy A
Tumas, Daniel
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Gerber, Hanspeter
Gerritsen, Mary E.
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Pan, James
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k; Pred. No. 19;
34; Mismatches
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19;
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OR APPLICATION NUMBER: 60/090252
OR APPLICATION NUMBER: 60/090252
OR APPLICATION NUMBER: 60/090254
OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/090254
OR APPLICATION NUMBER: 60/090349
OR FILING DATE: 1998-06-23
OR APPLICATION NUMBER: 60/090429
OR FILING DATE: 1998-06-24
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OR APPLICATION NUMBER: 60/090446
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19

70;

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287 245 245 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18

FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17

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OR PILING DATE: 1998-06-24
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OR FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090540
APPLICATION 1998-06-24
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OR PELICATION NUMBER: 60/090863
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091478
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091544
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APPLICANT: Ashkenazi, Avi J.
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Godowski, Paul J.
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Roy, Margaret Ann
Stewart, Timothy A.
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PRIOR PLING DATE: 1998-07-07 US-09-991-181-84
; Sequence 84, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION: Godowski, Paul J. Grimaldi, J.Christopher Gurney, Austin L. Kljavin, Ivar J. PLICANT: Ashkenazi, Avi J.
PLICANT: Baker, Kevin P.
PLICANT: Baker, Kevin P.
PLICANT: Botteein, David
PLICANT: Eaton, Dan I.
PLICANT: Ferrara, Napoleone
LICANT: Fong, Sherman
LICANT: Gorber, Manspeter
LICANT: Gorber, Manspeter
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LICANT: Gorber, Manspeter Goddard, Audrey E. 341 VPFYVRGP 348 306 LPFNTSTP 313 APPLICANT:
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4.2%; Score 79; DB 9; Length 867;
Best Local Similarity 23.8%; Pred. No. 19;
Matches 59; Conservative 34; Mismatches 85; Indels
PRIOR PEDLICATION NUMBER: 60/090557
PRIOR PELLING DATE: 1998-06-24
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Publication No. US20020198149A1
GENERAL INFORMATION:
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089440
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OR APPLICATION NUMBER: 60/091544
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OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091626
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OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
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DR FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090557
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC64
CURRENT APPLICATION NUMBER: US/09/989,734
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PRIOR APPLICATION NUMBER: 60/049787
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PRIOR PLING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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Sequence 84, Application US/09989734 Publication No. US20030003531A1 GENERAL INFORMATION:
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Gurney,Austin L.
Kljavin,Ivar J.
Napier,Mary A.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Grimaldi, J. Chris
                                                                                                                                            PLICANT: Ashkenazi, Avi J.
PLICANT: Baker, Kevin P.
PLICANT: Botstein, David
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Eaton, Dan L.
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DR APPLICATION NUMBER: 60/089907

DR APPLICATION NUMBER: 60/089908

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Matches 59
       246 QSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIR 305
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OR APPLICATION NUMBER: 60/091626
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OR APPLICATION NUMBER: 60/091633
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OR APPLICATION NUMBER: 60/091982
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R APPLICATION UMMBER: 60/091360

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R R APPLICATION NUMBER: 60/091478

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R FILING DATE: 1998-06-25

PR APPLICATION NUMBER: 60/090690

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NR APPLICATION NUMBER: 60/090429

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APPLICATION NUMBER: 60/090862
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APPLICATION NUMBER: 60/090540
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APPLICATION NUMBER: 6
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                                                                                                                                                                                                    LITNDSV-SFF--RTSKKMYPHRPVLMVISHAAPHGPEDSAPQY-----SRLFPNAS-QH
                                                                                                                                                                                                                                                                    FLDHQAVIKFFELETHFSYYP-----VSGFVAPH-----QYLSLLQDRYFPIASVMR 185
                                                                                                                                                                                                                                                                                                                                     TAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNY-TLCRNGVKEKHGSDYSKDY--LTD
                                                                                                                                                                                                                                                                                                                                                                                                     TPFFNRNL------WYRLL-SSRFSLWKSYC-----PRFFLDYLEAFGLLSD
                                                                                                                 TLDKONFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTL
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PRIOR PILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/05974
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CURRENT APPLICA
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OR FILING DATE: 1997-10-24

OR APPLICATION NUMBER: 60/062816

OR APPLICATION NUMBER: 60/063045

OR PILING DATE: 1997-10-24

OR APPLICATION NUMBER: 60/063045

OR APPLICATION NUMBER: 60/063082

OR FILING DATE: 1997-10-31

OR APPLICATION NUMBER: 60/063127

OR APPLICATION NUMBER: 60/063327

OR APPLICATION NUMBER: 60/063327
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Tumas, Daniel
Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Filvaroff, Ellen
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Sequence 20, Application US/10028072 Publication No. US20030004311A1 GENERAL INFORMATION:

APPLICATION NUMBER: US/10/028,072 FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/08332 PRIOR APPLICATION NUMBER: 60/08345 PRIOR APPLICATION NUMBER: 60/08460 PRIOR FILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/084627 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR PRIDRED FILING DATE: 1998-05-07 PRIOR PRIDRED FILING DATE: 1998-05-07 PRIOR PRIDRED FILING DATE: 1998-05-13 PRIOR PRIDRED FILING DATE: 1998-05-13 PRIOR PILING DATE: 1998-05-13 PRIOR PILING DATE: 1998-05-13 PRIOR FILING DATE: 1998-05-13 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-16 PRIOR PILING DATE: 1998-05-16 PRIOR PILING DATE: 1998-05-16 PRIOR PILING DATE: 1998-05-16 PRIOR PILING DATE: 1998-05-16 PRIOR PILING DATE: 1998-05-16 PRIOR PILING DATE: 1998-05-16 PRIOR PILING DATE: 1998-05-16 PRIOR PILING DATE: 1998-05-16 PRIOR PILING DATE: 1998-05-17 PRIOR PILING

16; 4.2%; Score 79; DB 9; Length 867; 23.8%; Pred. No. 19; tive 34; Mismatches 85; Indels Query Match Best Local Similarity 23.8% Matches 59; Conservative

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| Sequence 04. Application US/09989722  Sequence 04. Application US/09989722  Patent No. US2002007267A1  GENERAL INFORMATION  APPLICANT: Ashkenazi, Avi J.  APPLICANT: Baker, Kevin P.  APPLICANT: Baker, Kevin P.  APPLICANT: Gerimstali, J. Christopher  APPLICANT: Gerimstali, J. Christopher  APPLICANT: Gerimstali, J. Christopher  APPLICANT: Gerimstali, J. Christopher  APPLICANT: Majer, Mary A.  APPLICANT: Majer, Mary A.  APPLICANT: Napier, Mary A.  AP | Qy 139 FLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFFIASVMR 185  |
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|  | PRIOR APPLICATION NUMBER: 60/087609 PRIOR FILLING DATE: 1998-06-02 PRIOR APPLICATION NUMBER: 60/087759 PRIOR PLLING DATE: 1998-06-02 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/088021 PRIOR APPLICATION NUMBER: 60/088021 PRIOR APPLICATION NUMBER: 60/088025 PRIOR APPLICATION NUMBER: 60/088025 PRIOR APPLICATION NUMBER: 60/08025 PRIOR APPLICATION NUMBER: 60/08025 PRIOR APPLICATION NUMBER: 60/08026 PRIOR APPLICATION NUMBER: 60/08026 PRIOR APPLICATION NUMBER: 60/08026 PRIOR APPLICATION NUMBER: 60/08026 PRIOR FILLING DATE: 1998-06-04 PRIOR APPLICATION NUMBER: 60/08029 PRIOR FILLING DATE: 1998-06-04 PRIOR APPLICATION NUMBER: 60/08029 PRIOR PILLING DATE: 1998-06-04 |

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PRIOR FILING DATE: 1998-06-18

REIGN APPLICATION NUMBER: 60/089947

REIGN PELING DATE: 1998-06-19

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APPLICANT: Zhang, Zemin 1.

APPLICANT: Zhang, Zemin 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acide Encoding the Same FILE REPERRACE: P2730PLG2

CURRENT PILING DATE: 2001-11-19

CURRENT APPLICATION NUMBER: 60/69187

PRIOR APPLICATION NUMBER: 60/6616

PRIOR PILING DATE: 1997-60-16

PRIOR PILING DATE: 1997-60-16

PRIOR PILING DATE: 1997-11-12

PRIOR PILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/665311

PRIOR APPLICATION NUMBER: 60/665311

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PRIOR APPLICATION NUMBER: 60/66531

PRIOR APPLICATION NUMBER: 60/66570

PRIOR PILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/065710

PRIOR PILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/076945

PRIOR APPLICATION NUMBER: 60/075945
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                                                                                                                                   138 TAFFGKYLMEYNGSYVPPGWKEWVGLLKNSRFYNY-TLCRNGVKEKHGSDYSKDY--LTD 194
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                                                      70; Gaps
Query Match
4.2%; Score 79; DB 10; Length 867;
Best Local Similarity 23.8%; Pred. No. 19;
Matches 59; Conservative 34; Mismatches 85; Indels '
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Gerritsen, Mary E.
Geddard, Audrey
Goddwski, Paul J.
Godwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Rajer, Mary A.
Pan, James
Paoni, Nicholas F.
Pao, Wargaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Sequence No. US20020072092A1
GENERAL INFORMATION:
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Williams, P. Mickey
Wood, William I.
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Botstein, David
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PRIOR APPLICATION NUMBER: 60/091633
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PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
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| 4.2%; Score 79; DB 10; Length 867;<br>13.8%; Pred. No. 19;<br>.ve 34; Mismatches 85; Indels 70; Gaps 16;             | 99 TPFFNRNLWYRLL-SSRFSLWKSYCPRFFLDYLEAFGLLSD 138<br>      : | 139 FLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMR 185<br>  : : | 186 TLDKDNFSLTPDLIHDLIGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTL 245 246 ITPSYNYAPNPDKRWLQTL 287 | 246 QSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIR 305            |
|--|---|--|--|---|
| Query Match  4.2%; Score 79; DB  Best Local Similarity 23.8%; Pred. No. 19;  Matches 59; Conservative 34; Mismatches | NRNLWYRLL-SSRFSLWKSYC<br>:                                  | LDHQAVIKFFELETHFSYYPVSGFVAPH.<br> - : :                          | DNFSLTPDLIHDLLGHVPWLLHPSFSEFFIN<br> ::   | IAIVRCFWFTVESGLIENHEGRKAYGAVLIS:<br>::       :  <br>DSMETIYNMLVETGELDNTYIVYTADI |
| Match<br>local S   | 99 TPFF<br>     <br>38 TAFF                                 | S9 FLDH  | 36 TLDE<br>46 ITPS   | 46 QSNI<br> <br>88 MSVI   |
| Query Match<br>Best Local 8<br>Matches 59  | - QY 8  | Qy 13  | Qy 16  | 67<br>24<br>25  |

Search completed: January 9, 2003, 17:13:45 Job time: 52 secs

306 LPFNTSTP 313 :|| | 341 VPFVVRGP 348

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Page 1

| Sequence 20, Appl<br>Sequence 15, Appl<br>Sequence 15, Appl<br>Sequence 4, Appl<br>Sequence 4, Appl<br>Sequence 2, Appl<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli | Sequence 3, Applia<br>Sequence 2, Applia<br>Sequence 2, Applia<br>Sequence 2, Applia<br>Sequence 3, Applia<br>Sequence 3, Applia<br>Sequence 3, Applia<br>Sequence 3, Applia | Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 18, Appl<br>Sequence 18, Appl<br>Sequence 18, Appl<br>Sequence 18, Appl<br>Sequence 2, Appli<br>Sequence 2, Appli | Sequence 1, Appliance Sequence 1, Appliance 1, Appliance 1, Appliance 1, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 1, Appliance 12, Appli | Sequence 2, Appliance Sequence 2, Appliance 3, Appliance 2, Appliance 3, Appliance 2, Appliance 3, Appliance 2, Appliance 3, Appliance  |
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| GenCore version 5.1.3  Copyright (c) 1993 - 2003 Compugen Ltd.  protein search, using sw model  January 9, 2003, 14:46:38 , Search time 26 Seconds  (without alignments)  409.658 Million cell updates/sec  | US-09-438-185A-1047 score: 1889 1 VHYCERTLDPKYILKIALKLESIPLYNQEKYLSGFEVLCQ 362 table: BLOSUM62 Gapop 10.0 , Gapext 0.5 1: 262574 seqs, 29422922 residues                     | atisfying choser 2000000000 um Match 0% um Match 100%  | se: Issued Patents AA:*  1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:* 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:* 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:* 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:* 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* 6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* 6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* 6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* 6: /cgn2_6/ptodata/1/iaa/packfiles1.pep:* and is derived by analysis of the total score distribution.   | # # Query Dy analysis # # # Colory Decriped by analysis   Colory Decriped by analysis   Colory Decriped by a color Decriped by |

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RESULT 1
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GENERAL INFORMATION:
                                                        APPLICANT: GOLDSTEIN, Menek
APPLICANT: WU, Jing
APPLICANT: FILER, David
APPLICANT: FILER, David
APPLICANT: FILER, David
TITLE OF INVENTION: GENETICALLY MODIFIED TYROSINE
TITLE OF INVENTION: HYDROXYLASE AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY and NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
    STREET: 419 Seven
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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5, 5300436
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US-09-956-273-7
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Patent No. 5300436
GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Menek
APPLICANT: WIL, Jing
APPLICANT: FILER, David
APPLICANT: FILER, David
APPLICANT: FILER, GENETICALLY
TITLE OF INVENTION: GENETICALLY
TITLE OF INVENTION: HYDROXYLASE AND US
TITLE OF INVENTION: HYDROXYLASE AND US
TORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY and NEIMARK
STREET: 419 Seventh Street, N.W., Su
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/009,075
FILLING DATE: 19930126
FILLING DATE: 19930126
CLASSIFICATION NUMBER: US/08/009,075
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKST NUMBER: GOLDSTEIN=1A
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKST NUMBER: GOLDSTEIN=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
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COMPUTER: IBM PC compatible
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TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                             ADDRESSEE: BROWDY
STREET: 419 Sevent
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
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AND USES
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us-09-438-185a-1047.rai

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245 LQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELG-------- 286
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5.2%; Score 98.5; DB 4; Length 1024;
Bast Local Similarity 19.9%; Pred. NO. 0.13
Matches 68; Conservative 41; Mismatches 134; Indels 99; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564 QQTDSLXNLPSV----IGDILSETNVNKITLHAVKNNELLSLVETASTLKIKHL----- 613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      699 KSIRDLFADML-FGKSLESVNDSDSFIKINGSFTLKYHGDNINLLFNYHSLITKNVGYQI 757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          648 IKKVLFESENYKTLRKKYENEGFPGYHWAKFIVPGTFNSAENTFYSAI------DKT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 QNSQSLQRAYSTPYSYYRIILQKENKEK---QALARHKCISILEFFKNLLFVHLLSLSKN 85
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APPLICANT: Young, Richard A.
APPLICANT: Young, Richard M.
APPLICANT: Thompson, Craig M.
APPLICANT: Thompson, Craig M.
APPLICANT: Chao, David M.
TITLE OF INVENTION: No. 591966e1 Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Therefor NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
CITY: Lexington
CITY: Lexington
CITY: Lexington
CONVENTION OF ADDRESSEES
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,804
                                        APPLICATION NUMBER: AU PN7127
FILING DATE: 13-DEC-1995
ATTORNEY AGENT INPORMATION:
NAME: WINNER, Ellen P.
TELECOMMULICATION INPORMATION:
TELECHOUS: +1 303 499 8089
INPORMATION FOR ERG ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1024 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycoplasma genitalium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08540804 Patent No. 5919666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ORIGINAL SOURCE:
             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 QFSQDIG-----LASLGASDEBIEKLSTLS------WFTVEFGLCKQNGEVKAYG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 SSRFSLWKS-----YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHF 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
11.6%; Score 220; DB 1; Length 497;
Best Local Similarity 26.7%; Pred. No. 3e-15;
Matches 65; Conservative 38; Mismatches 10; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: The University of Melbourne TITLE OF INVENTION: Mycoplasma Recombinant Polypeptides and TITLE OF INVENTION: Vaccines
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/009,075
FILING DATE: 1930126
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: TOWNSEND, GUY K.
REGISTRATION NUMBER: 34,033
FEFERENCE/DOCKET NUMBER: GLESCHAMMICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-628-5197
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CONTRY: United States of America
ZIP: 80303
COMPUTE READABLE FORM:
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00803
FILING DATE: 13-DEC-1996
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FILING DATE: 12 JUNE 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 497 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-009-075-4
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CITY: Boulder
STATE: Colorado
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1226 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-540-804-12
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/521.
FILING DATE: 21-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218
APPLICATION NUMBER: US 08/218
FILING DATE: 25-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI9.
TELEPAN: 617-861-6240
TELEPAN: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                             Sequence 12, Application US/08218265 Patent No. 5922585
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5.0%; Score 95; DB 2; Length 1226;
Best Local Similarity 18.8%; Pred. No. 0.4;
Matches 98; Conservative 65; Mismatches 155; Indels 204; Gaps
GENERAL INFORMATION:
APPLICANT: Young, Richard A.
APPLICANT: Koleske, Anthony J.
APPLICANT: Thompson, Craig M.
APPLICANT: Thompson, Craig M.
TITLE OF INVENTION: No. 5922585el Factors Which Modify Gene
                                                                                                                                                                                                                                                                                  464 KTPLSIKIMVAEWYLSHLCSGILSSV---NRTVLLKIFKIFC 502
                                                                                                                                                                                                                                                                                                                                                                                     404 LLINLKISPLMKSQYNMVLRNVMEYDVKFYEIFNFDQLVEITEQIKMRILSNDITNLQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 LIENHEGRK-----QELGHAFID-- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 WSIHPSRQFDHYESN-----QLVAKLLLL-----RINSTDEDLHEFQIEDAIWSLVFQ- 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 WILHPS--FSEFFINMGRIFTKVIEKVQALPSKKQRIQTLQSNI--IAIVRCFWFTVESG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 DFQLTIVTCKQFPKLSCIQLNCIDTQFTKLLD-DNPTEFDWPTYVDQNPLTMHKIIQLIL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 HQYLSLLQDRYFPIASVM------RTLDKDN-----FSLTPDLIHDLLGHVP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 YKPLLFEIVSNADTNQNSDMKKKLELISYRNESLKNNSSIR------NVIMSASNÄN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKL--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAKNFSAQKRVVSYMMPSLYRLLNILITÝĞIIKVPTYIRKLÍSSGLLYLQDSNDKFVHVQ 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCPRFF-----LDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SILEFFKNLLF----VHLLSLSKNQREGCSTDMAVVST-----PFF------ 102
                                                                                                                                                                                                                                                                                                                              -----EWMLD---QGLLESIPLYNOEKYLSGFEVLC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YILE---KLIFDMTNHYNDSQQL-RTWKRQISYFLKLLGNCYSLRLINKE---IFHHWLV 65
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NAME: ATAINAM INFORMATION:
NAME: Granahan, Patricia
REGISTRATION UNMERR: 32,227
REFERENCE/DOCKET NUMBER: 432,227
REFERENCE/DOCKET NUMBER: WHI9-
FELEPHONE: 617-861-6240
FELEPAX: 617-861-6240
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1226 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: TYPE: protein
US-08-218-265-12
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,265
FILING DATE: 25-MAR-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
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NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                   344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167
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                                                                                                                                404 LLINLKISPLMKSQYNMVLRNVMEYDVKFYEIFNFDQLVEITEQIKMRILSNDITNLQLS 463
                                                                                                                                                                               292 ---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKL-------
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CITY: Lexington
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 YILE---KLIFDMTNHYNDSQQL-RTWKRQISYFLKLLGNCYSLRLINKE---IFHHWLV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 YILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRII-----LQKENKEKQALARHKCI 65
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ZIP: 02173
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                                KTPLSIKIMVAEWYLSHLCSGILSSV---NRTVLLKIFKIFC 502
                                                                                 -----EWMLD---QGLLESIPLYNQEKYLSGFEVLC 361
                                                                                                                                                                                                                                                                                                                                    WSIHPSROFDHYESN-----QLVAKLLLL----RINSTDEDLHEFQIEDAIWSLVFQ-
                                                                                                                                                                                                                                                                                                                                                                                   WLLHPS--FSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNL--IAIVRCFWFTVESG
                                                                                                                                                                                                                                                                                                                                                                                                                                       DFQLTIVTCKQFPKLSCIQLNCIDTQFTKLLD-DNPTEFDWPTYVDQNPLTMHKIIQLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HQYLSLLQDRYFPIASVM------RTLDKDN-----FSLTPDLIHDLLGHVP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKPLLFEIVSNADTNQNSDMKKKLELISYRNESLKNNSSIR-----NVIMSASNAN 236
                                                                                                                                                                                                                                LAKNFSAQKRVVSYMMPSLYRLLNILITYGIIKVPTYIRKLISSGLLYLQDSNDKFVHVQ 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCPRFF-----LDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n 5.0%; Score 95; DB 2; Length 1226;
Similarity 18.8%; Pred. No. 0.4;
98; Conservative 65; Mismatches 155; Indels 2
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5.0%; Score 95; DB 4; Length 1226;
Best Local Similarity 18.8%; Pred. No. 0.4;
Matches 98; Conservative 65; Mismatches 155; Indels 204; Gaps
                                                                                                                                                                                                     404 LLINLKISPLMKSQYNMVLRNVMEYDVKFYEIFNFDQLVEITEQIKMRILSNDITNLQLS 463
                                                                                                       344 LAKNFSAQKRVVSYMMPSLYRLLNILITYGIIKVPTYIRKLISSGLLYLODSNDKFVHVQ 403
                                                                                                                                                               292 ---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKL------333
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296 WSIHPSRQFDHYESN-----QLVAKLLLL-----RINSTDEDLHEFQIEDAIWSLVFQ- 343
                                                        ------QELGHAFID-- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Young, Richard A.
APPLICANT: Young, Richard A.
APPLICANT: Thompoon, Craig M.
APPLICANT: Thompoon, Craig M.
APPLICANT: Chao, David M.
TITLE OF INVENTION: No. 6214588el Factors Which Modify Gene
TITLE OF INVENTION: No. 6214588el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFEMATING STILEM: F. LOGS/H3. D. Version #1.30 COFFWRENT APPLICATION NATA: P. LOGS/H3. D. Version #1.30 COFFWRENT APPLICATION NATA: APPLICATION NUMBER: US/08/590,399 FILING DATE: 26-JAN-1996 CLASSIFICATION: A35 PRIOR APPLICATION NUMBER: US 08/540,804 FILING DATE: 11-OCT-1995 PRIOR APPLICATION NUMBER: US 08/521,872 FILING DATE: 31-AUG-1995 PRIOR APPLICATION NUMBER: US 08/218,265 FILING DATE: 32-MAR.1995 PRIOR APPLICATION NUMBER: US 08/218,265 FILING DATE: 25-MAR.1994 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                      334 ------EWMLD---QGLLESIPLYNQEKYLSGFEVLC 361
                                                                                                                                                                                                                                                                                                                     464 KTPLSIKIMVAEWYLSHLCSGILSSV---NRTVLLKIFKIFC 502
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RR: WHI94-03A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6214588
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 12:
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REGISTRATION NUMBER: 32,
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Lexington
STATE: Massachusetts
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                                                              264 LIENHEGRK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
5.0%; Score 95; DB 3; Length 1226;
Best Local Similarity 18.8%; Pred. No. 0.4;
Matches 98; Conservative 65; Mismatches 155; Indels 204; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 YILE---KLIFDMINHYNDSQQL-RIWKRQISYFLKLLGNCYSLRLINKE---IFHHWLV 65
                                                                                                                                         APPLICANT: Young, Richard A.
APPLICANT: Young, Anthony J.
APPLICANT: Thompson, Craig M.
APPLICANT: Chao, David M.
APPLICANT: Thompson, Craig M.
APPLICANT: Thompson, Craig M.
APPLICANT: Than Chao, David M.
TITLE OF INVENTION: No. 6015682el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Therefor
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---NRNLWYRLLSSRFSL-----
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CURRENT APPLICATION DATE: US/08/521,872
FILING DATE: 31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Granahan, Patricia
REGISTRATION NUMBER: 32-227
REFERENCE/DOCKET NUMBER: WH194-03A
TELECOMOUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,265
FILING DATE: 25-WAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                             Sequence 12, Application US/08521872
Patent No. 6015682
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1226 anino acids
TYPE: amino acid
TOPOLOGY: linear
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-521-872-12
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ZIP: 02173
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US-09-180-422B-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/09180422B
Patent No. 6444644
GENERAL INFORMATION:
                                                         TELEFAX: 7038164100 INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 KTPLSIKIMVAEWYLSHLCSGILSSV---NRTVLLKIFKIFC 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 LLINLKISPLMKSQYNMVLRNVMEYDVKFYEIFNFDQLVEITEQIKMRILSNDITNLQLS 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 ---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKL--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 LIENHEGRK-----QELGHAFID-- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 WSIHPSRQFDHYESN-----QLVAKLLLL-----RINSTDEDLHEFQIEDAIWSLVFQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 WLLHPS--FSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNL--IAIVRCFWFTVESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 HQYLSLLQDRYFPIASVM------RTLDKDN-----FSLTPDLIHDLLGHVP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 YYIVSSSKSMINDENYIINDIKKNNKIKLNILKILSSLILKIFQEQSLEVFIFPTSNWEI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 SILEFFKNLLF----VHLLSLSKNQREGCSTDMAVVST-----PFF----
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/09/180,422B
FILING DATE: 07-Dec-1998
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                         NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETTELAIE, CAMILLE
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
FROM APOLIPOPROTEIN B-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BRUCKDORFER, KARL R
ETTELAIE, CAMILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ĹAKŃFSAQKRVVSYMMPSLYRLLNILITYGIIKVPTYIRKLIŚSGLLYLQDSNDKFVHVQ 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFQLTIVTCKQFPKLSCIQLNCIDTQFTKLLD-DNPTEFDWPTYVDQNPLTMHKIIQLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKPLLFEIVSNADTNONSDMKKKLELISYRNESLKNNSSIR-----NVIMSASNAN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YILE---KLIFDMTNHYNDSQQL-RTWKRQISYFLKLLGNCYSLRLINKE---IFHHWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----EWMLD---QGLLESIPLYNQEKYLSGFEVLC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE, P.C.
STREET: 1100 NORTH GLEBE ROAD, BTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                   LENGTH: 4536 amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----LDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-180-422B-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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4.9%; Score 92; DB 4; Length 4536;
Best Local Similarity 20.7%; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Mamone
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
TITLE OF INV
                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sha, Dan
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                  REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION: (213) 489-1600
                                                                                                                                             APPLICATION NUMBER: 60/008,688
FILING DATE: December 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSeq Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4404 NFTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIAELSATAQEI -- IKSQAIA 4456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4344 SQELQQIHQYIMALREEYFDPSIVGWTVKYYELEEKIVSLIKNLLVALKDFHSEYIVSAS 4403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4286 NIKQLKEMKFTYLINYIQDEINTIFNDYIPY--VFKLLKENLCLNLHKFNEFIQNELQEA 4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4231 RKHKLIDVISMYREL----LKDLSKEAQEVFKAIQSLKTTEVL-RNLQDLLQFIFQLIED 4285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4184 YTREELCTMFIREVGTVLSQVYSKVHNGSEIL-----FSYFQDLVITLPFE----L 4230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 ---HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 ARHKCISILEFFKNLLFVHLLSISKNQREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 90071-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----HQYLSLLQDRYFPIASVMRT-----LDKDNFSLTPDLI------- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61; Conservative
                                          67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mamone, ...
                                                                (213) 955-0440
                                                                                                                                                                                                                                                                                                                                             Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM P.C.
                                                                                                                                                                                                                                                                                                                                                                      US/08/766,014
                                                                                                                                                                                                                                                           including application described below:
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48; Mismatches 118; Indels 68;
                                                                                                                                 223/104
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APPLICANT: Like, w. I.
APPLICANT: Like, Thomas
APPLICANT: Like, Stefanie
APPLICANT: Kliche, Stefanie
APPLICANT: Schender, Patrick A.
APPLICANT: Schender, Patrick A.
APPLICANT: Schenemann, Anette
TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous
TITLE OF INVENTION: System Diseases
NUMBER OF SUGURNES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Pulbright & Jaworski, L.L.P.
STREET: 865 South Figueroa Street, 29th Floor
CITY: Los Angeles
STATE: Galifornia
COUNTRY: USA
ZIP: GAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 QALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 YFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 SKKORIOTLOSNLIA------IVRCFWFTVESG----LIENHEGRKAY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 GAVLISSPQELGHAPIDNVRVLP--LELDQIIRLPFNTSTPQE-------315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 GPVLKTYSRSPVHTSTRNVRAAKGFIGFPQVIRQDQDTDHPENMEAYETVSAFITTDLKK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 -----TLFSIRHFDELVELTSKLEWM---LDQGLL-------ESIPLY-- 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 LWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 EWDSVYPKEPLRYDPPKGTGS-----RILVDVFLNDSSFDPYDVIMYVVSGAY---LHDP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 BGLTHEQCVDNWKSFAGVKF------GCFMPLSLDSD--LTMYLKDKALAALQR 46
                                                                                                                                                                                                                                                                                                                                                                                                          4.8%; Score 91; DB 3; Length 535;
20.6%; Pred. No. 0.31;
tive 46; Mismatches 119; Indels 136;
CLASSIFICATION: 435
ATORNEY AGENT INFORMATION:
NAWE: CHUCCHILL)
REGISTRATION NUMBER: 39,944
REGISTRATION NUMBER: 39,944
REPERENCE/DOCKET NUMBER: 1279-194XX
TELECOMMUNICATION INFORMATION:
TELEFAX: 213/690-4518
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39, Application US/08582776C; Patent No. 6077510; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 -NQE---KY-LSGFEVLCQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 PNDQIFIKYPMGGIEGYCQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 20.69 tes 78; Conservative
                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO
US-08-369-822C-24
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Matches
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APPLICANT: Briese, Thomas
APPLICANT: Briese, Thomas
APPLICANT: Kliche, Stefanie
APPLICANT: Kliche, Stefanie
APPLICANT: Schneider, Patrick A.
APPLICANT: Sthneemann, Anatte
APPLICANT: Schneemann, Anatte
TITLE OF INVENTION: Borna Disease Viral Sequences,
TITLE OF INVENTION: System Diseases
TITLE OF INVENTION: System Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----FTVESGLIENHEGRKAYGAVLISSP-QELGHAFIDNVRVLPLELDQIIR---LPFN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 KKLILISIEMPLVEVLKSMEVSGFTLDKEVLKELSQKIDDRIGEI---LDKIYKEAGYQFN 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 TSTPQE-TLESIRHFDELVELTSKLEWMLDQGLLESIPLYN-------OEKY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 IKENIENNKELAIMSKRLATIKRDIPIBIDFEBYKVKKFNEBK------LLELFNK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 MRTLDKDNFSLTPDLIHDLL------GHVPWLLHPSFSEFFINMGRLFT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 KVIEKVQALPS-----KKKQRIQTLQSNLIA---IVRCFW-------- 257
                                                                                                                                         Query Match
Best Local Similarity 17.5%; Pred. No. 0.57;
Matches 74; Conservative 70; Mismatches 141; Indels 139; Gaps
                                                                                                                                                                                                                                                                                                                             74 LLFVHLLSLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAF 133
                                                                                                                                                                                                                                                                                                                                                                        274 LEFFSLIDNIKKE----SSIEIVD------NHKVEKWSK-----VDIKELV 309
                                                                                                                                                                                                                                                                                                                                                                                                                       134 GLLSDFLDHQAVIKFFELETHFSYYPV-----SGFVAPHQYLSLLQDRYFPIASV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 TLLOD-----DL-STRNIAFYPLIYEGEIKKIAFSFGKDTVYIDVFOTE----DL 351
                                                                                                                                                                                                                                      14 LKIALKURQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fulbright & Jaworski, L.L.P. 865 South Figueroa Street, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IEM PC compatible
OPERATING SYSTEM: WINDOWS NT-WORDERFECT 8.0
OPERATING SYSTEM: WINDOWS NT-WORDERFECT 8.0
OPERATING SYSTEM: WINDOWS NT-WORDERFECT 1000
OFTEN APPLICATION NAMER: US/08/369,822C
APPLICATION NUMBER: US/08/369,822C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/08369822C Patent No. 6015660 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
  LENGTH: 872 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                               MOLECULE TYPE: peptide
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California
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ZIP: 90017-2571
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US-08-369-822C-24
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                                                                                                    US-08-766-014-2
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; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE; NO
US-08-582-776C-39
                                                                                                                                                 RESULT 12
US-08-434-831B-36
                                                                           Sequence 36, Application US/08434831B Patent No. 6113905 GENERAL INFORMATION:
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Best Local !
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APPLICATION NUMBER: US 08/349,822
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,831
PRILING DATE: 04-MAY-1995
ATTORNEY_AGENT INFORMATION:
NAME: Churchill, Margaret A.
REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 1279-194C2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEPAX: 213/680-4518
TINFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acid
APPLICANT: Lipkin, W. I.
APPLICANT: Briese, Thomas
APPLICANT: Kliche, Stefanie
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                                                                                                                                                                                                                                                                                                239 YCLNWRYETISLFAQR-LNEIYGLÞŚFFQWLHKRLETSVLYVSDÞHCÞÞDLDAHÍÞLYKV 297
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Local Similarity 20.6%; Pred. NO. 0.31;
Les 78; Conservative 46; Mismatches 119; Indels 136; Gaps
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                -----TLFSIRHFDELVELTSKLEWM---LDQGLL-----ESIPLY-- 348
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IBM PC compatible
SYSTEM: WINDOWS NT
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INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: Churchil, Margaret A. (Ph.D.)
REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 1279-194C1
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION NUMBER:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ORERATING SYSTEM: WINDOWS NT-WORDPERFECT 8.0
SOFTWARE: ASCII (DOS) TEXT
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APPLICANT: Stitz, Lothar
APPLICANT: Schneemann, Anette
TITLE OF INVERTION: Borna Disease Viral Sequences,
TITLE OF INVERTION: Dispostics and Therapeutics for Central Nervous
TITLE OF INVERTION: System Diseases
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APPLICATION NUMBER: US
FILING DATE: 04-MAY-15
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CITY: California
TTATE: California
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  349 -NQE---KY-LSGFEVLCQ 362
                                                                                                                                                                           179 GPVLKTYSRSPVHTSTRNVRAAKGFIGFPQVIRQDQDTDHPENMEAYETVSAFITTDLKK 238
                                                                           239 YCLNWRYETISLFAQR-LNEIYGLPSFFQWLHKRLETSVLYVSDPHCPPDLDAHIPLYKV 297
                                                                                                                                                                                                                     275 GAVLISSPQELGHAFIDNVRVLP--LELDQIIRLPFNTSTPQE--------
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                                                                                                                                                                                                                                                                                                                    237 SKKQRIQTLQSNLIA-------IVRCFWFTVESG----LIENHEGRKAY 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 QALARHKÇISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFPNRNLWYRLLSSRFS 116
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                                                                                                                                                                                                                                                                                                                                                                          EFNL-----SYSLQEKEIKE----
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1 Similarity 20.6%; Pred. No. 0.31;
78; Conservative 46; Mismatches 119; Indels 136; Gaps
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amino acid
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865 South Figueroa Street, 29th Floor
                                                                                                                        ---TLFSIRHFDELVELTSKLEWM---LDQGLL--
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В S us-09-438-185a-1047.rai

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PARENT. N. C. TREAMYTION:

APPLICANT: SARAKI, Keiko
APPLICANT: MORI, TAKAYUM.
APPLICANT: MORI, TAKAYUM.
APPLICANT: MORI, TAKAYUM.
APPLICANT: MORI, TAKAYUM.
TITLE OF INVENTION: ATTENDATES VIRUS VACCINE,
TITLE OF INVENTION: ATTENDATES SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
CORRESPONDENCE ADDRESS: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: ''. ATTENDATES OF THE SOUTH 23rd Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.8%; Score 91, DB 2, Length 2183;
20.6%; Pred. No. 2.6;
Live 46; Mismatches 119; Indels 136; Gaps
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                                                                                                                607 GPVLKTYSRSPVHTSTRNVRAAKGFIGFPQVIRQDQDTDHPENMEAYETVSAFITTDLKK 666
275 GAVLISSPOELGHAFIDNVRVLP--LELDQIIRLPFNTSTPQE---
                                                                                         ----TLFSIRHFDELVELTSKLEWM---LDOGLL----
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/905,817
FILING DATE: 04-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/348,891
FILING DATE: 25-NOV-1994
PRIOR APPLICATION NUMBER: US 08/348,400
FILING DATE: 10-NOW NUMBER: US 07/848,400
FILING DATE: 10-NAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: UP 3-293625
FILING DATE: 14-OCT-1991
ATTORNEY/ACBNT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: X2,925
REFERENCE/DOCKET NUMBER: KP-7501A
TELECOMMUNICATION INFORMATION:
TELEFAK: 703-521-2997
TELEFAK: 703-568-0533
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                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08905817
Patent No. 5824777
GENERAL INFORMATION:
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                                                                                                                                                                               349 -NQE---KY-LSGFEVLCQ 362
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Matches 78; Conserve
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US-08-905-817-7
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                                                                                                                                                                                  APPLICANT: SASAKI, Keiko
APPLICANT: WORI, Takayuki
APPLICANT: MORINO, Satoshi
TITLE OF INVENTION: ATTENDATED MEASLES VIRUS VACCINE,
TITLE OF INVENTION: CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           556 ----CQVIAENLISNGIGKYFKDNGMAKDEHDLTKALHTLAVSGVPKDLKESHRG---- 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

4.8%; Score 91; DB 1; Length 2183;
Best Local Similarity 20.6%; Pred. No. 2.6;
Matches 78; Conservative 46; Mismatches 119; Indels 136; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 QALLARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               429 EGLTHEQCVDNWKSFAGVKF------GCFMPLSLDSD--LTMYLKDKALAALQR 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 LWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 SKKORIQTLOSNLIA------INTOPPRETVESG----LIENHEGRKAY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,891A CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                Sequence 7, Application US/08348891A Patent No. 5654136 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  3: YOUNG & THOMPSON
745 South 23rd Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
       298 PNDQIFIKYPMGGIEGYCQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2183 amino acids
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                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPOLOGY:
                                                                                                 US-08-348-891A-7
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RESULT 15
US-08-484-105-6
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
STRANDEDNESS: sinci^
TOPOLOGY
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Patent No. 5589341
GENERAL INFORMATION:
                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION UNMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8701
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APPLICANT:
APPLICANT:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/484,105
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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TITLE OF I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YCLNWRYETISLFAQR-LNEIYGLPSFFQWLHKRLETSVLYVSDPHCPPDLDAHIPLYKV 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPVLKTYSRSPVHTSTRNVRAAKGFIGFPQVIRQDQDTDHPENMEAYETVSAFITTDLKK 666
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/ENTION: ORIGIN OF REPLICATION COMPLEX GENES
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HERSKOWITZ, Ira
LI, Joachim J
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BELL, Stephen P
KOBAYASHI, Ryuji
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Patent No. 5614618
GENERAL INFORMATION:
APPLICANT: STILLMAN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HERSKOWIT:
APPLICANT: LI, JOACH
APPLICANT: GAVIN, Kit
TITLE OF INVENTION: (
NUMBER OF SEQUENCES:
                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: OGMEAN Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8771
TELEPHORE: (415) 494-8771
                                                                                                                                                                                                                       ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: #10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: US/08/484,106
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 -QYLSLLQDRYFPIASYMRTLDKDNF-SLTPDL---IHDLLGHVPWLLHP-----SPSEF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 PRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPV-----SGFVAPH-- 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 MSYFFQNAFSV---FIDPVNVDFLNDDYLKIL-----SRCPTFMFFVEGLIK 369
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 LSLFFQNSQSLQRAYSTPYS-----YYRIILQKENKEKQALARHKCISILEFFKNLLF 76
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSYKSNIEDNLLSWEQVLPSLDKENYDTLSGDLDKIMAPVLGQLFKLYREANMTINIYDF 540
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                   910 277299
                                                                                                                                                                                                                                                                                                                                                                                                                         California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RINE, Jasper
FOSS, Margit
MCNALLY, Francis J
LAURENSON, Patricia
HERSKOWITZ, Ira
LI, Joachim J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAVIN, Kimberly VENTION: ORIGIN OF REPLICATION COMPLEX GENES
                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ryuji
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Sequence 3261, Application US/09134001C
Sequence 3261, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: WUBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 654
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4.8%; Score 90; DB 4; Length 654;
Best Local Similarity 20.1%; Pred. No. 0.53;
Matches 93; Conservative 61; Mismatches 152; Indels 116; Gaps
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3261
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US-09-134-001C-3261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
4.8%; Score 90.5; DB 1; Length 615;
Best Local Similarity 20.7%; Pred. No. 0.43;
Matches 64; Conservative 54; Mismatches 110; Indels 81; Gaps
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1 Similarity 20.5%; Pred. No. 0.5;
91; Conservative 71; Mismatches 172; Indels 110; Gaps
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PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LEWARTH. C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4504
           INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-106-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600 QSTKSYDLV 608
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US-09-134-001C-4504
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US-08-911-853-35
; Sequence 35, Applicat
; Patent No. 6048710
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match Similarity 22.4%; Score 89; DB 3; Length 392;
Best Local Similarity 22.4%; Pred. No. 0.31;
Matches 71; Conservative 40; Mismatches 104; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/699,09
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gerritse, Gijsbert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                        306 GÁVLSFEVKGGKÉAAWRFIDATŔVISITTNLGDTKTTÍAHPATŤŚHGRLSPQÉRASAGÍR 365
                                                                275 GAVL---ISSPQELGHAFIDNVRVLPL----ELDQIIRLPFNTS----TPQETLFS-IR 321
                                                                                                                248 WMFLKGLETLRIRMQAQSASALELAR--WLETQPGIDRVYYAGLPSHPQHELAKRQQSAF 305
                                                                                                                                                                                                        189 PALQQPLALGADMVMH-SATKFIDGQGRGLGGVVAGRRAQMEQVVGFLRTAGPTLSPFNA 247
                                                                                                                                                                                                                                                      196 PDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVI----EKV-----
                                                                                                                                                                                                                                                                                                   146 -----PNTKLLFVESPSNPLÄELVDIGALAEIAHARGALLAVDNCFCT 188
                                                                                                                                                                                                                                                                                                                                              149 FELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVM------RTLDKDNFSLT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                      90 CST-DMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLBAFGLLSDFLDHQAVIKF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 925 Page
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                           ----QALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE-----NHEGRK----AY 274
                                                                                                                                                                                                                                                                                                                                                                                           CSAGDHVLVSRSVF-----GSTISLFEKYLKRFGIEV--DYPPLADLDAWQAAFK- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STPQETL-----FSIRHFDELVELTSKLEWMLDQ-----GLLESIPLYNQ 350
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6048710
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TELEPAX: 650-845-000.

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LEMGTH: 392 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear
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US-09-479-409-35
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US-09-479-409-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFEX: 650-845-6504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTEEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/479,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMDATA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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CTTY: Palo Alto
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                                                                                                                                                                                                                                   189 PALQQPLALGADMVMH-SATKFIDGQGRGLGGVVAGRRAQMEQVVGFLRTAGPTLSPFNA 247
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                                             306 GAVLSFEVKGGKEAAWRFIDATRVISITTNLGDTKTTIAHPATTSHGRLSPQERASAGIR
                                                                                                                                        248 WMFLKGLETLRIŔMQAQSASALELAŔ--WLETQPĠIDRVYYAGLPSHPQHELAKRQQSÁF 305
                                                                                                                                                                                                                                                                                196 PDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVI-----EKV-----
                                                                                                                                                                                                                                                                                                                           146 -----
                                                                                                                                                                                                                                                                                                                                                                         149 FELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVM-----RTLDKDNFSLT 195
  322 HFDELVELTSKLEWMLD 338
                                                                                        275 GAVL---ISSPQELGHAFIDNVRVLPL----ELDQIIRLPFNTS----TPQETLFS-IR 321
                                                                                                                                                                                233 ----QALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE------NHEGRK----AY 274
                                                                                                                                                                                                                                                                                                                                                                                                                      98 CSAGDHVLVSRSVF------GSTISLFEKYLKRFGIEV--DYPPLADLDAWQAAFK- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 CST-DMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 4.7%; Score 89; DB 4; Length 392;
Similarity 22.4%; Pred. No. 0.31;
71; Conservative 40; Mismatches 104; Indels 102;
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925 Page Mill Road
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Quax, Wilhelmus J.
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                                                                                                                                                                                                                                                                                                                              --PNTKLLFVESPSNPLAELVDIGALAEIAHARGALLAVDNCFCT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXPRESSION SYSTEM EXPRESSION LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08/911,853
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163 FVAPHQYLSILQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMG 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 RLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFW-FTVESGLIEN-HEGRKAYGAVLIS 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CENSYYOTLVNSTSLYKN-CKKLLLENNK------NPTIKKNAEFEDQ-GYYSCVH 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 ISILBFF-----TPFFN-- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 DPKYL----LKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.6%; Score 87.5; DB 3; Length 309;
21.3%; Pred. No. 0.32;
tive 50; Mismatches 106; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: FIGHPY GIBE
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DE-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 12-MAA-197
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: UP 215,488/1997
FILING DATE: 38-JUL-1997
FILING DATE: 39-JUL-1997
FILING DATE: 39-JUL-1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                       ADDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W., Suite 300 STATE: D.C.
                                                                                                                                                                          APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, TAKANOAT
APPLICANT: KURIMOTO, MUSSENI
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                               RESULT 22
US-08-996-338-22
; Sequence 22, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TOF
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 21.3*
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
366 -- DNLVRVAVGLEDVVD 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-996-138-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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4.7%; Score 89; DB 4; Length 392;
Best Local Similarity 22.4%; Pred. No. 0.31;
Matches 71; Conservative 40; Mismatches 104; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 CST-DMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 CSAGDHVLVSRSVF------GSTISLFEKYLKRFGIEV--DYPPLADLDAWQAAFK- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 FELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVM--------RTLDKDNFSLT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 PDLIHDLIGHVPWLLHPSFSEFFINMGRLFTKVI-----EKV------ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 ----QALPSKKORIQTLOSNLIAIVRCFWFTVESGLIE------NHEGRK----AY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 WMFLKGLETLRIRMOAQSASALELAR--WLETOPGIDRVYYAGLPSHPOHELAKRQQSAF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 GAVL---ISSPOELGHAFIDNVRVLPL----BLDQIIRLPFNTS----TPQETLFS-IR 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 GAVLSFEVKGGKEAAWRFIDATRVISITTNLGDTKTTİAHPATTSHGRLSPQERASAGİR 365
                                                                                                                                                                                                    APPLICANT: Gerritee, Gijsbert
APPLICANT: Gerritee, Mihelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,453
                                                                                                                                                                                                                                                                                               CATY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GC361-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                     US-09-479-453-35
; Sequence 35, Application US/09479453
; Patent No. 6313283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 HFDELVELTSKLEWMLD 338
  366 -- DNLVRVAVGLEDVVD 380
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                    GENERAL INFORMATION:
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US-09-479-453-35
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; MOLECULE TYPE: US-08-996-338-20
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US-08-996-338-20
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 291,83
PILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25.618
REFERENCE/DOCKET NUMBER: TORIOTELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, App.
                                                                                                                                                                                                                                                 Best Local Similarity Matches 68; Conserv.
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TUKLUU-
APPLICANT: OKURA, Takanori
APPLICANT: KURIMOTO, Musashi
APPLICANT: KURIMOTO, POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-JUL-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
APPLICATION NUMBER: JP 215,488/1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 TPEGKWHA----SKVLRIE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 SPQELGHAFIDNVRVLPLE 299
                                         104 -RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSG 162
                                                                                  63 --VLEFWPVELNDTGSYFFQMKNYTQKWKLNVIRRNKHSCFTERQVTSKIVEVKKFFQIT 120
                                                                                                                           65 ISILEFF-----TPFFN-- 103
                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 22-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20004
                                                                                                                                                                    15 EPFYLKHCSCSLAHEIETTTKSWYKSSGSQEHVELNPRSSSRIAL------HDC 62
                                                                                                                                                                                                           9 DPKYI----LKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKC 64
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
CENSYYQTLVNSTSLYKN-CKKLLLENNK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                 4.6%; Score 87.5; DB 3; Length 521; llarity 21.3%; Pred. No. 0.7; Conservative 50; Mismatches 106; Indels 95;
                                                                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: JP 291,837/1997
09-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/996,338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TORIGOE=3
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                                                                                                                                                                                                                                                                                          DB 3; Length 521;
  -NPTIKKNAEFEDQ-GYYSCVH 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -MRIM
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US-08-604-333-2
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                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5776731
GENERAL INFORMATION:
APPLICANT: Parnet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 233-06-
TELEX: 756822
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 26.
TELECOMMUNICATION INFORMATION
TELEPHONE: (265) 597-0430
TELEPAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7
SOFTWARE: MICCOSOFT WORD,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 51
CITY: Seattle
CTY: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Parnet, Patricia et al.
TITLE OF INVERVION: Receptor Desig
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 FL--HH-----NGKLFNITK-----TENIT--IVEDRSNIVPVLLGPKLNHVAVELG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 TPEGKWHA----SKVLRIE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281 SPQELGHAFIDNVRVLPLE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 K---NVRLNCSALLNEEDVI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 RLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFW-FTVESGLIEN-HEGRKAYGAVLIS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 FVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMG 222
    188 FL--HH-----NGKLFNITK-----TFNIT--IVEDRSNIVPVLLGPKLNHVAVELG
                                      163 FVAPHQYLSLLQDRYFFIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMG 222
                                                                                  140 CENSYYQTLVNSTSLYKN-CKKLLLENNK------NPTIKKNAEFEDQ-GYYSCVH 187
                                                                                                                           104 -RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSG 162
                                                                                                                                                                    82 --VLEFWPVELNDTGSYFFQMKNYTQKWKLNVIRRNKHSCFTERQVTSKIVEVKKFFQIT 139
                                                                                                                                                                                                             65 ISILEFP-----TPFPN-- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 21 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 98101
                                                                                                                                                                                                                                                    34 EPFYLKHCSCSLAHEIETTTKSWYKSSGSQEHVELNPRSSSRIAL------HDC
                                                                                                                                                                                                                                                                                             9 DPKYI----LKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKC 64
                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2, Application US/08604333
5. 5776731
                                                                                                                                                                                                                                                                                                                                 68;
                                                                                                                                                                                                                                                                                                                               h 4.6%; Score 87.5; DB 1; Length 541; Similarity 21.3%; Pred. No. 0.75; 68; Conservative 50; Mismatches 106; Indels 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apple 7.1
ft Word, Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor Designated 2F1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
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                                                                                                                                                                                                                                                                                                                                   Gaps
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ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                   Sequence 28, Application US/09173151A Patent No. 6326472 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: LENGTH: 541 amino acids TYPE: amino acid STRANDEDNESS: not relevant
                                                                          281 SPQELGHAFIDNVRVLPLE 299
                                                                                                                   271 TPEGKWHA----SKVLRIE 285
  231 K---NVRLNCSALLNEEDVI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                       RESULT 26
US-09-173-151A-28
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                                   331 K---NVRLNCSALLNBEDVI------YMMFGEENGSDPNIHEEKE----MRIM 270
223 RLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFW-FTVESGLIEN-HEGRKAYGAVLIS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 RLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFW-FTVESGLIEN-HEGRKAYGAVLIS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 ISILEFF-----TPFFN-- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 -RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 FVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 4.6%; Score 87.5; DB 3; Length 541; Local Similarity 21.3%; Pred. No. 0.75; see 68; Conservative 50; Mismatches 106; Indels 95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 EPPYLKHCSCSLAHEIETTTKSWYKSSGSQEHVELNPRSSSRIAL-------HDC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 DPKYI----LKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKC 64
                                                                                                                                                                                                                      US-09-110-618-2

Sequence 2, Application US/09110618

Sequence 2, Application US/09110618

GENERAL INCEMATION:
APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2F1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation STREET: 5.1 University Street
CORRESPONDENCE SECURITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/110,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICALLC..
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/604,333
APPLICATION NUMBER: US/08/604,333
FILING DATE: 21-FBB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
"FILEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
                                                                                             281 SPQELGHAFIDNVRVLPLE 299
                                                                                                                                 271 TPEGKWHA----SKVLRIE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in EBNGTH: 541 amino acids
ryPB: amino acid
ryPB: amino acid
roPOLOGY: linear
MOLECULE TYPE: protein
US-09-110-618-2
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Matches
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APPLICANT: Timans, Jacqueline C.
APPLICANT: Theobets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Sana, Theodore R.
APPLICANT: Ratelein, Robert A.
APPLICANT: Ratelein, Robert A.
APPLICANT: Human Receptor Proteins, Related Reagents and Methods NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
-- YWMFGEENGSDPNIHEEKE----MRIM 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.6%; Score 87.5; DB 4; Length 541;
Best Local Similarity 21.3%; Pred. No. 0.75;
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SOFWARENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT 1998
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/05,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION NUMBER: US 60/078,008
FILING DATE: 17-NAR-1998
PRIOR APPLICATION NUMBER: US 60/091,883
FILING DATE: 12-APR-1998
PRIOR APPLICATION NUMBER: US 60/095,987
FILING DATE: 110-AUG-1998
PRIOR APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION NUMBER: US 60/095,987
FILING DATE: 110-AUG-1998
PRIOR APPLICATION NUMBER: US 60/078,416
FILING DATE: 110-AUG-1998
PRIOR APPLICATION NUMBER: US 60/078,416
FILING DATE: 115-OCT-1997
ATTORNEY AGAINT INDEMATION:
NUMBER: US 60/078,416
FILING DATE: TS-OCT-1997
ATTORNEY AGAINT INDEMATION:
NAME: Ching Edwin DATA:
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RESULT 27
US-09-578-178-2
; Sequence 2, Application US/09578178
; Patent No. 6451760
; Patent No. 6451760
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                                                                            US-09-578-178-2
    Ouery Match

4.6%; Score 87.5; DB 4; Length 541;
Best Local Similarity 21.3%; Pred. No. 0.75;
Matches 68; Conservative 50; Mismatches 106; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Parnet,
                                                                                                                                                 TELEFAX: (206) 233-0644
TELEFX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Receptor Design
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn h
                                                                                                 TYPE: amino acids
TYPE: amino acids
TOPOLOGY: 1:--
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/578,178
                                                                                                                                                                                                                                              NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 51 University Street
CITY: Seattle
STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 -RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSG 162
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US-08-392-625-20
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Patent No. 5
TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
RAPLICATION NUMBER: US 07/876,791
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: ESMODIA, ROBERT W.
REFIGISTRATION NUMBER: 32.893
REFERENCE/DOCKET NUMBER: 0652.09800
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 371-2600
TELECHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                              COMPUTER: IBM PC comparible COMPUTER: IBM PC comparible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATE: PTLING DATE: CLASSTER: US/08/392 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kupke, Thomas
APPLICANT: Jung, G nchar
APPLICANT: Kellner, Roland
TITLE OF INVENTION: Biosynthetic Process For The Preparation
TITLE OF INVENTION: Of Chemical Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 --VLEFWPVELNDTGSYFFQMKNYTQKWKLNVIRRNKHSCFTERQVTSKIVEVKKFFQIT 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
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5837485
                                                                                                                                                                                                                                                                                                                                                                                                                      D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Sterne, Kessler, 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wieland, Lunder Thomas
                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
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Klein, Cora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G tz, Priedrich
Schnell, No. 5837485bert
Augustin, Johannes
Engelke, Germar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenstein, Ralf
Kaletta, Cortina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Entian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Karl-Dieter
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                                                                            0652.0980002
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us-09-438-185a-1047.rai

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4.6%; Score 86.5; DB 2; Length 990; 23.1%; Pred. No. 2.4; tive 38; Mismatches 79; Indels 7:
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Patent No. 5962253
GENERAL INFORMATION:
APPLICANT: Roupe, Thomas
APPLICANT: Gotz, Friedrich
APPLICANT: Gotz, Friedrich
APPLICANT: Jung, Gunther
TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CIT's Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRAT APPLICATION DATA:
RPLICATION NUMBER: US/08/645,193B
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                  0652.0980004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/784,234
FILING DATE: 31-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Banand, ROBERT W.
REGISTRANION NUMBER: 32,893
REGISTRANION NUMBER: 0652.098000
TELECOMMUNICATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISCS:
                                                                                                                                                                                                                                                                                       LENGTH: 990 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-466-961A-20
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.1'
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 71
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US-08-645-193B-15
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                                                                                                                                            Query Match

4.6%; Score 86.5; DB 2; Length 990;
Best Local Similarity 23.1%; Pred. No. 2.4;
Matches 57; Conservative 38; Mismatches 79; Indels 73; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   764 FYIKFKEDEDFIK------LRLLREDEDYSQIYSFIKNW-KDYCLLNSELYDY 809
                                                                                                                                                                                                                                                                               601 FCPRIIYKNIILKPATWKINSEM---FSETENWLNRFATIRKWHIPKDVIIAFGDNRLLL 657
                                                                                                                                                                                                                                                                                                                               50 QKENKE----KQALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFF-- 102
                                                                                                                                                                                                                                                                                                                                                                                                                         103 ------NRNLWYRLLSSRFSLW----KSYCPRFFLDYLEAFGL---LSDFLDHQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    704 TSLKEQSFIIPKARNKHFNNLKDWFSIHLSIPKTYQDNFIQDYLLPFITELKVNNFINKF 763
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                                                                                                                                                                                                                                                                                                                                                                            658 NLLNDKHLIILKKELKKHGRIRILESF-----INESNNER-----MLEIVTPLYKK 703
                                                                                                                                                                                                                                          3 YCERTLDPKYILKIAL-KLRQSLSLFFQNSQSLQRAYSTPYSYY-----RIIL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Roland
TITLE OF INVENTION: Biosynthetic Process for the Preparation of
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/466,961A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
RICAN APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 New York Avenue, NW STRY: Washington
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G tz, Friedrich
Schnell, No. 5843709bert
Augustin, Johannes
Rogenstein, Ralf
Kaletta, Cortina
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APPLICATION NUMBER: US 08/392,625
PLING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,791
FILING DATE: 30-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-466-961A-20
; Sequence 20, Application US/08466961A
; Patent No. 5843709
; GENERAL INFORMATION:
                               LENGTH: 990 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-392-625-20
          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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13;
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73; Gaps
                                                                                                                                             601 FCPRIIYKNIILKPATWKINSEM---FSETENWLNRFATIRKWHIPKDVIIAFGDNRLLL 657
                                                                                                                                                                                                                                                50 QKENKE-----KQALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFF-- 102
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                                                                                3 YCERTLDPKYILKIAL-KLROSLSLFFQNSQSLQRAYSTPYSYY-----RIIL 49
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
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REFERENCE/DOCKET NUMBER: 0652
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 990 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: not relevant
MOLECULE TYPE: protein
US-08-645-193B-15
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TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4322
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US-09-134-001C-4322
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Patent NO. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: EDIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EDIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TILLE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR APPLICATION NUMBER: US/09/134,001C
PRIOR APPLICATION NUMBER: US/09/134,001C
PRIOR APPLICATION NUMBER: US/09/134,001C
PRIOR APPLICATION NUMBER: US/09/134,001C
PRIOR APPLICATION NUMBER: US/09/134,001C
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4322
                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 51
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Query Match
Query Match
Gest Local Similarity 21.7%; Pred No. 2.4;
Matches 62; Conservative 43; Mismatches 100; Indels 81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         810 YSIVDYVPEVYRYGGPHVIEDIENFFMYDSLLSINIIQSEFKIPKE 855
101 FFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPV 160
                                                                                                                                                                              369 CFQTVNPNNPAELLAEEKEVMDKLLLSFQQSEKLRRHMSFLMRKGKLYLPYNGNLLIHGC 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 HDLLGHVPWLLH------PSFSEFFINMGRLFTKVIEKVQALPSK 238
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                                                                                                                    48
                                                                                                                                                                                                                                                                                         / Match 4.6%; Score 86; DB 4; Length 656;
Local Similarity 22.5%; Pred. No. 1.5;
les 51; Conservative 28; Mismatches 78; Indels 70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 LQKENKE-----KQALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFF- 102
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                                                                                                                                                                                                                                     4 CERTLDPK---YILKIALKLRQSLSLFFQNSQSLQRAYS-----TPYS----YYRI 47
                                                          IPVDENGEMESFEIEGERLSGRELLDVFEYHVRRAFDH-----KESTEDISTDL------ 477
                                                                                                             ILQKENKEKQA-----LARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTF 100
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| RESUUS-00   | D 97 | 54 B 54  | 8 8 8   | Que<br>Best<br>Mat<br>Mat<br>Qy   | US-0<br>GPAESU<br>GPAESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>FRESU<br>F | Db<br>Db |
|---|------|--|---|---|--|----------|
| SSULT 33 \$-90-810-347-2 \$-90-810-347 Sequence 2, Application US/09810347 Patent No. 6461847 [GENERAL INFORMATION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES TITLE OF INVENTION: INFORMATION: HUMAN ENZYME PROTEINS, AND USES TITLE OF INVENTION: HERROF FILE REPERENCE: CL001169 CURRENT PILING DATE: 2001-03-19 NUMBER OF SEQ ID NOS: 6 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 3,72 | .Q   | GHVPWLLHPSFSEFFINMGRSHAPHGPEDSAPQFSKLYPNASQHITPSYNYA SHAAPHGPEDSAPQFSKLYPNASQHITPSYNYA KVQALPSKKQRIQTLQSNLIAIVRCFWFTVESG | 101 FFURNLMYRLLSSRFSLMKS-YCPRFFLDYLEAEGLLSDFLDHQAV 145  86 MCCPSRSSMLTGKYVHNHNVYTNNENCSSPSWQAMHEPRTFAVYLNNTGYRTAFFG 141  146 IKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFFIASVMRTLDKDNFSLTPDLIHDLL 203 | uery Match 4.5%; Score 84.5; DB 4; Length 360; est Local Similarity 19.6%; Pred. No. 0.85; atches 67; Conservative 51; Mismatches 117; Indels 107; Gaps 14  45 YRIILOKENKEKOALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTP 100 | SULT 32 :-09-810-347-4 :-09-810-347-4 :-09-810-347-4 PATENDER (A. ADDITION: DATE: ADDITION: APPLICANT: YE, Jane et al. TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CL001169 FULE REFERENC   | 478WTY   |
| <del></del>   |      |  |   |   | ••   |          |

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190 DNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNL 249
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JOS-1942-1952.

JOS-1942-1952.

JOSEPH TON 1965707

JOSEPH TAN 1965707

JOSEPH TAN 19697

JOSEPH TAN 19697

JOSEPH TON 19697

JOSEPH TON 19697

JULIE OF INVENTION: RAND. A NOVEL INHIBITOR OF

TITLE OF INVENTION: RANDIATED SIGNALING

NUMBER OF SEQUENCES: 15

CORRESPENDENCE ADDRESS: 19697

JOSEPH TON 19697

STREET: TWO Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTERO for Windows Version 2.0b
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/942,819
FILING DATE: 02-0CT-1997
464 VIDFARLEDSEVKEALGGIAVRAVNVSQGYPQRVG-
                                                               312 TPQETLFSIRHF----DELVELTSKLEWML 337
                                                                                                     506 SDKSVVNKİYELKNSTDNLTELKSFLETML 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 02-0cr-1997
CLASSIFICATION: 536
PRIDR APPLICATION NAMER: 60/058,520
APLICATION NUMBER: 60/058,520
ATTORNEY/ACBNT INFORMATION:
NAME: GEARADAN: Patricia
REGISTRATION NUMBER: 32,227
REPRENCE/DOCKET NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02173
COMPUTER READABLE FORM:
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 491 amino acid TYPE: amino acid
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Best Local Similarity 18.4%
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
COUNTRY: USI
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-942-819-2
                                                                                                                                                                         RESULT 35
US-08-942-819-2
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4.5%; Score 84.5; DB 4; Length 372;
Best Local Similarity 19.6%; Pred. No. 0.89;
Matches 67; Conservative 51; Mismatches 117; Indels 107; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.4%; Score 83.5; DB 6; Length 1365;
19.0%; Pred. No. 8.3;
tive 49; Mismatches 100; Indels 167; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 ----YLEAFGLLSDFLDH--- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 NGSRMSSIPQLKKILYTVPKEILVGADNKKQLHDLEPEELRELKLRVTSLISEFYQYKKD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 ------QAVIKFF----- 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 ITATLNFTKSIVNNPPLISKOLIKVSSVNKDIITSNEELNSKGFDYNMLGLYINGONWKI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 --VAPHQYLSLLQDRYFPIASVMRTLDK-----DNFSLTPDLIHDLLGHVPWL--- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 TSLTPYNLLTALKTEYQSLLKITNLLQELEPSKCILDSKFLLNKFSQFSLGKLQNLQPIK 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 --LH--PSFSFFFINMGRL----FTKVIEKVQAL--PSKKQRIQTLQSNLIALVRCFWF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 TVESGLIENHEGRKAYG----AVLISS----PQELGHAFIDNVRVLPLELDQIIRLPFNTS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 GCSTDMAVVSTPF--FNRNLWYRLLSS----RFSLWKSYC------------------ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 DKHWIMQYIGPMLPIHMEFINILQ------RKRLQILMSVDDSVERLYNMLVETGELE 307
                                                                                                                                                                                                                                                                                                                                                                                  196 TNESINYFKMSKRMYPHRPVMMVISHAAPHGPEDSAPQFSKLYPNASQHITPSYNYAPNM 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 YRIILQKENKEKQALARHKCISILEPPKNLLFVHLLSLSKNQR----EGCSTDMAVVSTP 100
                                                                                                                                                                                                                                                                101 F------PNRNLWYRLLSSRFSLWKS-YCPRFFLDYLEAFGLLSDFLDHQAV 145
                                                                                                                                                                                                                                                                                                           86 MCCPSRSSMLTGKYVHNHNVYTNNENCSSPSWQAMHEPRTFAVYLNNTGYRTAFFG---- 141
                                                                                                                                                                                                                                                                                                                                                      146 IKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRT--LDKDNFSLTPDLIHDLL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GHVPWILHPSFSEFFINMGR------ 223
                                                                                                                                                                                                          Patent No. 5194600

PAPPLICANT: BUSSEY, HOWARD, BOONE, CHARLES; SOMMER, STEVE S., HILL, KATHRYN, MEDSEY, PHILIP

TITLE OF INVENTION: GENES WHICH PARTICIPATE IN B-GLUCAN

ASSEMBLY AND USE THEREOF

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATE:

APPLICATION DATE: US/08/488,316

FILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 N----TYIIYTADHGYHIGQFGLVKGKSMPYDFD--IRVPF 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 NHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPF 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 19.0% nes 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1365
            TYPE: PRT
ORGANISM: Human
                                                  US-09-810-347-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 F-----HKIGQEVYK--QIKMPLEAMPYKRDLSIEEQSECTQDFYQNVAERMQT--- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 LFVHLLSLSKNOREGCSTDM--AVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 FGLLSDFLDH----QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVWRTLDK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S6 ELAERLQREBEBAFASSQSSQGAQSLTFSKFE---EKKTNEK----TRKVTTVKKFF--- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 KIALKLROSLSLFFONSQSLORAYSTPYSYYRIILOKENKEKQALARHKCISILEFFKNL 74
---LLPFSSD 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.4%; Score 83; DB 2; Length 491;
18.4%; Pred. No. 2;
tive 48; Mismatches 110; Indels 108;
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HENGTH: 284 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-159-2
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US-09-022-875-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-913-159-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.1
53; Conservative
                                                                                                                                                    Sequence 2, Application US/09022875
Patent No. 6071894
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08913159
Patent No. 6300109
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: DK 0
FILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
                                                               APPLICANT: Wallis, Nicola G.
TITLE OF INVENTION: NO. 6071
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT
                                                                                                                                                                                                                                                                                                                                                                             340 GLLESIPLY---NOEKYLSG-FE 358
                                                                                                                                                                                                                                                                                                                                                                                                                           111 KMS----EVERAARI------MYMLRVDFNGLYRVNSKNQFNVPYGRYKNPKIVDK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 PVNEEIPEVSDMVVKAITDIIEMDSK 281
                                                                                                                                                                                                                                                                                                                                 157 ELIESISEYLNNNSIKIMSGDFE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 NVRVLPLELDQIIRLPFNTSTPQETLFSIR-HFDELVELTSKLEW------MLDQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 PSKKQRIQTLQSNLIAIVRCFWFTVES--GLIENH--EGRKAYGAVLISSPQELGHAFID 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 MRTLDKDNFSLTPDL-----IHDLLGHVPWLLHPSFSEF---FINMGRLFTKVIEKVQAL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 PFNTSTPQETLFSIRHFDELVELTSK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 IAIVRCFWFTVESGLIENHEGRKAYGAVL---ISSPQELGHAFIDNVRVLPLELDQIIRL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 APQKAVINDFNSELINCYROMKDNPEQLIELLTNHQRENSKEYYLDLRSSDRD---GRID 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
CITY: Philadelphia
                     STREET:
                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNLLQKNKINLRPFTKWTGGKRQLLPHIQYLMPEKYNHFFEPFIGGGALFFE-----L 53
                   E: Dechert, Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --DQIEKHIMTRLYKFVFCPETTDDEKKDLAIQKRIRALHWVTPQMLCV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·4.3%; Score 82; DB 4; Length 284; 26.1%; Pred. No. 1.1; rative 29; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid-derived type II restriction-modification systems from Lactococcus lactis
                                                                                                                   No. 6071894el Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DK 0179/95
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                        1717 Arch Stre
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                                                                                                                                                            RESULT 38
US-09-810-347-5
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                                                                                       Sequence 5, Application US/09810347; Patent No. 6461847; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 861 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.3%; Score 82; DB 3; Length 861; Best Local Similarity 22.4%; Pred. No. 6; Matches 87; Conservative 66; Mismatches 144; Indels 92;
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEI
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 25-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION NDWAR:
APPLICATION NUMBER: US/09/022,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: ...
COUNTRY: USA
19103-2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  635 VTLLKQTRESMLQAERQLTHSNFLRSISHDIRTPLTTIMGNLDILVSHSKD------
                                                                                                                                                                                                                                                                                                              329 LTSKLEWMLDQGLLESIPLYNQEKYLSGF 357
                                                                                                                                                                                                                                                                                                                                                          745 RRHLKKRITVSSSVNLQFIHIDSKLILQALFNLIENAVKHTSTDTKINLSIRYASYEQIE
                                                                                                                                                                                                                                                                                                                                                                                                   270 GRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFD-ELVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    686 -MSIIEKEOLLVHSFQESQYLYLLVTNILSLTKLQSSNVQIKLQPYLVSELVEEIDMILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 FTKVIEKVQALP---SKKQRIQTLQSNLIAIVRCFWFTVE-----SGLIEN----HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 LSLLQDRYFPIASVMRTLDKDNF--SLTPDL---IHDLLGHVPWLLHPSFSEFFINMGRL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               596 TSPIK-----GILA--IDYQSSQVINPYDASILESMLNELSLA-----VEN 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 FSLWKSYCPRFFLDYLEAFGLLSDFLDHQA--VIKFFE---LETHFSYYPVSGFVAPHQY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 ----KTIPLONHIDNTTQQHEQALSWVIKNERQAGATTD-----TFPGINKW--LIPIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 KFQYSITKKQLYRTDLLFQFNDSIKQTYTVENLLINAGYQINQLLQQSITIYVINQSKVI 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 LARHKCISILEFFKNLLFVHLLSLS---KNQRE-GCSTDMAVVSTPFFNRNLWYRLLSSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 KYILKIALKLRQSLSLFFQNSQSLQRAYSTP----YSYYRI--ILQKE-----NKEKQA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                               FA-----VIDEG--PGISLEEQQKIFEPF 826
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                                              NUCLEIC
                           PROTEINS, AND USES
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Gaps

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Query Match
4.3%; Score 81.5; DB 1; Length 608;
Best Local Similarity 18.0%; Pred. No. 4;
Matches 67; Conservative 57; Mismatches 120; Indels 129;
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P.O. Box 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08493092
Patent No. 5728807
GENERAL INFORMATION:
GENERAL THORMATION:
APPLICANT: Tallioh, Yosef
APPLICANT: Collins, Francis S.
TITLE OF INVENTION: Ataxia-Telangiectasia Gene
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reiging, Ethington, Barnard & Perr
                        TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 608 amino acids
TYPE: amino acids
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide US-08-766-014-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 -----QEKYLSGF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 QLTKLKSTYIDGF 324
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                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.O
CITY: Troy
STATE: Mich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-493-092-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 NYAPNMDKHWIMQYTGPMLPIHMEFTNILQ------RKRLQTLMSVDDSVBRLYNMLV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 AVVSTPF-----FNRNLWYRLLSSRFSLWKS-YCPRFFLDYLEAFGLLSDF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 LDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRT--LDKDNFSLTPD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 LIHDLL----- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 YFTDLITNESINYFKMSKRMYPHRPVMMVISHAAPHGPEDSAPQFSKLYPNASQHITPSY 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93; Indels 99; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 AFVTTPMCCPSRSSMLTGKYVHNHNVYTNNENCSSPSWQAMHEPRTFAVYLNNTGYRTAF 86
                                                                                                                                                                                                                                                                                                                                                                               4.3%; Score 81.5; DB 4; Length 307;
19.8%; Pred. No. 1.4;
tive 39; Mismatches 93; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 ESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPF 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 ETGELEN----TYIIYTADHGYHIGQFGLVKGKSMPYDFD--IRVPF 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   One
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APPLICANT: Davis, Maria
APPLICANT: Davis, Maria
APPLICANT: Sta, Dan San, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, Dan SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, DAN SAL, 
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 60/008,688
FILING DATE: December 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 4.5" DISKETTE, 1.1 Mb
OPERATING SYSTEM: 11M P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
RPLING APPLICATION NUMBER: US/08/766,014
FILING DATE: Herewith
CLASSIFICATION: 435
                                    CURRENT APPLICATION NUMBER: US/09/810,347
CURRENT FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08766014 Patent No. 5744312 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 19.88
Matches 57; Conservative
        FILE REFERENCE: CL001169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
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ZIP: 90071-2066
                                                                                                                                                                                                                                                  TYPE: PRT
, ORGANISM: Human
US-09-810-347-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 39
US-08-766-014-3
                                                                                                                                                                             SEQ ID NO 5
LENGTH: 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 MNFIEEMDMKKLLLBIEMPLVEVLKSMEVSGFTLDKEVLKELSQKIDDRIGEI---LDKI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 IR---LPFNTSTPQE-TLFSIRHFDELVELISKLEWMLDQGLLESIPLYN----- 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 YKEAGYQFNVNSPKQLSEFLFEKLNLPVIKKTKTGYSTDSEVLEQLVPYNDIVSDIIEYR 311
                                                                 65 ISILEFFKNILFVHLISLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPR 124
                                                                                                                                                                                                         125 FFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPV-----SGFVAPHQYLSLLQ 174
                                                                                                                                                                                                                                                                                                                                                    175 DRYFPIASVMRTLDKDNFSLTPDLIHDLL-------GHVPWLLHPSFSEF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 FINMGRLFTKVIEKVQALPS------ZKQRIQTLQSNLIA---IVRCFW----- 257
                                                                                                                                   1 MKLLELFNKLEFFSLIDNIKKE----SSIEIVD------NHKVEKWSK---- 38
                                                                                                                                                                                                                                                                              39 --VDIKELVTLLQD-----NRNIAFYPLIYEGEIKKIAFSFGKDTVYIDVFQ 83
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RESULT 41
US-08-508-836A-2
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TOPOLOGY:
US-08-493-092-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08508836A Patent No. 5777093
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

4.3%; Score 81.5; DB 1; Length 1708;
Best Local Similarity 18.5%; Pred. No. 19;
Matches 61; Conservative 58; Mismatches 114; Indels 97; Gaps
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/08/508,836A
FILING DATE:
APPLICATION: 536
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
REGISTRATION: MUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-313 (TAU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGIH: 1708 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Shiloh, Yosef
APPLICANT: Tagle, Danilo A.
APPLICANT: Collins, Francis S.
TITLE OF INVENTION: Ataxia-Telangiectasia Gene
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 9-5
REFERENCE/DOCKET NUMBER: 9-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 689-3500
                                                                                                                                                                                                                                                                                                                                               STREET: P.O
CITY: Troy
STATE: Mich
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 KLVVNLLQLSKMAINHTGEKEVLEAVGSCL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 EVQKQVLDLL--KYL----VIDNKDNENLYITIKLLDPFPDHVVFKDLRITQQKIKYSRG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 ---HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV------ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 YINQRÞSCIMDVSÍRSFSÍCCDLÍSQVCQTAVTYCKDALENHL--HVIVGTLIPLVYEQV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 WKSYCPRFFLDY-LEAFGLLSDFLDH--QAVIKFFE--LETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
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STRANDEDNESS: siz
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Reising, Ethington, Barnard & Perry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 VYKKHRILKIYHLFVSLLL-----KDIKSGLGGAWA-----FVLRDVIYTLIH----- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 PKYILKIAL-----KLRQSLSLFFQNSQSLQRAYSTPYSYYRIIL---QKENKEKQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFSLLEEINH-FLSVSVYDALPLTRLEGLKDLRRQLELHKDQMVDIMRASQDNPQDGIMV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSHVIKATFAYISNCHKTKLKSILEILSK------SPDSYQKILLAICEQAAETNN 83
                                                                                                                                                                                                                                                                                                                        48099
                                                                                                                                                                                                                                                                                                                                                 Michigan
Y: US
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linear
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US-08-508-836A-8
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US-08-508-836A-2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,836A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
REGISTRATION UNUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-313 (TAU)
TELEPHONE: (810) 689-4071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08508836A
Patent No. 5777093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.3%; Score 81.5; DB 1; Length 1708; Best Local Similarity 18.5%; Pred. No. 19; Matches 61; Conservative 58; Mismatches 114; Indels 97; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Shiloh, Yosef
APPLICANT: Tsjle, Danilo A.
APPLICANT: Collins, Francis S.
TITLE OF INVENTION: Acaxia-Telangiectasia Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (810) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              ADUN-
STREET:
CITY: Troy
CITY: Michigan
US
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 EVOKOVLDLL -- KYL----VIDNKDNENLYITIKLLDPFPDHVVFKDLRITQQKIKYSRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1708 amir
TYPE: amino acid
STRANDEDNESS: sir
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P.O. Box 4390
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linear
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В Ś В á Db Ş 밁 á В Ś Вb Ş

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167 ---HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV----
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Patent No. 5955279
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ways Vensko, Nancy
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          619-235-8550
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                                                                                  ; ORGANISM: Homo sapiens
US-08-629-001A-3
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                     TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
  single
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OPERATING SYSTEM:
                   linear
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  STRANDEDNESS:
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US-08-874-266-2
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                                                                                                                                                                                                                                                                                     Query Match

4.3%; Score 81.5; DB 1; Length 3056;
Best Local Similarity 18.5%; Pred. No. 47;
Matches 61; Conservative 58; Mismatches 114; Indels 97; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 PWILHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
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                                                                                                                                                                                                                                                      10 PKYILKIAL-----KIRQSLSLFFQNSQSLQRAYSTPYSYYRIIL---QKENKEKQ 57
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; Sequence 3, Application US/08629001A
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ATAXIA TELANGIECTASIA GENE AND ITS
TITLE OF INVENTION: GENOMIC ORGANIZATION
NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
ADDRESSEE: 30500 No. 5858661thwestern Hwy.
CITY: Farmington Hills
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 ---HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV---
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COMPUTER: IBM PC Comparatible
COMPUTER: IBM PC Comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,001A
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CLASSIFICATION: 435
TATORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFRENCE/DOCKET NUMBER: 2290.00032
TELECOMMUNICATION INFORMATION:
TELEPAX: (810) 539-5050
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3056 amino acids
TYPE: amino acids
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INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 3056 amino acids TYPE: amino acid STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                           linear
                                                                                                        , TOPOLOGY:
US-08-508-836A-8
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1432 VYKKHRILKIYHLFVSLLL-----KDIKSGLGGAWA-----FVLRDVIYTLIH----- 1474
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Query Match
4.3%; Score 81.5; DB 2; Length 3056;
Best Local Similarity 18.5%; Pred. No. 47;
Matches 61; Conservative 58; Mismatches 114; Indels 97; Gaps
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APPLICATIONS IN THE ATM GENE
THIE OF INVENTION: ATAXIA-TELANGIECTASIA:MUTATIONS IN THE ATM GENE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
GITY: Newport Beach
GENERAL AND ADDRESSEES AND ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES ADDRESSEES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 3056
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-642-274D-3
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US-08-642-274D-3
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SEQ ID NO 3
LENGTH: 30
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Sequence 3, Application US/08642274D

Patent No. 6200749

GENERAL INFORMATION:

APPLICANT: Shiloh, Yosef

TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO TITLE OF INVENTION: SCREEN FOR A PARTIAL A-T PHENOTYPE

FILE REFERENCE: 229000033

CURRENT APPLICATION NUMBER: US/08/642,274D

CURRENT FILING DATE: 1996-05-03

NUMBER OF SEQ ID NOS: 220

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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TYPE: amino acid
STRANDENMESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                          1382 PSHVIKATFAYISNCHKTKLKSILEILSK-----SPDSYQKILLAICEQAAETNN 1431
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                                                  1475 YINQRPSCIMDVSLRSFSLCCDLLSQVCQTAVTYCKDALENHL--HVIVGTLIPLVYEQV 1532
                                                                                                                                                        1432 VYKKHRILKİYHLFVSLLL------KDIKSGLGGAWA-----FVLRDVIYTLIH----- 1474
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167 --- HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV-
                                                                                                  118 WKSYCPRFFLDY-LEAFGLLSDFLDH--QAVIKFFE--LETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 WKSYCPRFFLDY-LEAFGLLSDFLDH--QAVIKFFE--LETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                                        58 ALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSL 117
                                                                                                                                                                                                                                                                                                             10 PKYILKIAL-----KLRQSLSLFFQNSQSLQRAYSTPYSYYRIIL---QKENKEKQ 57
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                                                                                                                                                                                                                                                                                                                                                                   61; Conservative
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                                                                                                                                                                                                                                                                                                                                                          4.3%; Score 81.5; DB 4; Length 3056;
18.5%; Pred. No. 47;
ative 58; Mismatches 114; Indels 97; Gaps
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TELEPHONE: 810-539-5050
TELEPAX: 810-539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3056 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                  Best Local Similarity Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                Query Match
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Patent No. 6211336
GENERAL INFORMATION:
                                                                                                                                                                                        1382 PSHVIKATFAYISNCHKTKLKSILEILSK------SPDSYQKILLAICEQAAETNN 1431
                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KOhn, Kenneth I.
REGISTRATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1533 EVQKQVLDLL--KYL----VIDNKDNENLYITIKLLDPFPDHVVFKDLRITQQKIKYSRG 1586
1475 YINQRPSCIMDVSLRSFSLCCDLLSQVCQTAVTYCKDALENHL--HVIVGTLIPLVYEQV 1532
                                                                                            1432 VYKKHRILKIYHLFVSLLL------KDIKSGLGGAWA-----FVLRDVIYTLIH----- 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tagle, Danilo A.
APPLICANT: Collins, Francis S.
TITLE OF INVENTION: ATAXIA-TELANGIECTASIA GENE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Shiloh, Yosef
APPLICANT: Tagle, Danilo A.
APPLICANT: Collins, Francis
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                                              118 WKSYCPRFFLDY-LEAFGLLSDFLDH--QAVIKFFE--LETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 -----AYGAVL 278
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                                                                                                                                          58 ALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSL 117
                                                                                                                                                                                                                                       10 PKYILKIAL-----KLRQSLSLFFQNSQSLQRAYSTPYSYYRIIL---QKENKEKQ 57
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STREET: 30500 No. 6211336thwestern Hwy., Suite 410
CITY: Farmington Hills
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
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                                                                                                                                                                                                                                                                                     Conservative
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18.5%; Pred. No. 47;
ative 58; Mismatches 114; Indels 97; Gaps
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167 --- HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV---

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1533 EVQKQVLDLL--KYL----VIDNKDNENLYITIKLLDPFPDHVVFKDLRITQQKIKYSRG 1586
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                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Richard A. Gatti
APPLICANT: Richard A. Gatti
TITLE OF INVENTION: METHODS FOR DETECTION OF ATAXIA
TITLE OF INVENTION: TELANGIECTASIA MUTATIONS
FILE REFRENCE: 510015-22
CURRENT APPLICATION NUMBER: US/09/360,416
CURRENT PILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 143
SOFTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1647 KLVVNLLOLSKMAINHTGEKEVLEAVGSCL 1676
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US-08-540-804-18
Sequence 18, Application US/08540804
; Sequence 18, Application US/08540804
; Patent NO. 591966
; Patent NO. 591966

FENERAL INFORMATION:
                                                                                                                                                                                                                                   RESULT 46
US-00-360-416-3
'Sequence 3, Application US/09360416
; Patent No. 6458536
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Best Local Similarity
Matches 61; Conserv
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1382 PSHVIKATFAYISNCHKTKLKSILEILSK------SPDSYQKILLAICEQAAETNN 1431
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4.3%; Score 81.5; DB 4; Length 3056;,
Best Local Similarity 18.5%; Fred. NO.47;
Matches 61; Conservative 58; Mismatches 114; Indels 97; Gaps
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                                                              207 PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
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                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: ATAXTA-TELANGIECTASIA GENE AND ITS
TITLE OF INVENTION: GENOMIC ORGANIZATION
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSES: Kohn & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Kohn & Associates
STREET: 30500 No. 6265158thwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,014C
PILING DATE:
                                                                                                                                                                                 1646 KLVVNLLQLSKMAINHTGEKEVLEAVGSCL 1675
                                                                                                                                                267 -----AYGAVL 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: KODIN, Kenneth I.
REGISTRATION NUMBER: 30,995
REFERRICE/DOCKET NUMBER: 225
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 810-539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3056 amino acids
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: line
MOLECULE TYPE: I
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 ALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSL 117
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207 PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAJVRCFWFTVESGLIE 266
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APPLICANT: Koleske, Anthony J.
APPLICANT: Thompson, Craig M.
APPLICANT: Thompson, Craig M.
TITLE OF INVENTION: No. 5919666el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Therefor
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 3057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.3%; Score 81.5; DB 4; Length 3(18.5%; Pred. No. 47;
ive 58; Mismatches 114; Indels
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Two Militia Drive

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-661-5240
TELEPAY: 617-661-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
TYPE: molecular TYPE: protein
US-08-540-804-18
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US-08-218-265-18
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Sequence 18. Application US/08218265
Patent No. 5922585
GENERAL INFORMATION:
APPLICANT: Young, Richard A.
APPLICANT: Yoleske, Anthony J.
APPLICANT: Thompson, Craig M.
TITLE OF INVENTION: No. 5922585el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
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APPLICATION UNMBER: US/08/540,804
FILING DATE: 11-OCT-1995
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/521,872
FILING DATE: 21-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,265
FILING DATE: 25-MAR-1994
ANTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
RESERRENCE/DOCKET NUMBER: 32 227
RESERRENCE/DOCKET NUMBER: 32 127
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: FLOPPY DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Search completed: January 9, 2003, 17:00:47 Job time : 42 secs

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPAY: 617-861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
TYPE: protein
MOLECULE TYPE: protein
US-08-218-265-18
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Matches 56; Conservative 31; Mismatches 71; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,265
FILING DATE: 25-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI94-03
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
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STATE: MA
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| Q98c23 arabidopsis<br>Q9gf63 arabis alpi<br>Q4248 lates calca<br>Q9gf55 cardamine a<br>Q9gf31 cardamine p<br>Q9gf30 cardamine r<br>Q9f33 muhlanbergi<br>Q9f29 enneapogon<br>Q9f29 enneapogon<br>Q9f29 enneapogon<br>Q9f129 enneapogon<br>Q9f129 enneapogon<br>Q9f129 enneapogon<br>Q9f139 enneapogon | Oggi41 aubrieta de Oggi41 aubrieta de Oggi60 buchloe dac Ogge60 buchloe dac Ogge60 buchloe dac Ogge718 reederochlo Ogwa23 drosophila Oggi64 arabis alpi Ogwa23 oryza meyer Ogt244 dictyosteli Ogyane sulfolobus Ogwac5 aufclobus Ogwac5 forosophila Phyll phyll buch Oggi1 ebola virus Ogdi1 ebola virus Oggi1 ebola virus Oggi1 aggongon C Oggf21 grantus nory Oggi1 phyll methanosarc   | Oghico zeugites pi<br>Oghico zeugites pi<br>Oghis Gampylobact<br>Oghin musculu<br>Oggage caenorhabdi<br>Ogniga lymnaea sta<br>Ogniga lymnaea sta<br>Ogniga lymnaea sta<br>Ogniga lymnaea sta<br>Ogniga letif<br>Ogniga oryza aletif<br>Ogniga oryza aletif<br>Ogniga oryza grand<br>Ogfeo oryza aletif<br>Ogniga expis proc<br>Ogfeo oryza aletif<br>Ogniga expis proc<br>Ogfeo oryza aletif<br>Ogniga oryza indle<br>Ogniga oryza indle | Oggets pleurotus or Oggets pleurotus or Oggets cuclinimals Oggets crucinimals Oggets crucinimals Oggets crucinimals Oggets crucinimals Oggets crucinimals Oggets crucinimals oggets crucinimals oggets |
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| n 5.1.3 Compugen Ltd. ; Search time 81 Seconds (without alignments uppares/sec   | ω   | cted by chance to have a sof the result being printed,   | Description  Oppu40 gallus gall O96370 schistosoma Q2400 drosophila Q8sy55 drosophila Q8ty0 homo sapien Q9478 streptomyce Q23438 caenorhabdi Q9xxdl caenorhabdi Q9xxql caenorhabdi Q9xqf geodia cydo Q9wKz drosophila Q9647 geodia cydo Q9wKz drosophila Q9648 branchiosto   |
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RESULT
Q9PU40
ID QS
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DT 01
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Q9PU40;
01-MAY-2000
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          SEQUENCE FROM N.A.
STRAIN=PURRYOR RICAN;
STRAIN=PURRYOR RICAN;
MEDLINE=99348305; PubMed=10419488;
Hamdan F.P., Ribeiro P.;
"Characterization of a stable form of thuman parasite Schistosoma mansoni.";
J. Biol. Chem. 274:21746-21754(1999).
EMBL; AF031034; AAD01923.1; -
HSSP; P04177; 1TOH.
                                                                                                                      Schistosoma mansoni (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                     O96370 PRELIMINARY; PRT; 497 AA.
O96370;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tryptophan hydroxylase (EC 1.14.16.4).
TPH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cPhox-2 and Cash-1: evidence for distinct inductive stedifferentiation of chick sympathetic precursor cells."
Mech. Dev. 52:125-136(1995).
EMBL; AJ251387; CAB62388.1; -.
HSSP; P04177; ITOH.
HSSP; P04177; ITOH.
InterPro; IPR001273; Asa_hydroxylase.
Pfam; PF00351; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
PROSTIE; PS00367; BIOPTERIN HYDROXYL; 1.
TIGRCALS; TIGRO1269; Tyr 3_monoox; 1.
TIGRCALS; TIGRO1269; Tyr 3_monoox; 1.
TIGRCALS; TIGRO1269; Tyr 3_monoox; 1.
TIGRCALS; TIGRO1269; Tyr 3_monoox; 1.
TIGRCALS; TIGRO1269; Tyr 3_monoox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tyrosine hydroxylase.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The expression of tyrosine hydroxylase and the transcription factors cPhox-2 and Cash-1: evidence for distinct inductive steps in the differentiation of chick sympathetic precursor cells.";
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MEDLINE=96076133; PubMed=7577670;

Ernsberger U., Patzke H., Tissier-Seta J.P., Reh T., Goridis C.,

Rohrer H.;

Rohrer H.;
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InterPro; IPR001273; Aaa_hydroxylase
                                                                                                             NCBI_TaxID=6183;
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                                                                                                                                                                                                                                                                     387
                                                                                                                                                                                                                                                                                                                                                                                                      107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
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                                                                                                                                                                                                                                                                                                                                                                       159
                                                                                                                                                                                                                                                                                                                                                                                            226 WKEVYSTLKSLYPTHACK---EYLEAFNLLEKFCGYNENNIPQLEEVSRFLKERTGFQLR 282
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                                                                                                                                                                                                                                                                   LSSYGELIHSLSDEPEVRDFDPDAAAVQPYQDQNYQPVYFVSESFSD 433
                                                                                                                                                                                                                                                                                                                                                                      PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF
                                                                                                                                                                                                                                                                                        ISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDE 325
                                                                                                                                                                                                                                                                                                            QDIG-----YWFTVEFGLCRQNGIVKAYGAGL
                                                                                                                                                                                                                                                                                                                                                    PVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADKTFAQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                    66;
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                                                   tryptophan hydroxylase from the
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STRAINBERKELELS,

Adams M.D., Cellniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Cellniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Balazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Peese M.G.,

Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V.
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Drosophila, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                            96 VVSTPFFNRNLWYRLLSSRFSLWK-SYCPRFFLDYLEAFGLLSDFLDH-----QAVI 146
                                                                                                                                                                                                                                                                                                                                               201 IVEYTEIEKTTWGRIYRELTRLYKTSACHEF----QKNLGLLQDKAGYNEFDLPQLQVVS 256
                                                                                                                                                                                                                                                                                                                                                                                             147 KPFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLLHDLLGHV 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 PMLADPKFARFSQEIG-----LASLGTSDEEIKKLAT-----CYPFTIEFGLCR 360
                                                                                                                                                                                                                                        29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 QDNQLKAYGAGLLSSVARLQHALSDKAVIKPFIPMKVINEECLVTTFQNGYFFISSFED 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 NHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDE 325
                                                                                                                                                                              Match 11.9%; Score 224.5; DB 5; Length 497; Local Similarity 28.5%; Pred. No. 5.6e-11; es 68; Conservative 34; Mismatches 108; Indels 29;
                                                                                                                                497 AA; 57598 MW; F8964E4E4B2C361D CRC64;
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Last annotation update)
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Pfam; PF00351; biopterin H; 1.
PRINTS; PR00372; PYMPTKLASE;
TIGREAMS; TIGR01270; Trp 5 monoox; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
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NCBI_TaxID=7227;
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PLE OR CG10118.
                                                                                                          Oxidoreductase.
SEQUENCE 497
                                                                                                                                                                                          Query Match
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Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shide B.C., Siden-Kfalmos I., Sampson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun B., Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X., Wangsarman D.A., Weinstock G.M., Weissenbach J., Wang S.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Zhon W., Land B.C., Stan M., Zhong K.C., Wu D., Xang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri G.S., Zhan M., Zhang G., Zhao Q., Zheng I., Zhong K.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Globe R.A., Myers B.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 DYLEAFGLLSD---FLDH-----QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRXFP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 IASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | : : | : | : | | | | | | | | 389 STQYVRHVNSPYHTPEPDSIHELLGHMPLLADPSFAQFSQEIG------LASLGASD 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 --NVRVLPLE-------LDQIIRLPFNTSTPQETLFSIRHFD--ELVELT 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 PASTAVQPYQDQEYQPIYYVAESFEDAKDKFRRWVSTMSRPFEVRFN-PHTERVEVLDSV 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Gaps
                                                                                                                                                                                                                                STRAIN=CANTON S;
STRAIN=CANTON S;
BIDLINES-S9014502; PubMed=7929381;
Birman S., Morgan B., Anzivino M., Hirsh J.;
"A novel and major isoform of tyrosine hydroxylase in Drosophila is
generated by alternative RNA processing.";
J. Biol. Chem. 269:26559-26567(1994).
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Neckameyer W.S., Quinn W.G.;
"Isolation and characterization of the gene for Drosophila tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 QRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFID-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.6%; Score 219; DB 5; Length 579; 28.6%; Pred. No. 2e-10; tive 37; Mismatches 94; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CANTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydroxylase.
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Q8SY95;
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ID Q8SY6
D0 Q8Y1
DT 01-JI
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Drosophila melanogaster (Fruit fly)

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303

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RESULT
Q91WV1
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Best Local S
Matches 64
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Best Local
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Q91WV1;
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Q91WV1;
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Q91WV1;
Q1-DEC-2001 (TrEMBLrel. 19,
Q1-UN-2002 (TrEMBLrel. 21,
Q1-UN-2002 (TrEMBLrel. 21,
Q1-DEC-2001 (MOUSE),
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC013458; AAH13458 1; -.
InterPro; IPR001273; Aaa hydroxylase.
InterPro; IPR002912; ACT.
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                                                                                                                                                                                                                         TIGRFAMS; TIGR01268; Phe4hydrox_tetr; PROSITE; PS00367; BIOPTERIN_HYDROXYL;
                                                                                                                                                                                                                                                                                              Pfam; PF01842; ACT; 1.
Pfam; PF00351; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=KIDNEY;
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                                                                                                                                                                                       51899 MW;
                                      11.4%; Score 215.5;
27.8%; Pred. No. 2.96
tive 40; Mismatches
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28.6%; Pred. No. 2e-10;
ive 37; Mismatches
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551F181FA59DEA5B CRC64;
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O1-TUN-2002 (TrEMBLrel 21,
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                                                                Mammalia; Euther
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
        SEQUENCE FROM N.A.
                                                                                                                                                                                                                         Phenylalanine hydroxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPQPDICHELLGHVPLFSDRSFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSSFGELQYCLSDKPKLLPLELEKTACQEYTVTEFQPLYYVAESFNDAKE
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62; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LASLGAPDEYIEKLAT-----IYWFTVEFGLCKEGDSIKAYGAGL
                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51861 MW; DEF9DB9D6B8C800C CRC64;
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26.6%; Pred. No. 4.4e-10;
tive 44; Mismatches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
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                                                                                                               Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 452
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                                                                                                                                                 Vertebrata;
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                                                                                                               Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                               Homo
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Gaps

275 300 215 240 155 밁 Ş 밁 á 밁 Ś 밁 5 В

SO DE RECEPTOR DE LA COMPTANTA

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462 FEEAQO---KLRMFTNNMKRPFİVRYN--PYTESVEVL 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
      235 DALVTDG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taich A.;
                                                                                                                                                           023438
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U., Sanchez C., Chen M., Edwards D.J., Shen B.,
A locus encodaing nouribosomal peptide synthetase and polyketide
"A locus encodaing nouribosomal peptide synthetase and polyketide
synthase functions in the bleomycin producer Streptomyces verticillus
                                                                                                                                                                                                                                                                                                                                                                                                     301 QFSQEIG-----LASLGAPDEYIEKLAT-----IYWPTVEFGLCKQGDSIKAYG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHF 155
                                                                                                                                                                                                                                                                                                              184 KKTWGTVPKTLKŠLYKTHA----CYEYNHIPPLLEKYCGFHEDNIPQLEDVSQFLQTCTGF 240
                                                                                                                                                                                                                                                                                                                                                                         156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 HFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 LGGAILSSADEIRQCLDPACPVEPFDPBVVRFATYDILRLQSRYFAVEDLEEIESALADL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 VSTPP--FNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFL-DHQAVIKPFELET 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 FSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 YGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKL 333
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match

10.9%; Score 206.5; DB 2; Length 244;
Best Local Similarity 23.9%; Pred. No. 8.2e-10;
Matches 59; Conservative 48; Mismatches 123; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 VOEPYGPVDQEVWRHLYRQQAELVPAAAPPLYLEGLALLGLPTDHVPDLGQVNERLSAVS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces verticillus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycera. VCBI_TaxID=29309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 AVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 AGLLSSFGELQYCLSEKPKLLPLELEKTAIQNYTVTEFQPLYYVAESFNDAKE 397
                                                                                                                                                     Match 11.3%; Score 213.5; DB 4; Length 452; Local Similarity 26.6%; Pred. No. 4.4e-10; les 62; Conservative 44; Mismatches 100; Indels 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF340166, AAK27471.1;
InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF00351; biopterin H; 1.
SEQUENCE 244 AA; 27012 MW; 31962679A28916C7 CRC64;
                     Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCC2651; AAH26251.1; -
SEQUENCE 452 AA; 51790 MW; 018E9629BBDD640D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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TISSUE=LIVER;
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                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 RNLW---YRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 RKTWGIIYRKIR---ELHKKHACKQFLDNFELLERHCGYSENNIPQLEDICKFLKAKTGF 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 QFSQEIG-----LASLGASEEDLKKLATL------YFFSIEFGLSSDDAADSPVK 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 ---ENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402 ENGSNHERFKUYGAGLLSSAGELQHAVEGSATIIRFDPDRVVEQECLITTFQSAYFYTRN 461
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                                                                                                                                                                                            Caenorhabditis elegans.
Bukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
MCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
WALCESTON WAS EXECUTED.";
"Direct Submission.";
Submitted (SF2-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 10176; 1PHZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of C. elegans cosmid ZK1290.";
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypotherical protein. ---
SEQUENCE 522 AA; 59781 MW, B6205C4E932C21FA CRC64;
                                                                                              Last sequence update)
Last annotation update)
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   522 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pram, Pr00351; biopterin H; 1.
PRINTS; PR00372; FYMHYDRÄLASE.
TIGRFAMs; TIGR01270; Trp_5_monoox; 1.
                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequ
01-UTN-2002 (TrEMBLrel. 21, Last anno
Hypothetical 59.8 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
PRELIMINARY;
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Gaps

15;

190

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RESULT 11
Q9XYQ5
ID Q9XYQ
AC Q9XYQ
DT 01-VQ
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Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                                                               Q9XYQ5;
01-NOV-1999
STRAIN-BRISTOL N2;
Loer C.M., Davidson B., McKerrow J.;
"A phenylalanine hydroxylase gene from the nematode elegans is expressed in the hypodermis.";
J. Neurogenet. 0:00(1999).
EMBL; AF11938; AAD31643.1; -.
HSSP; P00439; 4PAH.
InterPro; IPR001273; ABA_hydroxylase.
InterPro; IPR002912; ACT.
                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Phenylalanine hydroxylase (EC 1.14.16.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sze J.Y., Ruvkun G.; "tph-1 encodes a C. elegans tryptophan hydroxylase."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF135186; AAD30115.1; -...HSSP; P04176; 1PHZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     u1-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-JUN-2002 (TrEMBLrel. 21,
Tryptophan hydroxylase.
TPH-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9XYQ5
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001273; Aaa_hydroxylase.
Pfam; PF00351; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
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Eukaryota; Metazoa; Nem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 FEEAQQ---KLRMFTNNMKRPFIVRYN--PYTESVEVL 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 RNLW----YRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKTWGIIYRKLR---ELHKKHACKOFLDNFELLERHCGYSENNIPQLEDICKFLKAKTGF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---ENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QFSQEIG-----LASLGASEEDLKKLATL------YFFSIEFGLSSDDAADSPVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGSNHERFKVYGAGLLSSAGELOHAVEGSATIIRFDPDRVVEQECLITTFQSAYFYTRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity 25.: 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR01270; Trp 5 monoox; 532 AA; 60863 MW; 8ACt
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.9%; Score 206.5; DB 5; 25.2%; Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Mismatches 116; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8AC6A51C7DD0121F CRC64;
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                                                                                                                                  Caenorhabditis
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Best Local :
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               Dev. Comp. Immunol. 22:469-478(1998).

EMBL; Y16353; CAA76184.1; -.

HSSP; P00439; ZPAH.

InterPro; IPR001273; Aaa_hydroxylase.
InterPro; IPR002912; ACT.

Pfam; PF01842; ACT; 1.

Pfam; PF00351; biopterin H; 1.

PFAINTS; PR00372; FYMYDRTARS.

TIGRFAMB; TIGR01268; Phe4hydrox tetr; 1

SEQUENCE 450 AA; 51204 MW; 69188021
                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Phenylalanine hydroxylase.
Geodia cydonium (Sponge).
Eukaryota, Metazoa; Porifera; Demospongiae; Tetracti
Astrophorida; Geodiidae; Geodia.
NCBI_TaxID=6047;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=99093257.
Wiens M., Kozioł C., Bateł R., Mueller W.;
"Phenylalanine hydroxylase from the sponge Geodia cydonium:
"mplication for allorecognition and evolution of aromatic as
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Pfam; PF01842; ACT; 1.

Pfam; PF01842; ACT; 1.

Pfam; PF00351; biopterin H; 1.

PRINTS; PR00372; FYMHYDRXLASE.

TIGRAD48; TIGR01268; Phe4Hydrox tetr; 1.

PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.

PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.

PROSITE; PS00192; CYTOCHROME_B_HEME; UNKNOWN_1.

Oxidoreductase.

Oxidoreductase.

SEQUENCE 457 AA; 52189 MM; 7A573B884B9EF6FC CRC64;
                                                                                                                                                                                                                  hydroxylases.";
Dev. Comp. Immu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.6%; Score 181.5; DB 5; Length 457; Local Similarity 21.8%; Pred. No. 2.4e-07; les 83; Conservative 66; Mismatches 137; Indels 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YNELTVMYPKNACQEF--NYI--FPLLQQNCGFGPDRIPQLQDVSDFLKDCTGYTIRPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSSRFSLW-KSYCPRFFLDYLEAFGLLSD-----FLDHQAVIKFFELETHFSYYPVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLSSFGELOYALSDKPEVVDFDPAVCCVTKYPITEYQPKYFLAESFASAKNKLKSWAATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LISSPQELGHAFIDNVRVLPLE--LDQIIRLPFNTSTPQETL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLLSPRDFLAGWAFRVFHSTQYIRHHSAPKYTPEPDICHELLGHVPLFADVEFAQFSQEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FFKNLL-----FVHLLSLSKNQREGCSTDMA------VVSTPFFNRNL--WYRL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSIRH--FDELVELTSKL 333
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                    ; Phe4hydrox_tetr; 1.
51204 MW; 691880218BB9725D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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406

317 346 277 306 221 246 161

CRC64;

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Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Wyers B.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, delta subdivision, Myxobacteria,
Myxococcales, Cystobacterineae, Myxococcaceae, Myxococcus.
NCBL TaxID=34
                                                                                                                                                                                                             Interpro; IPR001273; Aaa hydroxylase.
Interpro; IPR001273; Aaa hydroxylase.
Fram; PF01842; ACT.
Fram; PF001842; ACT.
Fram; PF00375; PYWHYDRXLASE.
IIGRAMS; TIGR01270; Try 5- anonox; 1.
PROSITE; PS00387; BIOPTERIM; HYDROXXL; 1.
SEQUENCE 555 AA; 61530 MW; 60D527EFB1FA791C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OFFDG3;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 LGHMPLLANSFAQFSQEIG----LASLGASDADIEKLATL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 GLCKQADSTFKVYGAGLLSSVAELQHA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                            EMBL; AE003470; AAF47444.1; -. HSSP; P04176; 1PHZ.
                                                                                                                                                                                     FlyBase; FBgn0035187; CG9122.
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RADAMEM M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RADAMEM M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RADAMEM G., Scherer S.E., Holt R.A., Eshburner M., Henderson S.N.,

RADAMEM G., Wordman J.R., Yandell M.D., Zhang Q., Chen L.K.,

RADAMEM G., Wordman J.R., Yandell M.D., Zhang Q., Chen L.K.,

RADAMI J.F., Agbayani A., An H.J., Andrews Pfannkoch C., Baldwin D.,

RADAMI J.F., Agbayani A., An H.J., Andrews Pfannkoch C., Baldwin D.,

RADAMI J.F., Agbayani A., An H.J., Andrews Pfannkoch C., Baldwin D.,

RADAMI J.F., Agbayani A., An H.J., Andrews Pfannkoch C., Baldwin D.,

RADAMI J.F., Agbayani A., An H.J., Andrews Pfannkoch C., Baldwin D.,

RADAMI J.F., Agbayani A., An H.J., Andrews Pfannkoch C., Baldwin D.,

RADAMI J.F., Agbayani A., Danke C., Davenport L.B., Davies P.,

RADAMI J.F., Doyle C., Barman B.P., Bhandari D., Bolshakov S.,

RADAMI J.F., Doyle C., Berman B.P., Bhandari D., Bolshakov S.,

RADAMI J.F., Doyle C., Davenport L.B., Davies P.,

RADAMI J.F., Doyle C., Davenport L.B., Davies P.,

RADAMI J.F., Doyle C., Davenport L.B., Davies P.,

RADAMI K.J., Brangelista C.C., Perract S., Fleischmann W.,

RADAMI K.J., Brangelista C.C., Perract S., Fleischmann W.,

RADAMI K.J., Harvey D., Heiman T.J., Harnandez J.R., Houck J.,

RADAMI M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,

Liu X., Mattel B., Morlnoch T.C., Moleod M. P., Morbherson D.,

RADAMI S.M., Moy M., Murphy B., Murphy L., Murshy D., Murshy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy
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Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,

Ereryotas, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,

Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                    186 WRIPTHLVDLFPTHACK---EHNHVPPLLQENCGYREDNIPQLEEVSGYLQSCTGFRLR 242
                                                                                                                                                                                                                                                                         302 QEIG------LASLGAPEEVVQQLAT------LYWFTIEFGLCKQDGQTKAYGAGL 345
                                                                                                                         107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                           159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                          219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                          Gaps
                                                                      80; Indels 35;
      9.4%; Score 178.5; DB 5; Length 450; 25.8%; Pred. No. 4.3e-07; Live 43; Mismatches 80; Indels 35.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
Query Match
Best Local Similarity 25.8%
Matches 55; Conservative
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-------YFFTVEF 387
                                                                                                                                143 QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDL 202
                                                                                                                                                                    284 QDVSVYLKRKTGFQLRPVAGYLSPRDFLSGLAFRVFHCTQYIRHSSDPFYTPEPDCCHEL 343
                                                                                                                                                                                                                                                      203 LGHVPWLLHPSFSEPFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVES 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 STDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 LETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLL 210
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SEQUENCE FROM N.A.

Sun H., Shi W.;

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"Genetic Studies of mrp, a Locus Essential for Cellular Aggregation of Myxococcus xanthus.";

"Bacteriol. 183:4786-4795 (2001).

EMBL, AF285263, AAF99327.1;

TherPro. IRROQLY33, AAR, Hydroxylase.

Pfam, PPRO9351; biopterin H; U. CB22E52F8A613AEB CRC64;
/ Match 9.4%; Score 178.5; DB 5; Length 555; Local Similarity 32.0%; Pred. No. 5.6e-07; Loss 47; Conservative 28; Mismatches 55; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Б
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RESULT 16
Q95LQ6
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ID 01749
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Best Local S
Matches 64
Q95LQ6;
Q95LQ6;
01-DEC-2001
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O17498;
O1-JAN-1998
O1-JAN-1998
O1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOI. Biol. Evol. 15:1373-1380 (1998).
EMBL; AJ001677; CAA04917.1; -.
HSSP; P04176; 1PHZ.
InterPro; IPR001273; Aaa hydroxylase.
InterPro; IPR002219; ACT.
InterPro; IPR002219; Histone_H2A.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phenylalanine hydroxylase (EC 1.14.16.1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00351; biopterin_H; 1.
TIGRPAMS; TIGR01268; Phe4hydrox tetr; 1.
PROSTIE; PS00046; HISTONE_HZA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Patton S.J., Luke G.N., Holland P.W.H.;

"Complex history of a chromosomal paralogy region: i
amphioxus aromatic amino acid hydroxylase genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase.
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                                                                                                                                                                                          389
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                                                                                                                                                                                                                                                                                                HRSESCRYCLTDKPDIRPFEPEKISVTKYPITEYOPIYFVADSFODAKEKVR--TWS---
                                                                                                                                                                                                                                                                                                                                                  SSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQ
                                                                                                                                                                                                                                                                                                                                                                                                       EIG-----LASLGAPDDFVMKLATL------YWFTVEFGLCRQDGEVKAYGRDCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAGLLSSRDFLAGLAFPVFHSTQYIRHHSKPLYTPEPDVCHELLGHAPLFADPSFAQFSQ
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                                                                                                                                                                                                                                               GLLESIPL----YNQEKYLSGFEVL 360
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                                                                                                                                                                                          HSIPRPFSVHYN--PYTQSVEIL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 AA; 49958 MW; 1619297DBDBF5EE7 CRC64;
   (TrEMBLrel. 19,
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                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.3%; Score 157; DB 24.1%; Pred. No. 2.9e tive 37; Mismatches
                                                    PRT;
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d insulin-related
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Q9SCZ3
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Best Local S
Matches 35
               InterPro; IPR000767; Disease resist.
InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
InterPro; IPR00182; NB-ARC.
InterPro; IPR000157; TIR domain.
Pfam; PP00560; LRR; 6.
Pfam; PP00582; TIR; 1.
PRINTS; PR00364; DISEASERSIST.
PRINTS; PR00364; DISEASERSIST.
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NON_TER
SEQUENCE
                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
EMBL; AL133452; Ch863020.1; -.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Delseny M., Berger C., Cooke R., Grellet F., Laudie M.,

Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.,

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ol-MAY-2000 (TrEWBLrel. 13, Created)
Ol-MAY-2000 (TrEWBLrel. 13, Last sequence update)
Ol-WIN-2002 (TrEWBLrel. 21, Last sention update)
Disease resistance-like protein.
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 INMG 222
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PF00351; biopterin_H; 1.
ps00367; biopterin_HydroxyL; UNKNOWN_1
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35; Conservative
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250 AA;
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250
28548 MW;
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Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Mewes
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                                                                                                                                                                                                                                                                                                                                                                                                                                H.W.,
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Gaps

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37; Mismatches 131; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IRR01273; Aaa hydroxylase.
Pfam; PF00351; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          266 E 266
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SEQUENCE
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Q9GF55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=AALP2;
Koch M., Mitchell-Olds T.;
EVOLUTIONARY BARIYSIS Of plastidic maturase K and nuclear chalcone synthase and their utility for phylogenetic reconstructions within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabis.
                                                                                                                 77 VHLLSLSKNQREGCS-----TDMAVVSTPFFNRNLWYRLLSS------RF 115
                                                                                                                                           421 IHLL------EGCGFFPRVEINVLVEKCLVSMA-EGRVVMHNLIQSIGRKIINGGKRRS 472
                                                                                                                                                                                          116 SLWKSYCPRFFLDYLEAFG---LLSDFLDHQAV-------IKFFEL----ET 153
                                                                                                                                                                                                                     473 RLWKPLIIKYFLEDRQVLGSEDIEAIFLDPSALSFDVNPMAFENMYNLRYLKICSSNPGN 532
                                                                                                                                                                                                                                                                   154 HFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSL-------TPD-- 197
                                                                                                                                                                                                                                                                                            198 -LIHDLIGHVPWLLHPSFSEFFINM-----GRL-----FTKVIE-----KVQ 233
                                                                                                                                                                                                                                                                                                                                                                                  593 MLKRIMLCHSQQLVGIQELQIALNMEVIDLQGCARLQRFLATGHFQHLRVINLSGCIKIK 652
                                                                                                                                                                                                                                                                                                                                                                                                                      234 ALPSKKORIQTL---QSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELG-HAF 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                   653 SPPEVPPNIEELYLKQTGIRSIPTVTFSPQDNSFIYDHKDHKFLNREVSSDSQSLSIMVY 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 IDNVRVLP----LELDQIIRLPFNT-----STPQETLFSIRHFDELVEL---TSKLEWM 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     713 LDNLKVLDLSQCLELEDIQGIPKNLRKLYLGGTAIKELPSLMHLSELVVLDLENCKRLHK 772
                                   ch 5.8%; Score 109.5; DB 10; Length 1253; l Similarity 20.3%; Pred. No. 1.2; B1; Conservative 61; Mismatches 130; Indels 127; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SINTLARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 106.5; DB 8; Length 506;
Pred. No. 0.73;
140809 MW; 4211ADE0566C2B01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast; mRNA processing.
SEQUENCE 506 AA; 60472 MW; 3BD5743D758B9F23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          773 LPMGIGNLSSLAVLNLSGCSELEDIQGIPRNLEELYLAG 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 LDQGL-----LESIPLYNQEXYLSG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                506 AA
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR012866; MatK_N.
Pfam; PF01348; Intron_maturae2; 1.
Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probable intron maturase (Maturase K)
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Best Local Similarity
  1253 AA;
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SEQUENCE
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                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                             101 FFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 SGFVAPHQYLSLLQDRYFFIASVWRTLDKDNFSLTPDLJHDLLGH----VPWLLHPSFSE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 -----DNIRIKLDNKIPISSIIGSLTKDKFC-----NLLGHPISKANW-TESSDSD 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 FFINMGRLFTKVIEKVQALPSKKQR------IQTLQSNLIAIVRCFWFTVESGLI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 FWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQE 315
                                                                                                                            190 YCNWKNFD----IKKKLILNPRFFLFLYNSHVCE-----YESIFFFLRKRSSHLRSTAY 239
                                                                                                                                                                                                         62 HKCISILEFFKNL----LPVH----LLSLSKNQ-----REGCSTDMAVVSTP----- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lates calcarifer (Barramundi).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Canthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Centropomidae; Lates.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 TLF----SIRHFDELVELTSKLEWMLDQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BARRAMUNDI;
Collet C., Candy J., Sara V.;
Tyrosine hydroxylase and insulin-like growth factor-II but no insulin are adjacent in the teleost species barramundi [Lates calcarifer].";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.6%; Score 106; DB 13; Length 129;
25.0%; Pred. No. 0.16;
tive 14; Mismatches 41; Indels 3
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EMBL; APO0794; AB64194-1; -.
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01-DEC-2001 (TrEMBLrel. 20, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Best Local :
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable intron maturase (Maturase K).
MATK.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9GF31;
Q9GF31;
01-MAR-2001
01-MAR-2001
01-MAR-2002
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Cardamine.
NCBI_TaxID=125588;
                                                                                                                                                                                                                       Cardamine penzesii.
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EMBL; AF144337; AAG43306.1; -
Interpro; IPRO00442; Intron maturse2.
Interpro; IPRO02866; MatK, N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK, N.
Chloroplast; PNA N. T.
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- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
- INTRONS (BY SIMILARITY).

- I- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
- AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
MITOCHONDRIAL INTRONS.
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Koch M., Mitchell-Olds T.,

"Evolutionary analysis of plastidic maturase K and nuclear chalcone
"Evolutionary analysis of plastidic maturase K and nuclear chalcone
synthase and their utility for phylogenetic reconstructions within the state of the synthase and their utility for phylogenetic reconstructions within the state of the synthase and their utility for phylogenetic reconstructions within the state of the synthase and their utility for phylogenetic reconstructions within the synthase and their utility for phylogenetic reconstructions within the synthase and their utility for phylogenetic reconstructions within the synthase and their utility for phylogenetic reconstructions within the synthase and their utility for phylogenetic reconstructions within the synthase and their utility for phylogenetic reconstructions within the synthase and their utility for phylogenetic reconstructions within the synthase and their utility for phylogenetic reconstructions within the synthase and their utility for phylogenetic reconstructions within the synthase and their utility for phylogenetic reconstructions within the synthase and their utility for phylogenetic reconstructions within the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and the synthase and 
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Cardamine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICRNISHYYSGSSKKKFLYRIKYILRLCCVKTLARKHKSTVRAFLKRLGSGLLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRIKL--DSKIPISSIIGSLAKDKFC-----NVLGHPISKVIW-THSSDSDILNRFVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRLLSSRFSLWKSYCERFFLDYLEAFGLLSDFLDHQAVIKEFELETHFSYYEVSGFVAPH 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----IQHFFKVFVNNFPAILGLLKDPFIHYVRYHGRSILATKDTPLLMNKWKYYFVNLW
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
tron maturase (Maturase K).
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                                                                                                                 Rosidae;
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Best Local
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Pfam; PF01824; MatK. N; 1.
Chloroplast; mRNA processing.
SEQUENCE 504 AA; 60292 MW; 94C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II INTRONS (BY SIMILARITY).
-I- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthase and
Brassicaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koch M., Mitchell-Olds T.; "Evolutionary analysis of plastidic maturase K and nuclear chalcone synthase and their utility for phylogenetic reconstructions within
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000442; Intron maturse2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
 414
                                231
                                                            362
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                                                                                                                                                    115
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                                                                                                                                                                                                                                                                          2 HYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MITOCHONDRIAL INTRONS.
                                                            DSKIPISSIIGSLAKDKFC------NVLGHPISKVIW-THSSDSDILNRFVRICRNISH
YYSGSSKKKKLYRIKYILRLCCVKTLARKHKSTVRAFLKRLGSGLLE
                              KVQALPSKKQR------IQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                             HVCE-----YESIFFFLRKRSSHLRSTSYEVLFERIFFYGKIQHFLKVFV 258
                                                                                         DRYFPIASVMRTLDKDNFSLTPDLIHDLLGH----VPWLLHPSFSEFFINMGRLFTKVIE
                                                                                                                       FQSQKVHIKQLSKDNLEFLGYLSSLRLNPLVVRSQMLE-----NSFLIDNVRIKL--
                                                                                                                                                FSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQ
                                                                                                                                                                                NNFPAILGLLKD-PFIHYV-----RYHGRSILATKDTPLLMNKWKYYFVNLWQCYFSVW
                                                                                                                                                                                                                HKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTP----FFNRNLWYRLLSSR 114
                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                        5.6%;
llarity 22.3%;
Conservative 4
                                                                                                                                                                                                                                                                                                      t; Score 106; DB 8; I
t; Pred. No. 0.81;
41; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                     94C5F9B8282127A7 CRC64;
                                                                                                                                                                                                                                                                                                                                     8; Length 504;
                                                                                                                                                                                                                                                                                                        Indels
460
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                                                                                                                                                                                                                                                                                                      Gaps
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Q9GF30;
01-MAR-2001
01-MAR-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Koch M., Mitchell-Olds T.;

"Evolutionary analysis of plastidic maturase K and
"Evolutionary analysis of plastidic maturase K and
synthase and their utility for phylogenetic reconst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cardamine rivularis.
Chloroplast.
Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Cardamine.
                                                                                                                                                                                                  Brassicaceae.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
--- FINCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=82338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probable intron maturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                    FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II INTRONS (BY SIMILARITY).
SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODE
                                                    MITOCHONDRIAL
     AF144365; AAG43334.1; -.
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                for phylogenetic reconstructions within
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                                                                                              POLYPEPTIDES ENCODED
                                                                                                                                                                                                                                                                                                                                                                                                                nuclear chalcone
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us-09-438-185a-1047.rspt

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SEQUENCE FROM N.A.
Hilu K.W., Alice L.A.;
Hilu K.W., Alice L.A.;
Hilu K.W., Alice L.A.;
A Phylogeny of Ciloridaideae (Poaceae) Based on matk Sequences.";
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: PROBABLY ASSITSI IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
--- SMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
--- AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast.
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Liliopsida; Poales; Poaceae; PACC clade;
Chloridoideae; Pappophoreae; Enneapogon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 KKWKSYLVNFSQYFLSFWTQPQRICLNOLTNSCFDFLGYRSSVPMQNFLVRNOMLENSFL 358
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    ----RLLSSRFSL----W 118
                                                        250 HFFRKMEH------FGVMYPGFFQKTIWFFMEPLMHYVRYQGKVILASKGTLLFQKKW 301
                                                                                                                                                    119 KSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYF 178
                                                                                                                                                                                                                          302 KSYLVNFSQYFFSFWAQPQRICLNOLTNSCFDFLGYRSNVPINTFLVTNQML----ENFF 357
                                                                                                                                                                                                                                                                                                     179 PIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTK-----V 228
                                                                                                                                                                                                                                                                                                                                                         229 IEKVQAL------PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 LDRFGRICRNLFHYHSGSSKKQTLYRLK----YILR---LSCARTLARKHK-----STV 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 LFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWY--------RLLSSRFSL--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 IFSRKME------HFGVMYPGFFWRTIWFFMDPLMHYVRYQGKAILASKGTLLLK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 --WKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLS---L 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60; Mismatches 131; Indels 92; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 QSLSLFFQNSQSLQR----AYSTPYSYYRIILQKENKEKQALARHKCISILE---FFKNL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.5%; Score 104; DB 8; Length 513; 20.3%; Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last annotation update)
01-MRA-2002 (TrEMBLrel. 20, Last annotation update)
Probable intron maturase (Maturase K) (Fragment).
    78 HLLSLSKNOREGCSTDMAVVSTPFFNRNLWY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF312360, AAK60051.1; -
InterPro; IPR000442; Introm_maturse2.
InterPro; IPR002866; MatK_N.
Pfam; PF01348; Introm_maturas2; 1.
Pfam; PF01824; MatK_N; 1.
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-!-SIMILARITY WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
EMBL. AFRIASS, AARKO046.1, -..
InterPro; IPR002866.1, -..
InterPro; IPR002866.Mark.N.
Pfam, PF01348; Intro. maturas2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade, Chloridoideae, Eragrostideae, Muhlenbergia.
                                                                                                                                                                                                                                                             Ouery Match
5.6%; Score 106; DB 8; Length 504;
Best Local Similarity 22.3%; Pred. No. 0.81.
Matches 64; Conservative 41; Mismatches 120; Indels 62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 KSIFLFSKDNKRLSRFLYNFYVSEYEFFLLFLKKQS-----SCLRLTSYGTFLBRI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
5.5%; Score 104; DB 8; Length 513;
Best Local Similarity 18.6%; Pred. No. 1.2;
Matches 67; Conservative 67; Mismatches 124; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 FQSQKVHIKQLSKDNLEFLGYLSSLRLNPLVVRSQMLE-----NSFLIDNVRIKL-- 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 DRYFPIASVMRTLDKDNFSLTPDLIHDLLGH----VPWLLHPSFSEFFINMGRLFTKVIB 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 HVCE------YESIFPFLRKRSSHLRSTSYEVLFERIFFYGKIQHFLKVFV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 HKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTP-----FFNRNLWYRLLSSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 FSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 QSLSLFFQNSQSLQR----AYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFV 77
                                                                                                                                                                                                                                                                                                                                                                                                                       2 HYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hilu K.W., Alice L.A.;
"A Phylogeny of Chloridoideae (Poaceae) Based on matK Sequences.";
submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414 YYSGSSKKKKLYRIKYILRLCCVKTLARKHKSTVRAFLKRLGSGLLE 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 KVQALPSKKQR-----IQTLQSNLIAIVRCFWFTVESGLIE 266
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002865; Matk N.*
InterPro; IPR01348; Intron_maturas2; 1.
Pfam; PF011348; Intron_maturas2; 1.
Pfam; PF011348; Matk N; 1.
Cfloroplast; Mark N; 0302 NW; 66AA07E8E2C48C64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast; mRNA processing.
SEQUENCE 513 AA; 61468 MW; 8D6AAD01B14BDEF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Probable intron maturase (Maturase K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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PRELIMINARY;

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MITOCHONDRIAL INTRONS.

EMBL, AF312349; AAK60040.1; -.

InterPro; IPR0004442; Intron maturse2.

InterPro; IPR002866; MatK.N.

Pfam; PF01348; Intron maturas2; 1.

Pfam; PF01824; MatK.N.

Chloroplast; mRNA processing.

SEQUENCE 513 AA; 61512 MW; FA97488C266572D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ol-DEC-2001 (TrEMBLrel. 19, Created)
Ol-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Ol-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Chloridoldeae; Eragrostideae; Monanthochloe.
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                                                                         456 MQRLGSVFLEEFFT---EEEQVFSLMFAKTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 SSGTFLERIHFSRKMEH-----FGVMYPGFFRKTIWFFMDPLMHYVRYQGKVILASKGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 FLLK---KENKRLSRFLYNS-----YVSEYEFFLLFLRKQS------SCLRLA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 LFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 ELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 KNLLFVHLLSLSKNOREGCSTDMAVVSTPFFNRNLWY------RLLSSRFSL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 YILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFF 71
                                                                                                                                  PQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                      --ESFFPIATRMKKFD-TTAPATP-LIGSISKAQFCTGLGHPISKPIWTDLSDWDILDRF 409
                                                                                                                                                                                                                                                                                                                                                                                                    LQDRYFPIASVMRTLDKDNFSLTPDLIHDL-----LGH-VPWLLHPSFSEFFI--NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFQKKWKSYLVNFSQYFFSFWTQPQRIRLNQLTNSCFDFLGYRSSVPINTFLVRNQML--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----WKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSL 172
                                                                                                                                                                                                       GRICRNLFH-YHSGSSKKRTLYRLK----YILR---LSCARTLARKHK-----STVRTF 455
                                                                                                                                                                                                                                                                     GRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLGSVFLEEFFT---EEEQVFSLMFTKTT-----HF-SFHGLHSERIWYLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.5%; Score 103.5; DB 8; Length 21.0%; Pred. No. 1.3; tive 59; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89; Gaps
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RX MEDLINE=20196006; PubMed=10731132;

RA Adams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Adams D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wordman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,

RA Baril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Ballew R.M., Beau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Beau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Barkewa D., Setchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Barkewa D., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Beeson K.Y., Beams D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Borkova D., Botchan M.R., Bouck J., Bavendar S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferriar S., Flesischmann W.,

RA Godek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

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RA Harris N.L., Harvey D., Heiman T.J., Hermandez J.R., Houck J.,

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RA Mount S.M., Moy M., Murphy L., Muzny D.M., Nelson D.L.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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01-MAY-2000 (Trem
01-JUN-2000 (Trem
CG11376 protein.
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                            574 ILEFPQSAIYNPHYSYRNLLFVSPKELNFSSRAGSARNIAVRVQLMAGETPKDAVNAIY- 632
                                                                                                                              110 LLSSRFSLWKSYCPRFFLDYLEAFGLLS-----DFLDHQAVIKFFELETH----FSYYP 159
                                                                                                                                                                                                                                                                 67 ILEF-----FKNLLFVHLLSLSKNQREGCSTDMAV-----VSTPFFNRNLWYR 109
                                                             -----GKSSCPKF---STEAFTAVNYHNKCPSFYDEIKIALPASIKQHHHLLFTIYH
                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                             5.5%; Score 103.5;
25.0%; Pred. No. 6.1
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                   96;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                Length 1782;
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                                                                                                                                                                                                                                                                                                                               Gaps
                                                                 681
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SEQUENCE FROM N.A. NCBI\_TaxID=160556; Monanthochloe littoralis.

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-1- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

KOCh M., Mitchell-Olds T.;

"Evolutionary analysis of plastidic maturase K and nuclear chalcone
"Evolutionary analysis of plastidic maturase k and nuclear chalcone
Brassicaceae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Aubrieta.
101 FFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 SGFVAPHQYLSLLQDRYFFIASVMRTLDKDNFSLTPDLIHDLLGH-----VPWLLHPSFSE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 -----DNIRIKLDSKIPISSIMGSLAKDKFC-----NVLGHPISKATWTDSSDFD- 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 -ILNRFVRICRNÍSHYYSGSSKKKNLYRIKYILRLCCVKTLARKHKSTVRAFLKRVGSGL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
5.5%; Score 103; DB 8; Length 504;
Best Local Similarity 21.9%; Pred. No. 1.5%
Marches 66; Conservative 37; Mismatches 113; Indels 86; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 L--FERILFYGKIHHFLKVFVNNFLTIPGLLKDPFLHYVRYHGKSILATKDTPLLMNKWK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 FYFVNLWQCYFSVWFQSQKVNINQLSKDNLEFLGYLSSIRLNPLVVRSQMLENSFLI--- 354
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                                                               204 GHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA-IVRCFWFTVES 262
                                                                                                   740 PGIXWL------DNHRAVFSINVEAVTA-----IHTLDSFLDRFFLICEYLDTRN 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                               263 GLIENHEGRKAYGAVLISSPQELGHAFID------NVRVLPLELDQIIRL 306
                                                                                                                                                                                      784 -- IPSHIGEN-----NIETELKKCLLDIEYANREPLVRHLPLVLDKLIEL 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast; mRNA processing.
SEQUENCE 504 AA; 60023 MW; 4620F813810B3AD8 CRC64;
                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable intron maturase (Maturase K).
                                                                                                                                                                                                                                                                                                 504 AA
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InterPro; IPR000442; Intron maturse2.
InterPro; IPR00286; MarK N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK N.
                                                                                                                                                                                                                                                                                                 PRT;
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Hilu K.W., Alice L.A.;
Hilu K.W., Alice L.A.;
"Phylogenetic relationships in subfamily Chloridoideae (Poaceae) based on matk sequences: A preliminary assessment.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopida; Poales; Poaceae; PACC clade; Chloridodeae; Cynodonteae; Bouteloua.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 NLFH-YHSGSSKKÖTLYRLK----YILR---LSCARTLARKHK-----STVRTFMQRLG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 KSYCPRFFLDYLBAFGLLSDFLD-HQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 KVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
5.5%; Score 103; DB 8; Length 513;
Best Local Similarity 22.0%; Pred. No. 1.5;
Matches 78; Conservative 59; Mismatches 127; Indels 90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 HLLSLSKNQREGCSTDMAVVSTPFFNRNLW------YR----LLSSRFSL----W 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 FPIASVMRTLDKDNFSLTPDLIHDL-----LGH-VPWLLHPSFSEFFI--NMGRLFT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 FLIATRMKKFD-TTVPATP-LIGSLSKAQFCTGLGHPISKPIWTDLSDWDILDRFGRICR 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 OSLSLFFQNSQSLQR----AYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTRONS (BY SIMILARITY).

-!- SIMILARITY: HITH CORRESPONDING ORP IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 HAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIR--HFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 SVFLEEFFT---EEBQVFSLMF----PKATHFSFHGSHSERI------WYLD 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast; mRNA processing.
SEQUENCE 513 AA; 61519 MW; 223EEA9CBA96DFEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
probable intron maturase (Maturase K).
                                            513 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF144578; AAF20334.1; -.
InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK_N; 1.
                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seqn
01-MAR-2002 (TrEMBLrel. 20, Last anno
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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                                            PRELIMINARY;
                                                                                                                                                                                      Bouteloua curtipendula.
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                                            Q9TIB8
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Q95F60
RESULT 28
Q9TIB8
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RESULT 30
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ID C95F5
AC Q95F5
DT 01-DE
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DE Proba
GN MATK.
OS Sched
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                                                   Schedonnardus paniculatus.
Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae; PACC clade;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Chloridoideae; Chlorideae; Schedonnardus.
NCBI_TaxID=160583;
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InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_W; 1.
Chloroplast; mRNA processing.
SEQUENCE 513 AA; 61509 MW; 1162FCC517CA1D1D CRC64;
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Hilu K.W., Alice L.A.;
"A Phylogeny of Chloridoideae (Poaceae) Based on matk Sequences.";
Submitted (OCT-2000) to the EMBL/GenBank/DDJ databases.
-i- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-i- SIMILARITY: HITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODER
   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl
Chloridoldeae; Chlorideae; Buchloe.
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L; AF312325; AAK60016.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVFLEEFFT---EEEQVFYLMF----PKTTHFSFHGSHSERI-----WYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIR--HFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLFH-YHSGSSKKRTLYRLK----YILR---LSCARTLARKHK-----STVRTFMORLG
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RESULT 31
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                   Chloroplast.
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnollophyta;
Chloridoideae; Eragrostideae;
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EMBL, AF31235; AAK60026.1;
InterPro; IPR000442; Intron maturse2.
InterPro; IPR00266; Matk N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; Matk N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hilu K.W., Alice L.A.;

"A Phylogeny of Chloridoideae (Poaceae) Based on matk Sequences.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

INTRONS (BY SIMILARITY).

-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,

AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chloroplast; mRNA processing.
SEQUENCE 513 AA; 61384 MW; 94861F9870BBF8EA CRC64;
                                                                                                                                                           SEQUENCE FROM N.A.
InterPro; IPR000442; Intron_maturse2
InterPro; IPR002866; MatK_N.
                                                                                                                                                                                  NCBI_TaxID=160560;
                                                                                                                                                                                                                                                           Reederochloa eludens.
                                                                                                                                                                                                                                                                                                                                                                                                                                    453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 PIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTK------V
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                                                                                                                                                                                                                                                                                                                                                                                                                                    RTFMORLGSVFLEEFFT---EEEQVFSLMFAKTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDRFGRICRNLFHYHSGSSKKQTLYRLK----YILR---LSCARTLARKHK-----STV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIATRMK-----KFDTTPPAT-PLIGSL-----SKSQFCTGSGHPISKPIWTDLSDWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLLSLSKNQREGCSTDMAVVSTPFFNRNLWY------RLLSSRFSL-----W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSIFLFSKENKRLSRFLYNFYVSEYEFFLLFLRKQSSCLRLTSSGTFLERIHFFRKM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSLSLFFQNSQSLQR----AYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISSPORTGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IEKVQAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----EHFGVMYPGFFQKTIWFFMEPLMHYVRYQGKVILASKGTLLFQKKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSYLVNFSQYFFSFWAQRQKICLNQLTNSCFDFLGYRSSVPINTFLVTNQML----ENFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.6%;
                                                                                                                                                                                                   Streptophyta; Embryophyta; Tracheophyta; yta; Liliopsida; Poales; Poaceae; PACC clade; eae; Reederochloa.

    k; Score 103; DB 8; Length 513;
    k; Pred. No. 1.5;
    64; Mismatches 127; Indels 1

                                                                                                                                                                                                                                                                                                                                                                                                                                   HFSFHGSHSERI-WYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102;
                                                         ENCODED
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EMBL; AE003617; AAF52504.2; -. HSSP; P08799; 1MND.
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Q9GF64;
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Q9GF64
ID Q9GF6
AC Q9GF6
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Holt R.A., Ehang C.A., Galle R.F.,
Change R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
A wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G,
Abril J.F., Apdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale U., Bayraktaroglu L., Beasley E.M.,
Abril J.F., Apdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Barman B.P., Bhandari D., Boldrier P.,
Ballew R.M., Cawley S., Dalwe C., Davenport L.B., Dollarkov S.,
Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahke C., Davenport L.B., Dinkov B.C., Dunn P.,
A burbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Ferraz S., Fleischmann W.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Harris M.,
A latali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alalali M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Ketchum K.A.,
Alalali M., Kalush F., Karpen G.H., Kavitz S., Kulp D., Lai Z.,
                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Brkaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophilia.
                                                                                                               5.5%; Score 103; DB 8; Length 513;
20.5%; Pred. No. 1.5;
tive 62; Mismatches 133; Indels 84; Gaps
                                                                                                                                                                                                                                                      199 KSIFLFKKENKRLSRFLYNSYVSEYEFFLLFLRKQS------SCLRLASSGTFL 246
                                                                                                                                                                                                                                                                                                       78 HLLSLSKNQREGCSTDMAVVSTPFFNRNLWY-------RLLSSRFSL----W 118
                                                                                                                                                                                                                                                                                                                                          119 KSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 PIASVMRTLDKDNFSLIPDLIHDL-----LGH-VPWLLHPSFSEFFI--NMGRLFTK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 PIATRWKKFD-TTAPATP-LIGSLSKAQFCTGLGHPISKPIWTDLSDWDILDRFGRICRN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 VIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGH 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 KSYLVNFSQYFFSFWTQPQRIRLNQLTNSCFDFLGYRSSVPINTFLVRNQML----ESFF 357
                                                                                                                                                                                                             22 QSLSLFFQNSQSLQR----AYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 AFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :: | | | : | 1 | 462 VFLEEFFT----EBEQVFSLMFAKTT------HFSFHGSHSERI-WYLD 499
                                              Chloroplast; mRNA processing.
SEQUENCE 513 AA; 61546 MW; 08330E6C2282C755 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01.MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1154 AA.
Pfam; PF01348; Intron maturas2; 1. Pfam; PF01824; MatK N; 1.
                                                                                                                                       Local Similarity 20.5% es 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NinaC protein.
NINAC OR CG5125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY;
                                                                                                                    Query Match
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20;
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattel B., McThcosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.M., Resinerle J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri, V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Shier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Shier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Shier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Shier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Shier E., Spradling A.C., Turner K., Venter E., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinscock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinscock G.M., Zhan G., Zhan G., Zhan G., Zhan G., Zhan G., Zhan G., Zhan K., Zhan G., Zhan K., Zhan S., Zhu X., Smith H.O.,
Glibbs R.A., Whers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  993 V----EMTKDNCRL---LFLRLKANEGWALGKTKVFLRYYNDEF---LARLYELQVKKV- 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1041 -----IKVQSMMRALLARKR----VKGGKVFKLGKKGPEHHD------VAASKIQKA 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 GHAFIDNVRVLPLELDQIIRL-----PFNTSTPQETLFSI-----RHFDELVELT 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 ALPSKKQRIQTLQSNLIAIVRCFWFTVESGLI-----ENHEGRKAYGAVLISSPQEL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 839 PEMIETFRSSLDESIMLMFTNOLTKAGNLTMP---FEAVOHKDESERKSYALNTLSAGCI 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 SILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSS-RFSLWKSYCPR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    896 SQVN-----NLRTLAANFRFTCLTLKMLSQ---NANLGVHFVRCIRADL--EYKPR 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 FF----LDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.4%; Score 102.5; DB 5; Length 1154;
22.7%; Pred. NO. 4.4;
tive 56; Mismarches 129; Indels 95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 PKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHK----CI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R Hybase; PEGN0002938; ninaC.
R InterPro; IPR00012938; ninaC.
R InterPro; IPR00012938; ninaC.
R InterPro; IPR00014609; myosin head.
R InterPro; IPR001245; Tyr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R Fam; PF000612; 1Q; 2.
R Pfam; PF00069; pkinase; 1.
R Pfam; PF00069; pkinase; 1.
R ProDom; PD000015; myosin head; 1.
R ProDom; PD000015; myosin head; 1.
R ProDom; PR00191; myosin head; 1.
R PROSITE; PS00101; PROTEIN KINASE DOM; 1.
R PROSITE; PS00101; PROTEIN KINASE DOM; 1.
R PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN_1.
R PROSITE: 1154 AA; 134334 MW; 211CD4A2F295B9A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      506 AA.
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RESULT 34

Q9MV23

ID Q9MV2

AC Q9MV2

DT 01-0C

DT 01-0C

DT 01-T

DE Probas

GM MATK.

OS OFFER

OG Chlor

OC Ebera

OC Spera

OC Spera

OC Spera

OC Spera

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Q9MV23;
01-OCT-2000 (TrE)
01-OCT-2000 (TrE)
01-JUN-2002 (TrE)
Probable intron 1
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Oryza meyeriana.
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01-JUN-2002
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Arabis alpina (Alpine rockcress)
Chloroplast
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Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabis.
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"Evolutionary analysis of plastidic maturase K and nuclear chalcone
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001 (TEMBLrel. 16, Last sequence update)
002 (TEMBLrel. 21, Last annotation updat
intron maturase (Maturase K).
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35; Mismatches 117;
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Pred. No. :
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                                                                                                                                                                                                tation update) (Fragment).
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SEQUENCE FROM N.A.

STRAIN-AX4;
Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Lear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K. Tunggal B., Cox B., Quail M.A., Platzer M., Rosenthal A., Noegel "Sequence and Analysis of Chromosome 2 of Dictyostelium.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=20056256; PubMed=10588717;
Ge S., Sang T., Lu B.R., Hong D.Y.;
"Phylogeny of rice genomes with emp
species";
Proc. Natl. Acad. Sci. U.S.A. 96:14
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NON_TER 519 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 LHYLSHIEIPYPIHLDILLQLLQYRIQDVPSLHLLRFFLNYYSSWNSFITSMKSI-LILK
                                                                                                                                                                                                                                                                                                                                                                                                                                   35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VHYCERTLDPKYI-LKIALKLRQ-----SLSL--FFQNSQSLQRAYSTPYSYYRIILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AKTTYFSFRGSHSDRI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSLAKAQFCTGSGHPISKPIWTDLSDWDILDRFGRICRNLFH-YHSGSSKKKTLYRLK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLNQLANSCFDFLGYFSSVPINSLLVRNQML----ENSFLIDTRMKKFD-TKVPATP-LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-HQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFFRKTVWFFMDPLMHYVRYQRKAILASKGTLLLKKKWKCYLVRLW-QYSFSFWTQSRRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFFNRNLWY------RLLSSRFSL-----WKSYCPRFFLDYLEAFGLLSDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KENKRLFRFLYNSYVSEYEFF--LLFLRKQSSCLRLTSSGTFLERIHFSRKMEHFGVMYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KENKEKQALARHKCISILEFFKNLLFVH----LLSLSKN----QREGCSTDM----AVVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTSTPQETLESIR--HEDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HDLL-----GH-VPWLLHPSFSEFFI--NMGRLFTKVIEKVQALPSKKQRIQTLQSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  519 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62257 MW; 0148830573EB14C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.4%; Score 101.5;
24.5%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55,
                                                                                                                                                                                                                                                                                       Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                      A.A.;
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183 SYFIQNHEIIFNISKGIWFLEIGVNASPYNSVSALINLNNKEVSQWLNKSRIPKLPDPLL 242
                                                                                                                                                                                                                                                                                              318 FSIRHFDELVELTSKLEWMLDQGLLESIP--LYNQEKYL 354
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                     1153 INRLNOSNFNENEDLFK-NYMIQIIEFGSRLSAKHIRSIFKSLEYGVDKSSLGN-DNYKE 1210
                                                                                                                                                                   STRÄIN=ZOW 10545 / 7;
PubMed=11572479;
Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Rawarzabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Octsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Msuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
                                                                           Indels 121; Gaps
                                                                                                                                                                                                     150 ---ELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV 206
                                                                                                                                                                                                                                                      207 PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                                                                                       NHEGRKAYGAVL-----ISSPQELGHAFIDNVRVLPL-------ELDQI 303
                                                                                                                                                                                                                                                                                                                                                         304 I-RLPFNTSTPQETLFSIRHFDELVELTSK------LEWMLDQGLLESIPLYNQ 350
                                                                                                                   95 AVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLL--SDFLDHQAVIKFF--- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.3%; Score 101; DB 17; Length 635;
19.8%; Pred. No. 2.9;
Live 69; Mismatches 123; Indels 128; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 SLFFQNSQSLQR-----AYSTPYSYYRIILQKENKE-KQALARHKCISILEFFK 72
                                                                                                  44 YYRIIL--QKENKEKQALARHKCIS-ILEFFKNLLFVHLLSLSKNQREGCSTD-----M 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus tokodaii.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                               5.4%; Score 101.5; DB 5; Length 1615; 20.3%; Pred. No. 8; Live 58; Mismatches 111; Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain?.";
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             ll protein.
1615 AA; 192460 MW; C1A5951F24D04A7A CRC64;
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BMBL, AP000985; BAB6140.1; -.
HYDChhetical proteome.
SEQUENCE 635 AA; 72823 MW; 5219B8F88204794F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein ST1107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  635 AA.
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EMBL; AC115613; AAM10775.1; -. Hypothetical protein. SEQUENCE 1615 AA; 192460 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 19.89
                                                            Best Local Similarity 20.3%
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                           351 EKYL 354
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                                                  Query Match
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EXURENCE FROM N.A.

REC STRAIN-BERKELEY,

RA Manatides P.G., Scherer S.E., 101 P.W., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Richards S., Ashburner M., Hendelson S.N.,

RA Amanatides P.G., Scherer S.E., 11 P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., 11 P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Hendelson S.N.,

RA Strandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Magbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Benos P.V., Berman B.P., Bhandari D., Bolbhakov S.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolbhakov S.,

RA Beeson K.Y., Cawley S., Dahler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahler K., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahler M., Dugan-Rocha S., Dunkov B.C.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Hout D., Houston K.A., Howland T.J., Heim M.-H., Ibegwam C.,

RA Harris N., Mattei B. M. McIncoh T.C., Kravitz S., Kulp D., Lai Z.,

RA Lakko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Harris N., Mattei B. M., McIncoh T.C., McLeod M. P., McBreson D.,

RA Harris N., Mattei B. M., Minchy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Hallon D.R., Nelson K.A., Nixon K., Nussker D.R., Pacled D.J.M.,

RA Nelson D.R., Pattman G.S., Pollard J., Purl Y., Resee M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403 NDLGLL--SVVKIYKALGLNYTLVLKEEKALNE-----SIIRYFWDNNSFAS 447
73 NLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEA 132
                                                                                                          243 KEYFLSLLLIKDDÖNPYLGT-FAASPSPIYLYS-WVR--DSAFSAIA-----LOQ 288
                                                                                                                                                                                                                          133 FGLLSDFLDHQAVIKFF------ELE-----THFSYY---PVSGFVAP-----------166
                                                                                                                                                                                                                                                                                                                                    289 AG-----HYNSALKYWLWMANAEQLQPGVWYTRYNFYNGEPDSSFGIPELDSIGLYEIG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 -HQYLSLLQDRYF-----PIASVMRTLDKDNFSLTP---DLIHDLLGHVPW---- 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | : | : | : | : | : | 343 VYDYYNLTHNITFLKLVLPRINESVEYQIQQIENDKYHLIPPDLSIWEDRLAYHFWTEAI 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 ----LLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFW----FTV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 BSG---LIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448 ALGISVLFENGKSEE----VLTPEPPS----IDSATLLPIDMGY---LPYNSN----- 489
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Sukaryotei, Metazosi, Arthropodai, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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Query Match
Best Local
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EMBL; AE003462; AAF47145.1; -. FlyBase; FBgD0034964; CG3173.
SEQUENCE 2042 AA; 233746 MW; 9144DB7B51F52EE5 CRC64;
                                                                                                                                                                                                                                                               P97517; P70468;
P97517; P70468;
P97517; P70468;
O1-MAY-1997 (TrEMBLrel. 03, Created)
O1-MAY-1997 (TREMBLrel. 03, Last sequence update)
O1-MAR-21097 (TREMBLrel. 03, Last sequence update)
O1-MAR-21092 (TREMBLrel. 20, Last annotation update)
Tyrosine hydroxylase (Fragment).
Tyrosine hydroxylase (Fragment).
Phodopus sungorus (Striped hairy-footed hamster) (Djungarian hamster)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Muridae; Cricetinae;
                                             Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Y09294; CAA70478.1; -.
HSSP; P04177; 1TOH.
InterPro; IPR0012713; Aaa_hydroxylase.
Pfam; PF00351; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
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                NON_TER
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                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE=HYPOTHALAMUS;
                                                                                                                                                                                                                           NCBI_TaxID=10044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339
                                                                                                                                                             Bockmann J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGLLESIPL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPQEQVQLLPDWLKLKMIRSSVDRLIEAALNDLTPDQIVLFVQNFGTPVNSMSKLLAMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPOELGHAFID -- NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IIHAF--IILLTYSNSNMPESIPILD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VMFNNYIIKLREYHEPY-----EWTEYPDLLMVQFDDGVQLP--LH-----IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAPHQYLSLIQDRYFPIASVMRTLDKDNFSLTPDLI---HDLLGHVPWLLHPSFSEFFIN 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQFITAHTLNDPVNEMLDHVIDMAQLIVERSTMFQHIIISQEDYDYVPDENRIQTLKCLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LE---AFGL---LSDFLDH-----QAVIKFFELETH-----FSYYPVSG-----F 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSGLKIIFRHSGDF--ENEW--LLKSLQQIPHFYEVKPFIIPQLRAACQVENCPELIMAY 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STDMAVV---STPFFNRNLWYRLLSS-------RFSLWKSYCPRFFLDY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IINEENSRDAEL-----VNFLRNLIFDGNLSHQIVCELLDYIFRRLSSTVKQSRVAA 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 5.3%; Score 101; Similarity 21.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
11433 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
  52241A9D5DB27795 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 122; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --YWFP-----PGRPAPVAFLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2042;
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RESULT 39
Q9DQD1
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Best Local S
Matches 62
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Best Local Similarity 29.3%;
Matches 27; Conservative 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9DQD1;
Q9DQD1;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF272001; AAG40171.1; -.
InterPro; IPR001297; FtBJ;
InterPro; IPR001016; Viral_RNA_pol_L.
Pfam; PF001728; FtBJ; 1.
Pfam; PF001728; FtBJ; 1.
Pfam; PF001728; FtBJ; 1.
SEQUENCE 2212 AA; 252692 MW; 5E334C0A291603D4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99171703; PubMed=10073695; Volchkov V.B., Volchkov V.A., Chepurnov A.A., Blinov V.M., Dolnik O., Netesov S.V., Feldmann H.; "Characterization of the L gene and 5' trailer region of Ebola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ebola virus (strain Zaire Mayinga) (Ebo).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=MAYINGA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11062045;
Volchkov V.E., Chepurnov A.A., Volchkova V.A., Ternovoj V.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=MAYINGA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=128952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ebola-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VICOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klenk H.D.;
"Molecular Characterization of Guinea Pig-Adapted Variants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                          125
                                                                                   409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 RVLPLELDQIIRLPFNTSTPQETLFSIRHFDE 325
                                                                                                                                                                 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 ALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                                                                                                                                                                          13 ILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
-HLDHPPLFSTKIISDLSIFIKDRATAVERTCWDAVFEPN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVRAFDPEAAAMQPYQDQTYQPVYFVSESFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLGASDERIEKLST-----VYWFTVEFGLCKQNGELKAYGAGLLSSYGELLHSLSEEP 62
                                        FFLDYLEAFGL----LSDFLDHQAVI-----KFFELETHFSYYPVSGFVAPHQYLSL 172
                                                                                   ---CVFKYSIAKHYFDSQGSWYSVTSDRNLTPGLNSYIKRNQFPPLPMIKELLWEFY---
                                                                                                                                                                 LIRLEMTPOOLCELF-----SIOKHWGHPVLHSETAIOKVKKHATVLKALRPIVIFETY- 408
                                                                                                                           NLLFVHLLSLSKNQREGCSTDMAVVS----TP----FFNRNLWYRLLSSRFSLWKSYCPR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virol. 80:355-362(1999)
                                                                                                                                                                                                                                                Similarity 23.1 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                             5.3%; Score 100.5;
23.1%; Pred. No. 14;
tive 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 100.5;
Pred. No. 0.35
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .35;
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                                                                                                                                                                                                                                                                                        DB 12; Length
                                                                                                                                                                                                                                                95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                  Indels
  - VLGYNPPHKFSTK 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Filoviridae;
                                                                                                                                                                                                                                                  69;
                                                                                                                                                                                                                                                                                          2212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ebola
                                                                                                                                                                                                                                             Gaps
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                                                                                   462
                                                                                                                                                                                                                                                  13;
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477 LMFAKTTHFSFHGSHSERIWYFDIIRIDDLV 507
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Q95F52;
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Q95F52
ID Q95F5:
AC Q95F5:
                                                RESULT 41
                                                                             qq
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                                                                                                                                                                                                                                                                                                                                                                                                              Hilu K.W., Alice L.A.; Phylogenetic relationships in subfamily Chloridoideae (Poaceae) based "Phylogenetic relationships in subfamily Chloridoideae (Poaceae) based on matK sequences: A preliminary assessment."; Beguences: Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTRONS (BY SIMILARITY).
SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHOUNRIAL INTRONS.
                                                                                                                                                                                                                                                                                                    Chloroplast.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Chloridoideae; Eragrostideae; Sporobolus.
                    515 RVPEQF-----LEQENFS-----IENVLSYAQKLEYLLPQYRNFSFSLKEKELNVGR 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 FLLKKENKRLFRFLYNSYVSEYEFF--LLFLRKQSSSLRLISSGTFLERIHFSMKMEHFG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 VVSTPFFNRNLWY------RLLSSRFSL----WKSYCPRFFLDYLEAFGLL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 SDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 DLIHDL-----LGH-VPWLLHPSFSEFFI--NMGRLFTKVIEKVQALPSKKQRIQTL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 -LIGSLSKAQFCTGLGHPISKPIWTDLSDWDILDRFGRICRNLFH-YHSGSSKKQALYQL 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 QSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIR 305
173 LODRYFPIASVMRTLDKONFSLTPDLIHDLLGHVPWL--LHPSFSEFF-----INMGR 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 EKFLHLHYLSHIEIPYPIHFEILVQLLEYRIQDVPSLHLLRFFLNYYSNWNSLITSMKSI 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 IILOKENKEKOALARHKCISILEFFKNLLFVHLLSLSKN------OREGCSTDM---A 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ERTLDPKYILKIALK-----LROSLSLFFONSOSLO--RAYSTPYSYR------ 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 5.3%; Score 99.5; DB 8; Length 513; Local Similarity 23.3%; Pred. No. 3; Local Similarity 23.3%; Mismatches 153; Indels 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chloroplast; mRNA processing.
SEQUENCE 513 AA; 61561 MW; BF6BB16048B3EC6A CRC64;
                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable intron maturase (Maturase K).
                                                                                                                                                                          513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 LPFNTST-----PQETLFSIRHFDELV 327
                                                                                     562 TFGK-----LPYPTRNVQTLCEALLA 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF144601; AAF20357.1; -.
InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; MarK_N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MarK_N; 1.
                                                             224 LETKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                     Sporobolus indicus (smut grass).
                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                          RESULT 40
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BY
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Chloridoideae; Chlorideae; Aegopogon.
NCBI_TaxID=160573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
5.2%; Score 99; DB 8; Length 513;
Best Local Similarity 19:1%; Pred. No. 3:3;
Matches 69; Conservative 63; Mismatches 124; Indels 106; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 KSIFLFSKENKRLSRFLYNFYVSEYEFFLLFLRKQS-----SCLRLTSYGTFLER 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 HLLSLSKNOREGCSTDMAVVSTPFRNRNLWYR-------LLSSRFSL----W 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 KSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 PIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTK-----V 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 LIATRMKKFD-TTAPATP-LIRSL-----SKAQFCTGSGHPISKPIWTDLSDWDI 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 IEKVQAL------PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   406 LDRFGRICRNLFHYHSGSSKKQTLYRLK----YILR---LSCARTLARKHK-----STV 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIR--HFDELVELTSKLEWM 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTRODUCE (SI SINILARII),

-1- SIMILARIYY WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARIYY TO MATURASE-LIKE POLYPEPTIDES ENCODED INTROCHONDRIAL INTRONS.

BMBL, AFA12324; AAK60015.1, -.

INTECTPO: IPRO0246; Intron maturse2.

Interpro: IPR00246; Matk.M.

Pfam; PF0148; Intron maturas2; 1.

Pfam; PF014824; Matk.M.; 1.

Chloroplast; mRNA processing.

SEQUENCE 513 AA; 61640 MW; E80743D3EA97F086 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 QSLSLFFQNSQSLQR----AYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hilu K.W., Alice L.A.;

"A Phylogeny of Chloridoideae (Poaceae) Based on matK Sequences.";

"A Phylogeny of Chloridoideae (Poaceae) Based on matK Sequences.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

INTRONS (BY SIMILARITY)

-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Probable intron maturase (Maturase K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                513 AA.
    513 AA
    PRT;
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PRELIMINARY;
                                                                                                                                                                                                                                                  Aegopogon cenchroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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27;

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RESULT 43
054921
ID 05492
AC 05492
AC 05492
DT 01-JU
DT 01-DE RECCS
OS RATCU
OC EUKARI
OC Mamma
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Best Local S
Matches 70
                                                            054921;
01-JUN-1998
01-JUN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A Phylogeny of Chloridoideae (Poaceae) Based on matk Sequences.";
Submitted (OCT-2000) to the EMBL/Genbank/DDBJ databases.

-- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).

--- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
MITOCHONDRIAL INTRONS.

EMBL, AF31233; AAK60024.1; --- EMBL, AF31233; AAK60024.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001
01-DEC-2001
01-MAR-2002
Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO00442; Intron_maturse2.
InterPro; IPRO02866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N; 1.
Pfam; PF01824; MatK_N; 1.
Chloroplast; mRNA processing.
SEQUENCE 513 AA; 61432 MW; 56F4A4
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                                                                                                                             054921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=160579;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 QSLSLFFQNSQSLQR----AYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFV 77
                                                                                                                                                                                                        6=6
                                                                                                                                                                                                                                                                  RTFMQRLGSVFLEEFFT---EEDQVFSLMF----PKTTHFSFHGSHSERI-----
                                                                                                                                                                                                                                                                                                ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIR--HFDELVELTSKLEWM 336
                                                                                                                                                                                                                                                                                                                               LDRFGRICRNLFHYHSGSSKKQTLYRLK----YILR---LSCARTLARKHK-----
                                                                                                                                                                                                                                                                                                                                                             IEKVQAL-
                                                                                                                                                                                                                                                                                                                                                                                          LIDTRMKKFD-TTAPATP-----LIGSL-----SKAQFCTGSGHPISKPIWADLSDWDI
                                                                                                                                                                                                                                                                                                                                                                                                                      PIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTK------V
                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSYLVNFSQYFFSFWTQPQRIRLNQLTNSCFDFLGYHSSVPINTFLVRNQML----ENFF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERIHFSRKMEH-----FGVMYPGFFWKTIWFFMDPLMHYVRYQGKVILASKGTLLLKKKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLLSLSKNQREGCSTDMAVVSTPFFNRNLWY------RLLSSRFSL-----W 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSIFLFSKENKRLSRFLYNSYVSEYEFFLLFLRKQS------SCLRLTSSGTFL 246
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                                                           (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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(TYEMBLrel. 19, Last sequence update)
(TYEMBLrel. 20, Last annotation update)
tron maturase (Maturase K).
                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.2%; Score 99;
19.3%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
 Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                           PRT;
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                                                                                                                             924
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   Euteleostomi;
; Murinae; Rat
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Q8TPH6
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Best Local
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Q8TPH6;
01-JUN-2002
01-JUN-2002
01-JUN-2002
STRAIN=C2A / ATCC 35395 / DSM 2834;

MEDLINE=21929760; PubMed=1193238;

Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown R.,

Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.

Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98070770; PubMed-9405631;
Kee Y. Yoo J.S. Hazuka C.D. Petterson K.E., Hsu S.C., Scheller R.H.;
"Subunit structure of the mammalian exocyst complex.";
Proc. Natl. Acad. Sci. U.S.A. 94:14438-14443(1997).
EMBL, AF032666; AAC01578.1; -.
InterPro; IPR002909; IPT_TIG.
                                                                                                                                                                    Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina.
                                                                                                                           SEQUENCE FROM N.A.
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[1]
                                                                                                                                                    NCBI_TaxID=2214;
                                                                                                                                                                                                                                   Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLSLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSSRF-----SLWKSYCPRFFLDYLEAF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVEGSMTQKLEN--VLNRASNTADTLFQEVLGRKDK---ADSTRNALNVLQRFK-FLFNL 286
                                                                                                                                                                                                                                                                                                                                                                                          RLAEKEDWIVDNEGLTSLPCQFEQSIVHSLQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HV-IQTIRLTYESLTALEIPNDMLQII-----QDLILDLRIHCIMVTLQHTAEEIK 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQRQNDFKKMIQEVMHSLVKLIRGALLPFSLREG-----DGRQ-YGGWEVQAELSGQWLA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQR-----IQTLQSNLIAIVR--CFWFTVESGLIENHEGRKAYGAVLIS---SPQELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRDDTWRYKTPHRVAFVEKLTKLVLSQLPNFWKLWISYVNGSLFSETAEKSGQIERSKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PWLLH-----VQALPSK
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VCE 924 AA; 104031 MW;
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(TremBLrel. 21, 1
(TremBLrel. 21, 1
al protein MA1936.
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                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.2%; Score 99; DB 11; Length 924; 19.9%; Pred. No. 6.7; tive 77; Mismatches 122; Indels 164;
                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1903C0593B113373 CRC64
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                                                                                                                                                                                        Methanosarcinales;
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                 Guss A.M.
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5.2%; Score 98.5; DB 16; Length 584;
20.2%; Pred. No. 4.2;
tive 67; Mismatches 154; Indels 99;
                                                                                                                                 Chloroplast; mRNA processing.
SEQUENCE 513 AA; 60865 MW; BFDC47C27343B94C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AL139079; CAB73666.1; -.
INPERPY: JRR001440; TPR.
Hypothetical processity. Complete proteome.
SRQUENCE 584 AA; 69439 MW; CFAD376B1562DE1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCT-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein Cj1679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 ELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              470 EEEQVFSLMF----AKTTRFSF-HGSQ----SERIWYLD 499
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Nature 403:665-668(2000).
             InterPro; IPR002866; MatK N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK N; 1.
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Matches 81; Conservative
                                                                                                                                                                                                                                                                                Best Local Similarity 22.08
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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NCBI_TaxID=197;
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"Phylogenetic relationships in subfamily Chloridoideae (Poaceae) based on matk sequences: A preliminary assessment.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Centotheceae; Zeugites.
Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Dearson E.C., Ferry J.G., Dearson E.C., Mitchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B., The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity."; Genome Res. 12:532-542(2002).

EMBL, ABOINGOS, AMMOSA40.1; EMBL, ABOINGOS, AMMOSA40.1; EMBL, BURDOS, AMMOSA40.1; EMBL, BURDOS, AMMOSA40.1; EMBL, BURDOS, AMMOSA40.1; EMBL, BURDOS, AMMOSA, LESSA, BURDOS, AMMOSA, LESSA, BURDOS, AMMOSA, LESSA, BURDOS, AMMOSA, BURDOS, AMMOSA, BURDOS, AMMOSA, BURDOS, AMMOSA, BURDOS, AMMOSA, BURDOS, BURDOS, AMMOSA, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, BURDOS, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 PHSLFESIFKFNEKVMLLYKSQDTEEIIEYKIQNQLSSAKIEIDNENYKKALNLLEDTKK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 SDKCVDLQKIHYDIMNLK-LKLCENQ-------FEENPENSFLKAQISV--- 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YCPRFFLDYLEAFGLLSDFLDHQAVI----KFFELETHFSYYPVSGFVAPHQYLSLLQDR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 -----TLEDFGI---FLINVKLIEKAKKIYEREIQILQDLLNKYPENEEYLSLIGSA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 YFPIASVMRTLD-----KDNFSLTPDLIHDLLGHVPWLLHPSFSEF-----FINMGRL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTKV------IBKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIEN 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 LSELGSIDEATNRYERALKVHIQFIERYPEIKQYHSSVLKNEFKLIESYFYCAENEI--N 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 HEGRKAYGAVLISSPOELGHAFI-----DNVRVLPLELDQIIRLPF-NTSTPOETLFSI 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 NQTKWMPFGEVIHMCEQYQDLFIKSDSEDERKKMLEPKIRSQIKFSFLDIEMQKKHELSA 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 PKYILKIALKLRQSLSLFFQNSQS---LQRAYSTPYSYYRIILQKENKEK-----QALA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.2%; Score 99; DB 17; Length 1078;
16.3%; Pred. No. 8;
tive 79; Mismatches 148; Indels 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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InterPro; IPR000442; Intron_maturse2.
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                                                                                                                                                                                                                                                     147 LHYLSH-IBIPYPLHLBI-LVQILEYRIQDVPSLHILRFFLNYYSNWNSLISSMKSILLL 204
                                                                                                                                                                                                                                                                                                                                                                                                                     205 KKENKRLFRFLYNSYVSEYEFF--LLFLRKQSSCLRLTSSGTFLERIHCCRKMEHFGVMC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 TPFFNRNLWY------RLLSSRFSL----WKSYCPRFFLDYLEAFGLLSDF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 PGFFRKTIWFFMDPLTHYVRYQGKAILASKGTLLLKKKWKSYLVN-FSQYFFSFGTQPQR 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 LD-HQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 IRLNQLTNSCFDFLGYLSSVPINTLLVGNQML----ENSFLIDTRMKKFD-TTVPATP-- 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 ---LIGSL-----SKAQPCTGSGHPISKPVWTDLSDRDILDRFGRICRNLFHYHSGSSK 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 KQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         426 KOTLYRLK----YILR---LSCARTLARKHK-----STVRTFMORLGSVFLEEFFT--- 469
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                                                                                                                                                                                                                                                                                                                                                              50 QKENKEKQALARHKCISILEFFKNLLFVH----LLSLSKN----QREGCSTDM---AVVS 98
                                                                                                                                                                                    1 VHYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQ--RAYSTPYSYYR-----IIL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 IHDLLGHVPWLLHPSFSEFFINMGRLFTK------VIEKVQAL------PSK
5.2%; Score 98.5; DB 8; Length 513; 22.0%; Pred. No. 3.6; tive 62; Mismatches 141; Indels 109;
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RESULT 47
Q94DZ7
ID Q94DZ
AC Q94DZ
AC Q94DZ
DT 01-DE
DT 01-DE
DT 01-MA
DE Putat
GN 0772A
OC Sherm
OC Sherm
OC Sherm
OC STRAI
RN [1]
RP SEQUE
RT Clone
RL Sassak
RT Clone
RT Strai
DR Inter
DR PEAM;
DR PROSE
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Best Local :
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Coryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
Clone:p0010B10.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003224; BAB63566.1; -
EMBL, AP003224; BAB63566.1; -
InterPro; IPR00143; Peptidase_M16;
Pfam; PF00675; Peptidase_M16; 1.
PROSITE; PS00143; INSULINASB; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative zinc protease.
P0010B10.10.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Q94DZ7;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                      KFPAILRKTPLSRLWYMPDMLFSTPKVHIVIDFHCPLTSHSPE-----AVIST-----S
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                                                                                                                                                                                                                                                                                                                                                                                                           FFQNSQSLQRAYSTPYSYYRII------LQKENKEK-----------
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                                                                                                                                                                                                                                                                                                                                   FEGTTDSVEPWYCTAYSVENVTPSMIQQWIQKAPTEKLCIPKPNIFIPKDFSLKEAHEKV 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.2%; Score 98.5; Dilarity 22.8%; Pred. No. 7.6; Conservative 43; Mismatches
                                      --DYLNAYGGYNDKMRILLDAIMKH---ISNFEVKPNRFC
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SEQUENCE FROM N.A.

CONTAINACTORL/GJ, TISSUE=TESTIS;

XX MEDLINE=2108560; PubMed=11217851;

XX MEDLINE=21085660; PubMed=11217851;

XX ARAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XX Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

XX Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XX Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XX Agdota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XX Agdota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XX Ashito T., Okazaki Y., Gojobori T., Bono H., Batalov S., Cosavant T.,

XX Ashito T., Lewis S., Matsuc Y., Nikaido I., Pesole G., Quackenbush J.,

XX Ashito T., Staubhi F., Suzuki R., Tomita M., Wagner L., Washio T.,

XX Ashito T., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

XX Ashito J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F.,

XX Ashito J., Boilt C., Fletcher C., Fujita M., Gariboldi M.,

XX Ashito J., Boll C., Fletcher C., Fujita M., Gariboldi M.,

XX Ashito J., Boll C., Fletcher C., Fujita M., Gariboldi M.,

XX Ashito J., Boll C., Fletcher C., Fujita M., J. Lee N.H.,

XX Ashito J., Ringgald M., Rodriguez I., Sakamoto N.,

XX Ashiti H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

XX Ashawi H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

XX Ashawi H., Sato K., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

XX Ashawi J., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

XX Ashawi H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

XX Ashawa B., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

XX Ashawa B., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Q9D4H1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AKO16522; BAB30290.1; -.
MGD; MGI:1913732; 2410030124Rik.
InterPro; IPR002999; IPT_TIG.
Pfam; PF01833; TIG; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152
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                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                             19 KLROSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFVH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                            AGIEDL---RELLLKKL-LETPSTLHDQKRYIRYLSDLHAPGDPAWQCIGAQHKWTLKLMQ
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                                                                                                                                                                                                                                                                                                                                                                         KVEGSMTOKLEN--VLNRASNTADTLFQEVLGRKDK---ADSTRNALNVLQRFK-FLFNL
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(TrEMBLrel. 17, Last seq
(TrEMBLrel. 17, Last ann
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        -RYFPIASVMRTLDKDNFSLTPDLIHDLLGHV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.2%; Score 98; DB 11; Length 924; 20.0%; Pred. No. 8.1;
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Last annotation updat
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121 YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYYPVSGFVAPHQYLSL 172
                                                                                                                                       DB 5; Length 1887;
19;
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
Hypochhetical protein.
SEQUENCE 1887 A4, 214207 WW, 992DDE7F409D2D84 CRC64;
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                                                                                                                                       Query Match 5.2%; Score 98; DB 98st Local Similarity 23.3%; Pred. No. 19; Metches 71; Conservative 34; Mismatches
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NCBI_TaxID=6523;
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387 DCKEGHMKSLKGHPGPHSPM-----LDLDN-----DVRPSVLGHLSQTASLKRGSSFQS 435
                                                                                                   436 GRDDTWRYKTPHRVAFVEKLTKLVLSQLPNFWKLWISYVNGSLFSETAEKSGQSERSKNV 495
                                                                                                                                                                                                                                           239 -----KQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLIS---SPQELGHA 288
                                                                                                                                                                                                                                                                                       496 RQRQNDFKKMIQEVMHSLVKLIRGALLPLS----LREGDGRQ-YGGWEVQAELSGQWLAHV 551
                                                                                                                                                                                                                                                                                                                                                                               289 FIDNVRV---------HPDELDQIIRLPFNTSTPQETLFSIR--------HFDELVEL 329
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF067217; AAF99977.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
Murray J., Rohlfing T., O'Neal D., Wilson R.;
"The sequence of C. elegans cosmid F56A6 ";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 214.2 kDa protein.
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SMART; SM00242; MYSc; 1.
SMART; SM00314; RA; 1.
SMART; SM003124; RA; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 TSKLEWMLDQGLLESIPLYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602 AEKEDWVVDNEGLTSLPCQFEQSIVHSLQSL 632
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InterPro; IPR001609; myosin head.
InterPro; IPR001609; RAGGAP.
InterPro; IPR000189; RAGGAP.
Pfam; PP00130; DAG PE-bind; 2.
Pfam; PP006612; IQ; 4.
Pfam; PP006612; IQ; 4.
Pfam; PP006618; RA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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InterPro; IPR000048; IO region.
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PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_heav
SMART; SM00109; Cl; 2.
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MEDINE-21295676; PrbMed=11466431;
MEDINE-21295676; PrbMed=11466431;
Sort C.E., Spencer G.E., van Minnen J., Li K.W., Geraerts W.P.,
Syed N.I., Smit A.B., van Kesteren R.E.;
"Functional implications of neurotransmitter expression during axonal regeneration: Berconin, but not peptides, auto-regulate axon growth of an identified central neuron.";
J. Neurosci. 21:5597-566 (2201).
HSSP; P04176; 1PR2.
HSSP; P04176; 1PR3.
PRO01273; Aaa_hydroxylase.
PRINTS; PR001273; PYWHYDEXILASE.
PRINTS; PR00372; FYWHYDEXILASE.
PRINTS; PR00372; FYWHYDEXILASE.
PRONTE; PR00372; FYWHYDEXILASE.
                                                                                                                                                                                                                                                                                     154
                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 NNNSSRFG-----KFIKINYREN-GMVSG-----ANVEIYLLEKSRIIFQTKGERNYH 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 VFYYLLEGADEEERKKYFLLKPHDYKYLNQNEPFALEGVN---ERNEF-----DRLK 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 HA-----MSSVGFCAKTQQTIFGIISAV-----LLLGNITYIKRHGYHSDESGY 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 FKNLLFVHLLSLSKNQREGCSTDMAV----VSTPFFNR----NLWYRLLSSRFSLWKS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 FKDTVY------RQRRKIITDLAMKYAHGTEIPYVEYTEVEVETWGIVFRELMKLYPT 144
92; Indels 108; Gaps
                                                                                                                                                                                                                                       61 RHKCISI------DEFFKNLLFVHLLSLSKNQREGCSTDMAVVST-----PFFNRNLWY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 FSYYPVSG------FVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 HVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGL 264
                                                                                                                                                    217 NPKY-----ARLYFOS----KRLGSLPPHIFAIADVCYHNMLRIKEN----- 254
                                                                              9 DPKYILKIALKLRQSLSLFFQNSQSLQRAYSTP-----YSYYRIILQKENKEKQALA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Tryptophan hydroxylase (Fragment).
Lymnaea stagnalis (Great pond snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
                                                                                                                                                                                                                                                                                                                                                                                           109 RLLSSRFSLWKSYCPRFF-LDYLEAFGLLSDFLDHQAVIKFFELET-------H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.2%; Score 97.5; DB 5; Length 239; Best Local Similarity 21.7%; Pred. No. 1.7; Matches 34; Conservative 30; Mismatches 64; Indels 29
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중 유 145 HACR---EYLANIPLLVEHCGYREDNVPQLEDIGRFLKERTGFTLRPVAGYLSSRDFLAG 201

Search completed: January 9, 2003, 16:59:53 Job time: 90 secs

дδ

|  |   |  |   |  |  |  |  |  | 58<br>60<br>61<br>61<br>63<br>63<br>63                      |   |           |  |                    |  |  |                    |  |  |  |                    |                    |  |                    |                    |  |  |                                     |                    |  |  |
|--|---|--|---|--|--|--|--|--|---|---|-----------|--|--------------------|--|--|--------------------|--|--|--|--------------------|--------------------|--|--------------------|--------------------|--|--|-------------------------------------|--------------------|--|--|
| 5.1.3<br>Compugen Ltd.                       |   | . Search time 43 Seconds<br>(without alignments)<br>809.318 Million cell updates/sec | ESIPLYNQEKYLSGFEVLCQ 362  |  | 89                                       | eters: 283224                                      |  |  |   | dicted by chance to have a<br>re of the result being printed,<br>l score distribution.  | S         | Description                                  | aromatic amino aci | aromatic amino aci<br>phenylalanine-4-hy | phenylalanine-4-hy<br>tryptophan 5-monoo | phenylalanine hydr | tryptophan 5-monoo<br>tyrosine 3-monooxy | tryptophan 5-monoo<br>tryptophan 5-monoo | tyrosine 3-monooxy                                       | tyrosine 3-monooxy | tyrosine 3-monooxy | tyrosine 3-monooxy<br>phenylalanine 4-mo | phenylalanine 4-mo | tyrosine 3-monooxy | pnenylalanine 4-mo<br>hypothetical prote | tryptophan 5-monoo<br>phenylalanine 4-mo | phenylalanine-4-hy                  | phenylalanine 4-mo | disease resistance<br>174K ninaC protein |  |
| GenCore version<br>Copyright (c) 1993 - 2003 | OM protein - protein search, using sw model | Run on: January 9, 2003, 15:15:23;<br>(<br>8   | Title: US-09-438-185A-1047 Perfect score: 1889 Sequence: 1 VHYCERTLDPKYILKIALKI | Scoring table: BLOSUM62<br>Gapop 10.0 , Gapext 0.5 | Searched: 283224 segs, 96134422 residues | Total number of hits satisfying chosen parameters: | Minimum DB seq length: 0<br>Maximum DB seq length: 200000000 | Post-processing: Minimum Match 0%<br>Maximum Match 100%<br>Listing first 150 summaries | Database : PIR 73:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution. | SUMMARIES | Result Query<br>No. Score Match Length DB ID | 1886 99.8 362 2    | 256.5 13.6 289 2                         | 235.5 12.5 262 2<br>231.5 12.3 444 1     | 229.5 12.1 262 2   | 229.5 12.1 491 2                         | 227.5 12.0 444 1<br>226.5 12.0 447 2     | 11 225.5 11.9 498 2 JN0068<br>12 223.5 11.8 481 2 151567 | 223 11.8 498 1     | 220 11.6 528 1     | 219 11.6 579 1<br>214 11.3 453 1         | 213.5 11.3 452 1   | 211.5 11.2 491 2   | 206.5 10.9 575 2                         | 197 10.4 453 1<br>194 10.3 452 2         | 189.5 10.0 294 2<br>178.5 9.4 404 2 | 175.5 9.3 457 2    | 109.5 5.8 1253 2<br>108.5 5.7 1501 1     |  |

| phenylalanine 4-mo<br>genome polyprotein<br>probable transcrip<br>exodeoxyribonuclea<br>NUP133 protein - y<br>exocyst complex pr<br>hypothetical prote<br>hypothetical prote<br>hypothetical prote<br>cytochrome P450 2L<br>exodeoxyribonuclea | glucose-6-P dehyro glucose-6-P dehyro grobable membrane exceoxyribonuciea large tegument pro hypothetical prote probable zinc prot SRB protein - yea cell communication probable cation-tr hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote protein F09C3.1 [i heterocyst maturat hypothetical prote hypothetical prote hypothetical prote gene A protein - y 265 proteane - y                      | mark protein (Irrik lamin B receptor - apolipoprotein B-1 spermidine synthas hypothetical protein B-9. K hypothetical minor inner core p DNA topoisomerase genome polyprotein probable signal pe ORC3 protein - yea hypothetical protein phycobilisome anch hypothetical protein hypothetical h | hypothetical prote phosphotidylinosit hypothetical prote hypothetical prote hypothetical prote hypothetical prote sensor probable sensor fo probable sensor fo probable sensor fo probable sensor fo probable sensor fo probable sensor fo probable sensor fo probable sensor fo probable sensor fo probable manalectical prote hypothetical prote hypothetical prote probable membrane polymerase I uu probable membrane polymerase — Berne apolipoprotein B - |
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| 000000000000000000000000000000000000000  | 512 2 786520<br>529 2 862468<br>2059 2 862468<br>2059 2 1472041<br>2059 2 7472041<br>536 2 870066<br>1477 2 84246<br>1477 2 84246<br>1477 2 861321<br>293 2 747139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 872139<br>618 2 87213<br>618 2 87213<br>618 2 87213<br>618 2 87213<br>618 2 87213<br>618 2 87213<br>618 2 87213<br>618 2 87213<br>618 2 87213<br>618 2 87213<br>618 2 87213<br>618 2 87213<br>618 2 87213 | 000000000000000000000000000000000000000  | 28 4 3 3 5 5 6 6 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8  |
|  | พ พ พ พ พ พ พ พ พ พ พ พ พ ഷ ഷ ഷ ഷ ഷ ഷ ഷ   |  | <b> </b>  |
| 106.5<br>104.5<br>102.1<br>102.1<br>100.5<br>99.5<br>98.5<br>98.5  | ᲓᲓ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ  | 9999 898 899 891 892 898 898 899 899 899 899 899 899 899   | M M D D D D D D D M M M M B B B B B B B   |
|  | 4 4 4 4 4 4 4 4 4 W W W W W W W W W W W   |  |   |

| Query Match 99.8%; Score 1886; DB 2; Length 362;                        | A;Accession: B72002 A;Status; preliminary A;Status; preliminary A;Molecule type: DNA A;Residues: 1-362 <arn> A;Accession: Brain CBL001685; GB:AE001363; NID:g4377378; PIDN:AAD19183.1; PID:g437738 A;Cross-references: GB:AE001685; GB:AE001363; NID:g4377378; PIDN:AAD19183.1; PID:g437738 A;Experimental source: strain CWL029 C;Genetics: C;Genetics: C;Genetics: C;Genetics:</arn> | R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999 A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606; PMID:10192388 | aromatic amino acid hyroxylase - Chlamydophila pneumoniae (strain CWL029) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000 C:Accession: R72002 | RESULT 1  | 50 84 4.4 240 2 270409 Conserv           | 49 84.5 4.5 1107 L<br>48 84.5 4.5 1748 1<br>49 84.5 4.5 3068 1   | 84.5 4.5 820 2 TZ7909 hypotheti<br>84.5 4.5 1070 2 G84982 exodeoxyv | 43 84.5 4.5 719 2 C88216  | 84.5 4.5 531 2 B84442 hypothetical   | 85 4.5 938 2 G70472 hypothetical 84.5 4.5 2 T22823 hypothetical 84.5 4.5 2 G71152 hypothetical   | 85 4.5 567 2 B69166 hypothetical 85 4.5 717 2 S78177 hypothetical                   | 85 4.5 493 2 H95209<br>85 4.5 549 2 F64640 | 131 85 4.5 328 2 132210 Nypochetical proce<br>132 85 4.5 462 1 YSBYTM threonine-tRNA 11g<br>133 85 4.5 471 2 F71618 adenylosuccinate l | 85 4.5 2039 2 864340<br>85 4.5 238 1 864313 | 85.5 4.5 1613 2 D90129 hypothet<br>85.5 4.5 1808 2 AB1847 serine/t | 85.5 4.5 816 2 T25788<br>85.5 4.5 1489 2 T38842                  | 85 4.6 1405 1 DUZER<br>86 4.6 1822 2 S4849<br>85.5 4.5 321 2 D90154  | 86 4.6 512 2 D98074<br>86 4.6 565 2 D72222                       | 86 4.6 339 2<br>86 4.6 422 2  | 86.5 4.6 990 2 \$23416<br>86.5 4.6 990 2 \$23416                        | 86.5 4.6 120 2 Mn2322 nypothetical pro<br>86.5 4.6 533 2 T27589 hypothetical pro | 87 4.6 324 1 A48953 choloylglycine hy 87 4.6 741 490607 attp-dependent hel | 87.5 4.6 181/ 2 H/1611 prodable Section 87 4.6 293 2 F64558 conserved hyp | 87.5 4.6 1122 2 A97814 transcript internal inter | 87.5 4.6 542 2 JQ0201 hypothetical 65K<br>87.5 4.6 694 2 D81280 polyphosphate kin | 87.5 4.6 334 2 E71680<br>87.5 4.6 454 2 AH0469   |
|---|--|---|---|---|--|--|---|---|--|--|---|--|--|---|--|--|--|--|---|---|--|--|---|--|---|--|
| Qy 241 RIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL 300 | Qy         121 YCPRFFLDYLAAFGLLSDFLDHQAVIKFFLETHFSYYPVSGFVAPHQYLSLLQDRYFPI         180   | 61 RHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKS<br>   | Qy 1 VHYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALA 60  | Query Match 99.8%; Score 1886; DB 2; Length 362;<br>Best Local Similarity 99.7%; Pred. No. 2e-144;<br>Matches 361; Conservative 1; Mismatches 0; Indels 0; Gaps | ntal source: strain J138<br>3;<br>5)1046 | A;Residues: 1-362 <sto> A;Residues: 1-362 <sto> A·Croser-references: GRADODOB: NTD-C8070419: DIDN-BAA00253 1: GSDDB-GNDD14</sto></sto> | A;Accession: C86621<br>A;Status: preliminary                        | A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  A;Reference number: A86491; MUID:20330349; PMID:10871362 | R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; S | C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae<br>C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 | C86621 aromatic amino acid hyroxylase [imported] - Chlamydophila pneumoniae (strain | RESULT 2                                   | Db 361 CQ 362  | Qy 361 CQ 362                               | 301 DQIIRLPENTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL   | 301 DQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL | QY 241 KIQTIQSNLIALYKCFWETVESGLLENHSKKANGAVLLSSPQELGHAFIDNVKVLDELEL 300  DD 241 KIQTIQSNLIALVKCFWETVESGLLENHSKKANGAVLLSSPQELGHAFIDNVKVLDELEL 300 | 181 ASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSBFFINMGRLFTKVIBKVQALPSKKQ | QY 181 ASYMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ 240 | Db 121 YCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPI 180 | Qy 121 YCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPI 180          | Db 61 RHKCISILEFFKNLLFVHLLSISKNQREGCSTDMAVVSTPFFNRNLMYRLLSSRFSLMKS 120     | QY 61 RHKCISILEFFKNILFVHLLSLSKNOREGCSTDMAVVSTPFFNRNLMYRLLSSRFSLWKS 120    | Db 1 MHYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALA 60   | VHYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQAI                       | .  Best Local Similarity 99.7%; Pred. No. 2e-144;  Marches 361; Conservative 1; Mismatches 0; Indels 0; Gaps |

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7%; Pred. No. 2e-144;
1; Mismatches 0; Indels 0; Gaps

$; Score 1886; DB 2; Length 362;
$; Pred. No. 2e-144;
1; Mismatches 0; Indels 0; Gaps

                                                                                                                                                                                                                                                                            8; NID:g8979419; PIDN:BAA99253.1; GSPDB:GN00142
J138
                                                                                                                                                                                                                                                                                                                                                                 enome sequences of chlamydia pneumoniae J138.
ID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                                                                            moto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.
14, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                        [imported] - Chlamydophila pneumoniae (strain J138)
coniae, Chlamydia pneumoniae
revision 02-Mar-2001 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL 300
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ESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ 240
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RESULT 3

361 361

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A; Description: catalyzes the oxidation of tryptophan to 5'-hydroxytryptophan by tetrahydd A; Pathway: melatonin biosynthesis; scrotconin biosynthesis; tryptophan catabolism C; Superfamily: phenylalanine 4-monooxygenase C; Superfamily: phenylalanine 4-monooxygenase; wetalloprotein; monooxygenase; c; Keywords: biopterin; iron; melatonin biosynthesis; metalloprotein; monooxygenase; oxidc F; SGM aite: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicte F; 260,443/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status F; 277,217,317/Binding site: iron (His, His, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecule type: mRNA
1,Molecule type: mRNA
1,Residues: 1-444 <BOLD:
1,Residues: 1-444 <BOLD:
1,Residues: 1-444 <BOLD:
1,Residues: 1-444 <BOLD:
1,Residues: 1-644 <BOLD:
1,Residues: 1-644 <BOLD:
1,Ribeatro, P.; Kaufman, S.
1,Titpesr, J.P.; Citron, B.A.; Ribeatro, P.; Kaufman, S.
1,Titchen: Biophys. 315, 445-453, 1994
1,Reference number: S51199; MUID:95077422; PMID:7986090
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A,Molecule type: mRNA
35, G', 437-444 «TTP»
AjCross-references: GB:L29306; NID:g531192; PIDN:AAA67050.1; PID:g531193
                                       A;Cross-references: GB:AE004522; GB:AE004091; NID:g9946768; PIDN:AAG04261.1; GSPDB:GN001:
A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 RVLQATTGWRVARVPALIPFQTFFELLASQQFPVATFIRTPEELDYLQEPDIFHEIFGHC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
12.3%; Score 231.5; DB 1; Length 444;
Best Local Similarity 27.8%; Pred. No. 5.8e-11; Undels 27; Gaps Matches 64; Conservative 43; Mismatches 96; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                            93 DMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 -----THFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 PLLTNPWFAEFTHTYGKLGLKA-----SKEER-----VFLARLYWMTIEFGLVE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 NHEGRKAYGAVLISSPQELGHAFID---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHF 323
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        13 DNGFIHYPETEHQVWNTLITRQLKVIEGRACQEYLDGIEQLG-----LPHERIPQLDEIN 67
                                                                                                                                                                                                                         Query Match
12.5%; Score 235.5; DB 2; Length 262;
Best Local Similarity 24.5%; Pred. No. 1.4e-11;
Matches 61; Conservative 52; Mismatches 103; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:120732; OMIM:191060
A;Map position: 11p15.1-11p14.3
C;Punction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 DELVELTSK 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE004410; GB:AE003853; NID:g9658244; PIDN:AAF96726.1; GSPDB:GN001
A;Experimental source: serogroup Ol; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phenylalanine-4-hydroxylase VCA0828 [imported] - Vibrio cholerae (strain N16961 serogrou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fileddelberg, UST; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.R.R.; Metalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 200
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Reference preliminary
A;Reference to the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Reference number: ARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Vibrio cholerae
Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                         301 DQIIRLPFNISTPQETLFSIRHFDELVELISKLEMMLDQGLLESIPLYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 RIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL 300
                                                                              DQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 VWHELITRQQEVVKTRACQAYLDGLNMLNLPTDRLPQLPEINRVLQRETGWQVEPVPALI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 FTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 LGHAFIDNV-RVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSK----LEWM-LD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 LWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDPLDHQAVI-KFFELETHFSYYPVSGFV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 APHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.6%; Score 256.5; DB 2; Length 289; Best Local Similarity 25.6%; Pred. No. 3.2e-13; Matches 65; Conservative 56; Mismatches 108; Indels 25;
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A; Map position: 2

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A; Gene: VCA0828 C;Genetics:

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A;Status: preliminary A;Molecule type: DNA A; Accession: F83535

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tryptophan 5-monooxygenase (EC 1.14.16.4) - rabbit (Species: Oryottolagus cunicullus (domestic rabbit) (C;Bate: 15.Jul-1995 #sequence_revision 19-Apr-1996 #text_change 31-Mar-2000 C;Accession: S51199; A32699 R;Tipper; J.P.; Citron, B.A.; Ribeiro, P.; Kaufman, S. Arch. Biochem. Biophys 315, 445-453, 1994 A;Title: Cloning and expression of rabbit and human brain tryptophan hydroxylase cDNA A;Reference number: S51199; MUID:95077422; pMID:7986090 A;Accession: S51199
A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-444 <TIP> A;Cross-references: GB:L29305; NID:g531213; PIDN:AAA67051.1; PID:g531214
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A; Residues: 1-262 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Zhao, G.S.; Xia, T.; Song, J.; Roy, R.A.
Proc. Natl. Acad. Sci. U.S.A. 91, 1366-1370, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEIG-----LASLGASEEAVQKLAT-----CYFFTVEFGLCKQDGQLRVFGAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVLQATTGWRVARVPALIPFQTFFELLASQQFPVATFIRTPEELDYLQEPDIFHEIFGHC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNGFIHYPETEHQVWNTLITRQLKVIEGRACQEYLDGIEQLG-----LPHERIPQLDEIN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSSISELKHALSGHAKVKPFDPKITCKQECLITTFQDVYFVSESFEDAKE 384
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            219
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            INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
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tyrosine 3-monooxygenase (BC 1.14.16.2) - quail
N;Alternate names: tyrosine 3-hydroxylase
C;Species: Phasianidae gen. sp. (quail)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 31-Mar-2000
C;Accession: A28582; PHI524
R;Fauquet, M.; Grima, B.; Lamouroux, A.; Mallet, J.
J. Neurochem. 50, 142-148, 1988
A;Title: Cloning of quail tyrosine hydroxylase: amino acid homology with other hydro.
A;Reference number: A28582; MUID:88089590; PMID:2447231
A;Accession: A26582
A;Molecule type: mRNA
A;Residues: 1-491 <FAU>
A;Residues: 1-491 <FAU>
A;Cross-references: GB:M24778; NID:g213649; PIDN:AAA49514.1; PID:g213650
R;Faunnet M. Rami C
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A;Molecule type: mRNA
A;Residues: 1-101,'L'
                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-30 cFA2>
A;Residues: 1-30 perA2>
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: biopterin; catecholamine biosynthesis; iron; metalloprotein; oxidoreduct
F;324,329,369/Binding site: iron (His, His, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Fauquet, M.; Boni, C.
J. Neurochem. 60, 274-281, 1993
A;Title: The quail tyrosine hydroxylase gene promoter contains A;Reference number: PH1524; MUID:93107923; PMID:8093261
A;Accession: PH1524
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A;Title: Full-length cDNA for rabbit tryptophan hydroxylase: functional domains A;Reference number: A32699; MUID:87289638; PMID:3475690
A;Accession: A32699
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                                                                                                                            WKEVYSTLKSLYPTHACK---EYLEAFNLLEKFCGYNENNI PQLEEVSRFLKERTGFQLR 282
                                                                                                                                                                                                        WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
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PVRGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADKTFAQFS 342
                                                                PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                        12.1%; Score 229.5;
29.1%; Pred. No. 9.
                                                                                                                                                                                                                                                                            34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Mismatches
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thes 97;
                                                                                                                                                                                                                                                                                                        9.7e-11
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                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                                             Length 491;
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                                                                                                                                                                                                                                                                                27;
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RESULT 9

셤 ð

::| :::| :::| :::| ::::| 343 QDIG----LASLGATDEEIEKLATL--

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Appropriation bounce: Drain and the Morgan, W.W. J. Sharp, Z.D. submitted to the EMBL bota Library, June 1990 Appearance to the EMBL Data Library, June 1990 Appearance number: $2132 Appearance number: $2132 Appearance number: $2132 Appearance number: $2132 Appearance number: $2132 Appearance number: $2132 Appearance number: $2132 Appearance number: $2132 Appearance number: $2132 Appearance number: $2132 Appearance number: $2132 Appearance number: $2132 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance number: $2032 Appearance num
                                A mouse tryptophan 5-monooxygenase (EC 1.14.16.4) - mouse tryptophan 5-monooxygenase (EC 1.14.16.4) - mouse (Specias: Mus musculus (house mouse)
C. Specias: Mus musculus (house mouse)
C. Accession: A34582
R. Stoll, J. Grak, C.A.; Goldman, D.
Genomics 7, 88-96, 1990
A.Title: Characterization and chromosomal mapping of a cDNA encoding tryptophan hydroxyle A.Reference number: A34582; MUID:90243261; PMID:2110547
A.Reference number: A34582; MUID:90243261; PMID:2110547
A.Reference number: A34582
A.Residues: pre-liminary
A.Residues: 1447 <STO>
A.Residues: Tel-47 <STO>
A.Residues: Tel-47 <STO
A.Residues: Tel-47 STO
A.Rocersania translated the codon AAC for residue 405 as Gln
A.Cross references: GB = Monooxygenase
C. Superfamily: phenylalainine + monooxygenase
C. Stepverfamily: phenylalainine + monooxygenase
C. Stepverfamily: phenylalainine + monooxygenase
C. Stepverfamily: phenylalainine + monooxygenase
C. Stepverfamily: phenylalainine + monooxygenase
C. Stepverds: biopterin; iron; metalloprotein; oxidoreductase; phosphoprotein
F;275,280,320/Binding site: iron (His, His, Glu) #status predicted
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NyAlternate names: tyrosine hydroxylase
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 31-Mar-2000
C;Accession: UN0068; S1322_revision 31-Dec-1991 #text_change 31-Mar-2000
C;Accession: UN0068; S1322_revision 31-Dec-1991 #text_change 31-Mar-2000
C;Accession: UN0068; S1322_revision 31-Dec-1991 #text_change 31-Mar-2000
A;Reference number: Ommun. 176, 1610-1616, 1991
A;Reference number: JN0068; MUID:91248263; PMID:1674869
A;Molecule type: mBNA
A;Residues: 1498 atCH>
A;Cross-references GB:MG9200; NID:g201997; PIDN:AAA40434.1; PID:g201998
A;Experimental source: brain
R;Morgan, W.W.; Bermudez, J.: Sharr 7 n.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 WGTIFRELNKLYPTHACR---EYLRNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.0%; Score 226.5; DB 2; Length 447; ilarity 27.4%; Pred. No. 1.5e-10; Conservative 43; Mismatches 97; Indels 27;
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Best Local Similarity
Matches 66; Conserva
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A;Residues: 1-44 <KIM>
A;Residues: 1-44 <KIM>
A;Residues: 1-44 <KIM>
A;Experimental source dorsal raphe nucleus
R;Darmon, M.C.; Grima, B.; Cash, C.D.; Maitre, M.; Mallet, J.
FEBS Lett. 206, 43-46, 1986
A;Title: Isolation of a rat pineal gland cDNA clone homologous to tyrosine and phenylala
A;Reference number: A24367; MUID:87005247; PMID:2875901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Description: catalyzes the oxidation of tryptophan to 5'-hydroxytryptophan by tetrahyd A, Pethway; malatonin biosynthesis; serotonia biosynthesis; tryptophan catabolism (c. Superfamily; phenylalanine 4-monooxygenane) (c. Superfamily; phenylalanine 4-monooxygenasis; metalloprotein; monooxygenase; oxid F;58 Manding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict F;260,447)Binding site: phosphate (Ser) (covalent) (by campadont kinase) #status predict F;272,277,317/Binding site: inon (His, His, Glu) #status predicted
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A; Cross-references: GB:X53501; NID:g57760; PIDN:CAA37579.1; PID:g57761
A; Experimental source: pineal gland gland
B; Experimental source: pineal gland gland
B; Kim, K.S.; Wessel, T.C.; Stone, D.M.; Carver, C.H.; Joh, T.H.; Park, D.H.
Brain Res. Mol. Brain Res. 9, 277-283, 1991
A; Filtle: Molecular cloning and characterization of cDNA encoding tryptophan hydroxylase
A; Reference number: A60034; MUID:91245924; PMID:1645430
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A;Residues: 167-261 - DA2>
A;Cross-references: GB:M28000; NID:g207432; PIDN:AAA42262.1; PID:g207433
C;Comment: This enzyme has different physical properties in pineal gland and in dorsal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tryptophan 5-monooxygenase (EC 1.14.16.4) - rat

N.Alternate names: tryptophan 5-hydroxylase
C,Alternate names: tryptophan 5-hydroxylase
C,Species: Rattus norvegicus (Norway rat)
C,Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 03-Mar-2000
C,Accession: JL0034; A60034; A24367
R;Darmon, M.C.; Guibert, B.; Leviel, V.; Ehret, M.; Maitre, M.; Mallet, J.
A; Neurochem. 51, 312-316, 1988
A; Title: Sequence of two mRNAs encoding active rat tryptophan hydroxylase.
A; Reference number: JL0034; MUID:88244702; PMID:337941
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----YWFIVEFGLCRONGIVKAYGAGL 386
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12.0%; Score 227.5; DB 1; Length 444;
Best Local Similarity 27.4%; Pred. No. 1.2e-10;
Matches 63; Conservative 43; Mismatches 97; Indels 27; Gaps
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A; Status: not compared with conceptual translation

C; Function:

A; Molecule type: mRNA A; Accession: JL0034

279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328 335 LSSISELRHALSGHAKVKPFDPKVACKQECLITSFQDVYFVSESFEDAKE 384 ò

Gaps

à g ò

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tyrosine 3-monooxygenase (EC 1.14.16.2) - rat
NyAlternate names: tyrosine 3-hydroxylase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 03-Mar-2000
C;Accession: A00510; A44714; S03026; IS8264
R;Grima, B; Lamouroux, A.; Blanot, F; Faucon Biguet, N.; Mallet, J.
Proc. Natl. Acad. Sci. U.S.A. 82, 617-621, 1985
Proc. Natl. Acad. Sci. U.S.A. 82, 617-621, 1985
A;Title: Complete coding sequence of rat tyrosine hydroxylase mRNA.
A;Reference number: A00510; MUID:85113249; PMID:2857492
A;Accession: A00510.
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 31-Mar-2000
C;Accession: I51567
A;Molecule type: mRNA
A;Residues: 1-498 <GRI>
A;Cross-references: GB:M10244; NID:g207408; PIDN:AAA42257.1; PID:g207409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-481 cGRE>
A;Residues: 1-481 cGRE>
A;Cross-references: GB:L20679; NID:g450644; PIDN:AAA21306.1; PID:g450645
A;Cross-references: GB:L20679; NID:g450644; PIDN:AAA21306.1; PID:g450645
C;Superfamily: phenylalanine 4-monoxygenase
C;Keywords: biopterin; iron; metallogrotein; oxidoreductase
C;Keywords: biopterin; iron; metallogrotein; oxidoreductase
C;Keywords: biopterin; iron; metallogrotein; oxidoreductase
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R;Green, C.B.; Besharse, J.C.
J. Neurochem. 62, 2420-2428, 1994
A;Title: Tryptophan hydroxylase expression is regulated A;Reference number: I51567; MUID:94246419; PMID:8189245
A;Accession: I51567
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I51567
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tyrosine 3-monooxygenase (EC 1.14.16.2) - bovine c;Species: Bos primigenius tearrus (cattle) c;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Mar-2000 C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Mar-2000 C;Accession: 145983  
R;D'Wello, S.R.; Weisberg, B.P.; Stachowiak, M.K.; Turzai, L.M.; Gioio, A.E. J. Neurosci. Res. 19, 440-449, 1988 equence of a cDNA clone encoding bovine a A;Title: Isolartion and nucleotide sequence of a cDNA clone encoding bovine a A;Reference number: 145983; MUID:88259287; PMID:2898537 A;Accession: 145983  
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
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Nucleic Acids Res. 15, 2363-2384, 1987
A;Title: Identification and cell type specificity of the tyrosine hydroxylase gene
A;Reference number: I58264; MUID:87174758; PMID:2882469
A;Recession: I58264
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-30 RES>
A;Residues: 1-30 RES>
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A;Molecule type: protein
A;Rolecule type: protein
A;Residues: 2-12;16-24;38-47;151-157 <CAM>
A;Residues: 2-12;16-24;38-47;151-157 <CAM>
A;Bonnefoy, E.; Ferrara, P.; Rohrer, H.; Gros, F.; Thibault, J.
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J. Biol. Chem. 261, 10489-10492, 1986
A;Title: Identification of four phosphorylation sites in the N-terminal region of tyr
A;Reference number: A44714; MUID:86278113; PMID:2874140
A;Accession: A44714
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A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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A, Status: translation not shown
A, Molecule type: DNA
A, Residues: 35-61 < ICH2>
    JE0014
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A; Molecule type: mRNA
A; Gross-references: GB:M17589; NID:9339680; PIDN:AAA61179.1; PID:9339681
B; Le Bourdelles, B.; Boularand, S.; Boni, C.; Horellou, P.; Dumas, S.; Grima, B.; Mallet
J. Neurochem. 50, 988-991, 1988
A; Title: Analysis of the 5' region of the human tyrosine hydroxylase gene: combinatorial
A; Reference number: A60201; MUD:88117543; PMID:2892893
A; Accession: A60201
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-65 < LBB:NA4790; NID:9556223; PIDN:AAA61174.1; PID:9556224
B; Kobayashi, K.; Kaneda, N.; Ichinose, H.; Kishi, F.; Nakazawa, A.; Kurosawa, Y.; Fujita
J; Biochem: 103, 907-912, 1988
A; Title: Structure of the human tyrosine hydroxylase gene: alternative splicing from a shareference number: JE0012; MUD:89008200; PMID:2902075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine 3-monooxygenase (EC 1.14.16.2), splice form 4 - human
NiAlternate names: Vyrosine 3-hydroxylase
NiContains: tyrosine 3-monooxygenase, splice form 1; tyrosine 3-monooxygenase, splice for C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1989 #text_change 16-Jun-2000
C;Dates: 31-Mar-1989 #text_change 16-Jun-2000
C;Datesibn: A30002; A26825; A60201; US0012; US0013; US0014; A27791; B27791; PNQ
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A;Residues: 1-528 «NAG1»
A;Cross-teferences GB:M17589; NID:g339680; PIDN:AAA61179.1; PID:g339681
R;Kaneda, N.; Kobayashi, K.; Ichinose, H.; Kishi, F.; Nakazawa, A.; Kurosawa, Y.; Fujita
Biochem. Biophys. Res. Commun. 146, 971-975, 1987
A;Title: Isolation of a novel cDNA clone for human tyrosine hydroxylase: alternative RNA
A;Reference number: A90136; MUID:87298614; PMID:2887169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;Molecule type: DNA
.;Rosidues: 1-30,62-135 <KOB1>
.;Cross-references: GB:D00269; NID:g220099; PIDN:BAA25094.1; PID:g2951764
.;Experimental source: splice form 1
                                                                                                                                                                                                                                                                                                                     2
A;Residues: 1-491 <DXM>
A;Cross-references: GB:M36794; NID:g163750; PIDN:AAA30779.1; PID:g163751
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: biopterin; iron; metalloprotein; monooxygenase; oxidoreductase
F;324,329,369/Binding site: iron (His, His, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 PAAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPECCHELLGHVPMLADRTFAQFS 342
                                                                                                                                                                                                                                                                                                                                                                                         107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 QDIG------LASLGVSDEEIEKLST-----LYWFTVEFGLCKQNGEVKAYGAGL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTSKLE 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387 LSSYGELLHSLSEEPEIRAFDPDAAAVQPYQDQTYQPVYFVSESFSDAKDKLRSYASRIQ 446
                                                                                                                                                                                                                                11.7%; Score 221.5; DB 2; Length 491;
ilarity 27.1%; Pred. NO. 4.3e-10;
Conservative 42; Mismatches 102; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              226 WKEVYSTLRGLYPTHACR---BHLEAFELLERFCGYREDRIPQLEDVSRFLKERTGFQLR 282
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A;Residues: 1-34,62-135 <KOB2>
A;Cross-references: GB:D00269; NID:g220099; PIDN:BAA25097.1; PID:g2951767
A;Experimental source: splice form 2
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submitted to GenBank, December 1987
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Matches 65; Conserve
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A, Modecule type: DNA
A, Residues: 1-30,35-135 < KOB3>
A, Residues: 1-30,35-135 < KOB3>
A, Residues: 1-30,35-135 < KOB3>
A, Residues: 1-30,35-135 < KOB3>
A, Residues: 1-30,35-135 < KOB3>
A, Residues: 1-30,35-135 < KOB3>
A, Residues: 1-30,35-135 < KOB3>
A, Residues: 1-30,35-135 < KOB3>
A, Note: this splice form is produced by an alternative donor site within exon 1
R, Grima, B, L, Lamourcoux, A, Boni, C, Julien, J.F.; Javoy-Agid, F.; Mallet, J.
A, Rightla: A single human gene encoding multiple tyrosine hydroxylases with different predi A, Reference number: A93393; MUID:8713064; PMID:2882428
A, Residues: 1-30,62-528 < GRII>
A, Residues: 1-30,62-528 < GRII>
A, Roberimental source: splice form 1
A, Note: this splice form is produced by an alternative donor site within exon 1
A, Residues: 1-34,62-528 < GRIZ>
A, Residues: 1-34,62-528 < GRIZ>
A, Residues: 1-34,62-528 < GRIZ>
A, Residues: 1-34,62-528 < GRIZ>
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A, Residues: 1-34,62-528 < GRIZ>
A, Residues: 1-34,62-528 < GRIZ>
A, Residue
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Ayrcesosion: Cariston and characterization of the human tyrosine hydroxylase gene: identific Ayrcesosion: 152396
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A;Scatus: pre-infinary; translated from GB/EMBL/DDBJ
A;Scatus: pre-infinary;
A;Residues: 1-30,35-528 «KOB4>
A;Cross-references: EMBL:Y00414; NID:g37126; PIDN:CAA68472.1; PID:g37127
A;Cross-references: EMBL:Y00414; NID:g37126; PIDN:CAA68472.1; PID:g37127
A;Cross-references: EMBL:Y00414; NID:g37126; PIDN:CAA68472.1; PID:g37127
A;Cross-references: M.; M.; Martin, B.M.; Weller, M.; O'Malley, K.L.; LaMarca, M.E.; McAll
J; Biol. Chem. 263, 7466-7410, 1988
A;Title: Expression of human tyrosine hydroxylase cDNA in invertebrate cells using a back
A;Reference number: 155282; MUID:88213428; PMID:2896667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: 30,35-528 <GRI3>
A;Cross-references: GB:X05290; NID:g32501
A;Experimental source: splice form 3
A;Note: this isozyme is produced by use of an alternative donor site within exon 1
R;Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
Biochem. Biophys. Res. Commun. 195, 158-165, 1993
A;Title: Increased heterogeneity of tyrosine hydroxylase in humans.
A;Reference number: PN0575, MUID:93371398; PMID:7689834
A;Status: translation not shown
1;Molecule type: DNA
;Residues: 19-30 <ICH1>
;Residues: 19-30 <ICH1>
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-30,62-64 <GINI>
A;Cross-references: GB:M20911; NID:g339636; PIDN:AAA61167.1; PID:g339637
A;Accession: 170056
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tyrosine 3-monooxygenase (EC 1.14.16.2), major splice form - fruit fly (Drosophi)
N;Alternate names: tyrosine 3-mydroxylase, type 1; tyrosine 3-hydroxylase, type 1;
N;Contains: tyrosine 3-monoxygenase, minor splice form
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: A55369; B55489; JN0010
R;Birman, S.; Morgan, B.; Anzivino, M.; Hirsh, J.
J. Biol. Chem. 269, 26559-26567, 1994
A;Title: A novel and major isoform of tyrosine hydroxylase in Drosophila is gene: A;Reference number: A55369; MUID:95014502; PMID:7929381
A;Accession: A55369; MUID:95014502; PMID:7929381
A;Cossion: A55369; MUID:95014502; PMID:7929381
A;Coss-references: GB:U14395; NID:9595799; PIDN:AAA62876.1; PID:9595800
A;Note: authors translated the codon CGC for residue 219 as Ser, and TCC for residues: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
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Best Local S
Matches 65
Residues: 1-61,133-579 <BIR2>
Cross-references: GB:U14395;
Note: authors translated the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGLLSSYGELLHCLSEEPEIRAFDPEAAAVQPYQDQTYQSVYFVSESFSDAKDKLRSYAS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVLISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLRPVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABEIATWKEVYTTLKGLYATHACGEHLEAFALLERFSGYREDNIPOLEDVSRFLKERTGF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSRFSLWKS-----YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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  NID:g595799; PIDN:AAAA62877.1; PID:g595801 codon CGC for residue 219 as Ser, and TCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -WFTVEFGLCKQNGEVKAYG
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3-hydroxylase, type II
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A;Gene: FlyBase:ple
A;Gene: FlyBase:ple
A;Gross-references: FlyBase:FBgn0005626
A;Map position: 31 65B
A;Map position: 31 65B
A;Introns: 23/3; 61/1; 101/1; 132/1; 405/2; 447/3
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: alternative splicing; biopterin; iron; metalloprotein;
F;409,414,454/Binding site: iron (His, His, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Neckameyer, W.S.; Quinn, W.G.
Neuron 2, 1167-1175, 1989
A;Title: Isolation and characterization of the gene for drosophila tyrosine hydroxyl
A;Reference number: JN0010, MUID:90166583; PMID:2483109
A;Accession: JN0010
A;Accession: JN0010
A;Molecule type: mRNA
A;Restdues: 1-61,133-579 <NEC>
A;Cross-references: GB:X76209; NID:g433469; PIDN:CAA53802.1; PID:g433470
C;Genetis:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 DYLEAFGLLSD---FLDH-----QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFP 179
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                                                                  SKLEWMLDQGLLESIPLYN 349
                                                                                                                                                                                                                                                                                EEIEKLST-----VYWFTVEFGLCKEHGQIKAYGAGLLSSYGELLHAISDKCEHRAFE 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKK 239
DKLETLVHQMNTEILHLTN 570
                                                                                                                                    PASTAVQPYQDQEYQPIYYVAESFEDAKDKFRRWVSTMSRPFEVRFN-PHTERVEVLDSV
                                                                                                                                                                                                          --NVRVLPLE----ELVELT 330
                                                                                                                                                                                                                                                                                                                                                  QRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFID-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 11.6%; Score 219; DB 1; Similarity 28.6%; Pred. No. 8.4e-10; 74; Conservative 37; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 579
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                                                                                                                                                                                                                                                                                                                                                      291
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where
phenylalanine 4-monooxygenase (EC 1.14.16.1) - rat
N;Alternate names: phenylalanine 4-hydroxylase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec.1996 #sequence revision 19-Oct-1995 #text\_change 03-Mar-2000
C;Accession: A25321; A00509; Ā14970
R;Dahl, H.H.M.; Mercer, J.F.B.
J. Biol. Chem. 261, 4148-4153, 1986
A;Title: Isolation and sequence of a cDNA clone which contains the complete coding r.
A;Reference number: A25321; MUID:86140234; PMID:2869038
A;Accession: A25321
A;Molecule type: mRNA
A;Residues: 1-453 < CDAH;
A;Cross-references: GB:M12337; NID:g206120; PIDN:AAA41843.1; PID:g206121
A;Molecule type: mRNA
A;Residues: KJ-H.; Beattie, W.; James, R.J.; Cotton, R.C.H.; Morgan, F.J.; Woo, S.L.C
Biochemistry 23, 5671-5675, 1984
A;Reference number: A00509; MUID:85122617; PMID:6098294
A;Accession: A00509
A;Molecule type: mRNA
A;Residues: 208-453 <ROB;
A;Cross-references: GB:K02599; NID:g205961; PIDN:AAA41794.1; PID:g205962
R;Wretborn, M.; Humble, E.; Ragnarsson, U.; Engstrom, L.
Biochem. Biophys. Res. Commun. 93, 403-408, 1980
A;Accession: A14970
A;Molecule type: protein
A;Residues: 12-16; B;/18-19, ZZ: <MRE>
C.Complay: homodiver: homodive

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Query Match
11.2%
Best Local Similarity 29.9%
Matches 61; Conservative
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A; Description: catalyzes the 4'-hydroxylation of phenylalanine to tyrosine by tetrahydrd A; Pathway: tyrosine biosynthesis; phenylalanine catabolism c; Superfamily: phenylalanine 4-monooxygenase C; Keywords: biopterin; homodimer; iron; metalloprotein; monooxygenase; oxidoreductase; p; F;16/Painding site: phosphate (Ser) (covalent) (by calmodilin-dependent kinase) #status p; P;285,290,330/Painding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict P;285,290,330/Painding site: iron (His, His, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phenylalanine 4-monooxygenase (EC 1.14.16.1) - human
NyAlternate names: phenylalanine 4-hydroxylase
NyAlternate names: phenylalanine 4-hydroxylase
C;Decies: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 21-Jul-2000
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 21-Jul-2000
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 21-Jul-2000
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change
B;Ochemistry 24, 556-561, 1985
A;Title: Nucleotide sequence of a full-length complementary DNA clone and amino acid seq
A;Reference number: A00508; MUID:85199778; PMID:2986678
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A; Residues: 131-144 < COT>
A; Residues: 131-144 < COT>
B; Residues: 131-144 < COT>
B; Rang, Y: Trefz, F.K.; Lichter-Konecki, U.; Moo, S.L.
Biochemistry 31, 8363-8368, 1992
A; Title: Structural characterization of the 5' regions of the human phenylalanine hydrox A; Recence number: 152416; MUID: 92399453; PMID: 1326329
A; Accession: 152416
A; Status: preliminary; translated from GB/BML/DDBJ
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A, Cross-references: GB.844225; NID:9255493
R;Abadie, V.; Jaruzelska, J.; Lyonnet, S.; Millasseau, P.; Berthelon, M.; Rey, F.; Munni Hum. Mol. Genet. 2, 31-34, 1993
A, Title: Illegitimate transcription of the phenylalanine hydroxylase gene in lymphocytes A, Reference number: 154346; MUID:93258345; PMID:8098245
A, Accession: 154346
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A) Cross-references: GB:KO3020, NID:g189936; PIDN:AAA60082.1; PID:g189937
A) Cross-references: GB:KO3020, NID:g189936; PIDN:AAA60082.1; PID:g189937
B) Cocton, R.G.H.; McAdam, W.; Jennings, I.; Morgan, F.J.
Biochem. J. 255, 193-196, 1988
A) Title: A monoclonal antibody to aromatic amino acid hydroxylases. Identification of A); Reference number: S02687; WUID:89061656; PMID:2461704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 SLGAPDEYIEKLAT-----IYWFIVEFGLCKEGDSIKAYGAGLLSSFGELQYCLSDKP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 FSLWKSYCPRFFLDYLEAFGLLSDFLDH-QAVIKFFELETHFSYYPVSGFVAPHQYLSLL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 QDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 ALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNV 293
                                                                                                                                                                                                                                                                                                                                                                                                                            28; Gaps
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A;Molecule type: mRNA
A;Residues: 381-389, 'G', 391-405 <ABA>
A;Cross-references: GB:S61296; NID:g300410; PIDN:AAD13926.1; PID:g4261626
A;Experimental source: lymphocytes, mutant form
R;Kowlessur, D.; Gitron, B.A.; Kaufman, S.
Arch. Biochem. Biophys: 333, 85-95, 1996
                                                                                                                                                                                                                                                                                                                                 Ouery Match
11.3%; Score 214; DB 1; Length 453;
Best Local Similarity 28.4%; Pred. No. 1.56-09;
Marches 61; Conservative 37; Mismatches 89; Indels
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A; Residues: 1-20 < KON>
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A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DMA
A,Rote: mutant sequence found in patients with phenylketonuria
A,Gross-references: GB.862392; NID:9238240; PIDN:AAB20205.1; PID:9238241
A,Genetics: mutant sequence found in patients with phenylketonuria
C,Genetics: DB:119470; OMIM:261600
A,Genetics: Lidy GB:119470; OMIM:261600
A,Map position: 12q24.1-12q24.1
A,Note: a defect in this gene can cause phenylketonuria
C,Genetics: homodimer
C,Genetics: homodimer
C,Function:
A,Description: catalyzes the 4'-hydroxylation of phenylalanine to tyrosine by tetrahydroh
A,Pescription: catalyzes the 4'-hydroxylation of phenylalanine catabolism
C,Superfamily: phenylalanine 4 monooxygenase
C,Keywords: biopterin; homodimer; iron; metalloprotein; monooxygenase; oxidoreductase; p?15/Binding site: phosphate (Ser) (Govalent) (by calmodulin-dependent kinase) #status predicte
F;285,290,330/Binding site: iron (His, His, Glu) #status predicted
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phenylalanine 4-monooxygenase (EC 1.14.16.1) - mouse
cispecias: Mus musculus (house mouse)
Cispecias: Mus musculus (house mouse)
Cispecias: Mus musculus (house mouse)
Ciaccesion: S1578; 808678
Rieddey, F.D.; Gremett, H.E.; Dunbar, B.S.; Woo, S.L.C.
Biochem. J. 267, 399-406, 1990
A;Title: Mouse phenylalanine hydroxylase. Homology and divergence from human phenylalanine
A;Recence number: S15758; MUID:90241147; PMID:2334400
A;Accession: S15758
A;Accession: S15758
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-453 <-LED>
A;Cross-references: EMBL:X51942; NID:953683; PIDN:CAA36205.1; PID:953684
C;Superfanily: phenylalanine d-monooxygenase
C;Keywords: biopterin; iron; metallopyrotesin, oxidoreductase; phosphoprotein
F;285,290,330/Binding site: iron (His, His, Glu) #status predicted
A;Title: Recombinant human phenylalanine hydroxylase: novel regulatory and structural pro A;Reference number: S74142; MUID:96400381; PMID:8806757
A;Accession: S74142
A;Molecule type: protein
A;Residues: 2-21 eXGWN
A;Residues: 2-21 eXGWN
R;Eigel, A; Dworniczak, B.; Kalaydjieva, L.; Horst, J.
Hum. Genet. 87, 739-741, 1991
A;Title: A frameshiff mutation in exon 2 of the phenylalanine hydroxylase gene linked to A;Reference number: 154257; MUID:92039642; PMID:1682235
A;Accession: 154257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 RLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFA 300
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tyrosine 3-monooxygenase (EC 1.14.16.2) - bovine
tyrosine 3-monooxygenase (EC 1.14.16.2) - bovine
G;Apecies: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 31-Mar-2000
C;Accession: JL0039; A27687
R;Saadat S; Stehle, A.D.; Lamouroux, A.; Mallet, J.; Thoenen, H.
J. Neurochem. 51, 572-578, 1988
A;Title: Predicted amino acid sequence of bovine tyrosine hydroxylase and its similarity
A;Reference number: JL0039; MUID:88274405; PMID:2899135
A;Accession: JL0039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 153-158,160,162-169 <ABA>
A;Residues: 153-158,160,162-169 <ABA>
A;Residues: 153-158,160,162-169 <ABA>
A;Residues: 153-158,160,162-169 <ABA>
A;Residues: 153-158,160,162-169 <ABA>
C;Comment: This protein is the rate-limiting enzyme in the biosynthesis of catecholamine C;Superfamily: phenylalanine 4-monoxygenase
C;Superfamily: phenylalanine 4-monoxygenase #status predicted <AMI>
C;Keywords: biopterin; iron; metalloprotein; oxidoreducted <AMI>
F;24-49/Product: tyrosine 3-monoxygenase #status predicted kinase) #status predicted
F;8/Binding site: phosphate (Ser) (covalent) (by unidentified kinase) #status predicted
F;19/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
F;324,329,369/Binding site: tron (His, His, Glu) #status predicted
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A;Experimental source: adrenal medulla
R;Abate, C.; Smith, J.A.; Joh, T.H.
Biochem. Biophys. Res. Commun. 151, 1446-1453, 1988
A;Title: Characterization of the catalytic domain of bovine adrenal tyrosine hydroxylase
A;Reference number: A27687; MUID:88183482; PMID:2895648
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phenylalanine 4-monooxygenase
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A; Residues: 1-491 < SAA >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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Best Local
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                                                                                                                                                          387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                   279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTSKLE 334
                                                                                                                                                                                                                                                                                                                                                 219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 WKEVYSTLRGLYPTHACR---EHLEAFELLERFCGYREDRIPQLEDVSRFLKERTGFQLR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104
                                                                                                                                                                                                                                                                                    QDIG--
                                                                                                                                                                                                                                                                                                                                                                                                             PVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLAHGPMLADRTFAQFS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSSFGELQYCLSDKPKLLPLELEK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEIG------LASLGAPDEYİEKLAT-----IYWFTVEFGLCKEGDSIKAYGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFAQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSPQELGHAFIDNVRVLPLELDQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNLW---YRLLSSRFSLWKSYCPRFFLDYLEAF-GLLSDFLDH-QAVIKFFELETHFSYY
                                                                                                                                                          LSSYGELLHSLSEEPEIRAFDPDAAAVQPYQDQTYQPVYFVSESFSDAKDKLRSYASRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                       LASLGVSDEEIEKLST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.2%;
26.7%;
   (EC 1.14.16.1) - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s; Score 211.5; DB 2;pred. No. 2.7e-09;41; Mismatches 104;
                                                                                                                                                                                                                                                                                       ----LYWFTVEFGLCKONGEVNAYGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 31;
                                                                                                                                                                                                                                                                                       386
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294

RKTWGIIYRKLR---ELHKKHACKQFLDNFELLERHCGYSENNIPQLEDICKFLKAKTGF 350

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RESULT 22
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                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-575 <TAI>
A;Cross-references: EMBL:U21308; PIDN:AAB93319.1; GSPDB:GN00020; CESP:ZK1290.2
A;Experimental source: strain Bristol N2; clone ZK1290
                                                                                                                                                                                                                                                                                                                                                                              submitted to the RMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid ZK1290
A;Reference number: Z21535
A;Accession: T34509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein ZK1290.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T34509
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C;Rupwords: biopterin; iron; metalloprotein; monooxygenase; oxidoreductase; phenylke:
F;285,290,330/Binding site: iron (His, His, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 93, 213-219, 1990
A;Title: Sequence and expression of the Drosophila phenylalanine hydroxylase mRNA.
A;Reference number: JQ0766; MUID:91033030; PMID:2121612
A;Accession: JQ0766
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A; Residues: 1-453 < MOR>
                                                                                                                                                         A; Introns: 49/3;
                                                                                                                                                                                                          A;Gene: CESP:ZK1290.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: FlyBase: FBgn0005770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: FlyBase:Tph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                      Matches
                                                                                Query Match
Best Local :
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                                                                                                                                                                                   position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398
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  104 RNLW---YRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WGIIFRNLTKLYKTHACR---EYNHVFPLLVDNCGFREDNIPQLEDVSNFLRDCTGFTLR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTIKFANSIPRPFGVRYN--AYTQSVEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGL--LESIP----LYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEIG------LASIGAPDDYIEKIST-----IFWFTVEYGLLAKEGELKAYGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVAGLLSSRDFLAGLAFRVFHCTQYIRHPSKPMYTPEPDVCHELMGHVPLFADPSFAQFS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSSYGELEYCLTDKPQLKDFE-----PESTGV---TKYPITQFQPLYYVADSFETAKE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISSPOSLGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                   70;
                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Requena, J.M.; Jimenez-Ruiz, A.; Lopez, M.C.; Ugarte, M.; Alonso,
                                                                                                                                                      72/2; 105/3; 223/1; 257/3; 280/2; 310/2; 346/1; 391/2; 433/3; 523/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:M32802; NID:g158035; PIDN:AAA69513.1; PID:g158036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.0%;
                                                                           10.9%; Score 206.5; DB 2
25.2%; Pred. No. 8.5e-09;
                                                   47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 207; DB 2; Length 453 Pred. No. 5.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 109;
                                                      Mismatches 116;
                                                                                                  DB 2;
                                                                                                  Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                      Indels
                                                      45;
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                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347
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| OY 156 SYXPVSGFVAPHQYLSLLQDRXFPIASVMRTLDKDNFSLTPDLIHDLGHVPWLLHPSFS 215   | Biochem. Biophys. Res. Commun. 225, 238-242, 1996 A.Title: Structure of the phenylalanine hydroxylase gene in Drosophila melanogaster and e A; Reference number: JC4888; MUID:96332435; PMID:8769124 A; Accession: JC4888  |
|--|--|
| 216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLI   | A.potecule type: makes A.potecule (1912 - 1912 - 1912 - 1912 - 1912 - 1913 - 19 |
| Cy 266EMBGRANGARULISCOBLEHAFIONURULDIBLODIRLIPPRYSTPOETLESIRH 322  Db 455 ENGSNHERFKVYGAGLLSSAGELQHAVEGSATIIRFDPDRVVEQECLITTFÇSAYFYTRN 514  Cy 323 PDELVELTSKLEWMLDQGLLESIPLYNOEKYLSGFEVL 360  Cy 12 PDELVELTSKLEWMLDQGLLESIPLYNOEKYLSGFEVL 360  Ch 516 EPERACO - YI DMFTWANDDBFTUNN | C;Genetics. A;Gene: Pah A;Introns: 10/3; 235/1; 322/3; 399/2 A;Introns: 10/3; 235/1; 322/3; 399/2 A;Introns: 10/3; 235/1; 322/3; 399/2 C;Superfamily: phenylalamine 4-monooxygenase C;Keywords: biopterin; iron; metalloprotein; oxidoreductase F;284,289,329/Binding site: iron (His, His, Glu) #status predicted   |
| SULT 23  | Query Match<br>Best Local Similarity 27.1%; Pred. No. 6.38-08;<br>Matches 73; Conservative 39; Mismatches 111; Indels 46; Gaps 10;   |
| tryptophan 5-monooxygenase (EC 1.14.16.4) - fruit fly (Drosophila sp.) N,Alternate names: tryptophan hydroxylase C,Species: Drosophila sp.   | QY 107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYY 158   :  |
| 0008-1M41-   | QY 159 PVSGFVAEHQYLSLLQDRYFPIASYWRTLDKDNFSLTPDLIHDLGHVPWLLHPSFSEFF 218   |
| #/iller A Bingle locus encodes both phenylaranine nydroxylase and tryptophan nydroxylas A;Reference number: A42271; MUID:92156168; PMID:1371286 A;Accession: A42271 A;Molecule type: mRNA  | QY 219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278  1   |
| Ayrestudus: 1-455 cNEC> Ayrestudus: 1-455 cNEC> Ayrestudus: 1-455 cNEC> CGenetics: equence extracted from NCBI backbone (NCBIN:82902, NCBIP:82903)   | Cy 279 ISSEQELGHAFIDNVRVLELELDQIIRLPENTSTPOETLFSIRHFDELVELTSKLEMMLD 338  |
| A,Cross-references: FlyBase:FBgn0005770<br>C,Superfamily: PhenyLalmine 4-monoxoxygenase<br>C;Keywords: blopterin; iron; metalloprotein; monoxygenase; oxidoreductase; phosphoprote<br>F;284,289,329/Binding site: iron (His, His, Glu) #status predicted                             | 339 QGL-LESIPLYNQEKYLSGFEVL 360 ::   |
| Query Match 10.4%; Score 197; DB 1; Length 453;<br>Best Local Similarity 27.5%; Pred. No. 3.66-08;<br>Matches 74; Conservative 38; Mismatches 111; Indels 46; Gaps 10;   | RESULT 25<br>C87449  |
| QY 107 WYRLLSSRFSLWKSYCPRFFLDXLEAFGLLSDFLDHQAVIKFFELETHFSYY 158  | phenylalanine-4-nydzoxylase (imported) - Caulobacter crescentus<br>C;Species Caulobacter crescentus<br>C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001<br>C;Accession: C87449  |
| QY 159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTHDLLGHVPWLLHPSFSEFF 218  | <pre>Kinlerman, W.C.; Fedloaryum, T.V.; Fadlsen, 1.1.; Nelson, A.E.; Elsen, U.; Hethelberg, U.; B.; Laud, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001</pre>  |
| QY 219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIALVRCFWFTVESGLIENHEGRKAYGAVL 278  | AjTile: Compider Genome Sequence of Caulobacter crescentus. AjReference number: A87249; MUID:21173698; PMID:11259647 AjRecesion: C87449 AjStatus: preliminary  |
| 279 ISSPQELGHAPIDNVRVLPLELDQIIRLPF<br>   | A.Mouseule Lype; Juna<br>A.Reaidues: 1-294 «STO»<br>A.Cross-references: GB:AE005673; NID:g13423011; PIDN:AAK23591.1; GSPDB:GN00148<br>C.Genetics:<br>A.Gene: CC1612  |
| QY 339 QGLESIPLYNQEKYLSGFEVL 360<br>: :  | Query Match<br>Best Local Similarity 24.1%; Pred. No. 8.2e-08;<br>Matches 63; Conservative 43; Mismatches 108; Indels 47; Gaps 6;  |
| RESULT 24<br>JC4888<br>Phenylalanine 4-monooxygenase (EC 1.14.16.1) - fruit fly (Drosophila melanogaster)<br>N.Alternate names: phenylalaninase. phenylalanine 4-hydroxylase   | OY 118 WKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFBLETHFSYYP  |
| C;Species: Drosophila melanogaster<br>C;Date: 10-Sep-1996 #sequence_revision 18-Oct-1996 #text_change 20-Jun-2000<br>C;Accession: JG488<br>R;Ruiz-Vazquez, P.; Moulard, M.; Silva, F.J.  | Qy 160VSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSF 214  |

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phenylalanine 4-monooxygenase (EC 1.14.16.1) K08F8.4 (similarity) - Caenorhabditis elega C,Species: Caenorhabditis elegans C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 19-May-2000 C,Accession: T23494
R;Smye, R.
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Mosldwes: 1-409 AHEN
A;Cross-references: EMBL:U80836; PIDN:AAB37888.1; GSPDB:GN00020; CESP:B0432.5
A;Experimental source: strain Bristol N2; clone B0432
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A;Introns: 117/2; 183/1; 273/2; 302/3; 369/3
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: biopterin; oxidoreductase
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submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid B0432.
A;Reference number: Z20038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tyrosine 3-monooxygenase (EC 1.14.16.2) B0432.5 [similarity] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 19-May-2000 C;Accession: T25453
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to the EMBL Data Library,
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                                                                                                                                                                                                                                                                                                        GAVLISSPOELGHAFID 291
                                                                                                                                                                                                                                                                                                                                                             AQMSQDIG-----LMSLGASDEHIEKLST-----VYWFIVEFGLCKEDGKLKÄI 290
                                                                                                                                                                                                                                                                                                                                                                                                         SEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEEEHATWKAVYEKLGDLHLSHTCAVYRQNLKILQEEKVLTADRIPQIRDVNKFLQKKTG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LE----AFGLLSDF-LDHQAVI-----KFFELETH 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------PTTDPRHPGHGDVAYIARRKFLND---QALEFKFGDEIGY-----VDY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQA-LARH------KCISILE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGAIYERLASVSDIGVAEIVP 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAVLISSPQELGHAFID-NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELT--- 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADY------MOAYGEGGRRALGL-GRLANLARLYWYTVEFGLMNTPAGLRIY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELRPCSGLLSARDFLASLAFRVFQTTTYLRHHKSPHHSPEPDLIHELLGHVPMFSDPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESYYPVSGEVAPHQYLSLLQDRYFFIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSF 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLIHSAELLTQNHVAL----TKFSIFAKKLSDEKNQSQIWFPRHISELDQCSKCITKYE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGIVSSRTESIFALDDESPNRIGEDLERVMRTLYRIDDEQQVYEVIDSIQTLQEVTLRD 248
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  October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 114; Indels 85; Gaps
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A;Reference number: Z19747

A;Accession: T23494

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-457 <WIL>
A;Cross-references: EMBL:Z66497; DTDN.Cananara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease resistance-like protein - Arabidopsis thaliana
N;Alternate names: protein F26013.200
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T45787
C;Accession: T45787
R;Delseny, M; Berger, C; Cooke, R; Grellet, F; Laudie, M; Mewes, H;W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:KO8F8.4
A;Map position: 2
A;Introns: 12/3; 51/3; 116/1; 170/2; 236/1; 281/2; 323/3; 400/2
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: biopterin; oxidoreductase
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A;Experimental source: clone K08F8
C;Genetics:
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A; Residues: 1-1253 < DEL>
A; Cross-references: EMBL: AL133452
A; Experimental source: cultivar Cc
C; Genetics:
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A; Introns: 138/2;
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
  198
                                          533
                                                                                        154
                                                                                                                                                                                   116 SLWKSYCPRFFLDYLEAFG---LLSDFLDHQAV-----IKFFEL-----ET 153
                                                                                                                                                                                                                                421 IHLL------EGCGFFPRVEINVLVEKCLVSMA-EGRVVMHNLIQSIGRKIINGGKRRS 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 LAESFASAKNKLKSWAATINRPFQIRYNAYTQRVEILDKV 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDL 202
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                                                                                                                                                                                                                                                                             77 VHLLSLSKNQREGCS------TDMAVVSTPFFNRNLWYRLLSS------
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                                                                                                                                     RÍWKPLIIKYFLEDRQVLGSEDIEAIFÍDPSÁLSFDVNPMAFENMYNLRYLKICSSNPGN 532
-LIHDLLGHVPWLLHPSFSEFFINM----
                                                                                        HFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSL------TPD-- 197
                                          HYALHLPKGVKSLPEELRLLHWEHFPLLSLPQDFNTRNLVILNMCYSKLQRLWEGTKELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIEFGICQQDGEKKAYGAGLLSSFGELQYALSDKPEVVDFDPAVCCVTKYPITEYQPKYF 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLE--LDQIIRLPFNTSTPQET 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGHVPWLLHPSFSEFFINMGRLF----TKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGHVPLFADVEFAQFSQEIGLASLGAPDDVIEKLATL--
                                                                                                                                                                                                                                                                                                                           81;
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                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                             5.8%; Score 109.5;
20.3%; Pred. No. 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Columbia;
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  -GRL---
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-FTKVIE----KVQ
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phenylalanine 4-monooxygenase (BC 1.14.16.1) - Chromobacterium violaceum
N.Alternate names: phenylalaninase, phenylalanine 4-hydroxylase
(Species: Chromobacterium violaceum
C,Species: Chromobacterium violaceum
C,Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 31-Mar-2000
C,Accession: A40996 #84096
R,Onishi, A.; Liotta, L.J.; Benkovic, S.J.
J. Biol. Chem. 266, 18454-18459, 1991
A,Fieference number: A40996; MUID:92011593; PMID:1655752
A,Fieference number: A40996; MUID:92011593; PMID:1655752
A,Accession: A40996
A,Molecule type: Drotein
A,Fesidues: 1-296 <AONI
A,Rocession: B40996
A,Molecule type: protein
A,Rocession: A40996
A,Molecule type: protein
A,Fesidues: 1-20 <AONI
A,Fesidues: 1-20 <AONI
A,Fesidues: 1-20 <AONI
A,Fesidues: 1-20 <AONI
A,Fesidues: 1-20 <AONI
A,Fesidues: 1-20 <AONI
A,Fesidues: 1-20 <AONI
A,Fesidues: Strain ATCC 12540
C,Keywords: biopterin; oxidoreductase
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R;Bukreyev, A.A.; Volchkov, V.E.; Blinov, V.M.; Dryga, S.A.; Netesov, S.V. submitted to the BWBL Data Library, January 1994 **
A;Description: Full-length nucleotide sequence of Marburg virus Popp strain: The comparis A;Reference number: 844054
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A;Residues: 1-231 aBNDA
A;Cross-references: EMBL:X68494; NID:g296962; PIDN:CAA48508.1; PID:g296963
A;Experimental source: strain Popp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: genomic RNA
A;Residues: 1-231 -8018.
A;Cross-references: EMBL:229337; NID:g450908; PIDN:CAA82542.1; PID:g450915
A;Experimental source: strain Popp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 FLDYLEAFGLLSDFL-DHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFFIASVM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 FLEGLERLEVDADRVPDFNKLNEKLMAATGWKIVAVPGLIPDDVFFEHLANRRFPVTWWL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Description: The partial nucleotide sequence of Marburg virus genome.
A;Reference number: S32.75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.6%; Score 106.5; DB 2; Length 296; Best Local Similarity 27.3%; Pred. No. 0.4; Matches 27; Conservative 22; Mismatches 49; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: parainfluenza virus RNA-directed RNA polymerase;
Keywords: ATP; nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 REPHQLDYLQEPDVFHDLFGHVPLLINPVFADYLEAYGK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome polyprotein - Marburg virus (strain Popp)
NiAlternate names: structural protein L
NiContains: RNA-directed RNA polymerase (EC 2.7.7.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 RTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGR 223
    : : : | | |
---QQVHIYNQ 1150
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A;Variety: strain Popp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S32776
                                    1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cisuperfamily: Inlact protein; myosin motor domain homology; protein kinase homology cisuperfamily: Inlact protein; myosin motor domain homology; protein kinase homology (cisuperfamily: actin binding; alternative splicing, APP; nucleotide binding; P-loop; phosph F:14-282/Domain: protein kinase homology «KMIN»
F:14-282/Domain: protein kinase homology «KMIN»
F:135-1022/Domain: myosin motor domain homology «MMCT»
F:135-1022/Domain: mucleotide-binding motif A (P-loop)
F:135-132/Region: nucleotide-binding motif A (P-loop)
F:1054-1501/Domain: carboxyl-terminal «CBT»
F:156-1501/Domain: carboxyl-terminal «CBT»
F:45,60.145/Active site: lys, Glu, Asp #status predicted
F:431/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: B29813
R;Montell, C.; Rubin, G.M.
(Cell 52, 757-772, 1988
A;fitle: The Drosophila ninaC locus encodes two photoreceptor cell specific proteins wit A;Reference number: A90898; MUID:88151067; PMID:2449973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .041 -----IKVQSMMRALLARKR-----VKGGKVFKLGKKGPEHHD------VAASKIQKA 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1083 FRGFRDRVRLPPLVNEKSGQLNENTADFIRPFAKKWREKSIFQVLLHYRAARFQDFVNLS 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174K ninaC protein - fruit fly (Drosophila melanogaster)
N/contains: protein kinase (BC 2.7.1.-)
C.Species: Drosophila melanogaster
C.Pate: 31-Dec.1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 FF----LDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 IASVMRTLDKDNFSLTPDLIHDL-----LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 ALPSKKQRIQTLQSNLIAIVRCFWFTVESGLI-----ENHEGRKAYGAVLISSPQEL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 GHAFIDNVRVLPLELDQIIRL-----PFNTSTPQETLFSI-----RHFDELVELT 330
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713 LDNLKVLDLSQCLELEDIQGIPKNIRKLYLGGTAIKELPSLMHLSELVVLDLENCKRLHK 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     943 SFHSDVVQQQMKALGVLDTVIARQ---KGFS----SRLPFDEFLRRYQFLAFDFDE--P 992
                                                                                                                      234 ALPSKKQRIQTL---QSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELG-HAF 289
                                                                                                                                                                                                                                                                             290 IDNVRVLP----LELDQIIRLPFNT-----STPQETLFSIRHFDELVEL---TSKLEWM 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 108.5; DB 1; Length 1501;
22.4%; Pred. No. 2.4;
tive 58; Mismatches 130; Indels 107; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
Residues: 1-1501 -kNNA
(Cross-references: GB:M20230; NID:g157967; PIDN:AAA28721.1; PID:g157968
                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LESIPLYNOEKYLSG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | | : | | : | | 173 LPMGIGNLSSLAVLNLSGCSELEDIQGIPRNLEELYLAG 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: FlyBase: FBgn0002938
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Best Local Similarity 22.4%
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   337 LDQGL-----
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A;Gene: SPDB:SPAC3H8.08c
A;Map position: 1
C;Superfamily: transcrip
F;14-50/Domain: GAL4 zin
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A;Molecule type: DNA
A;Residues: 1-563 <GEN
A;Residues: 1-563 <GEN
A;Residues: 1-563 <GEN
A;Residues: 1-563 <GEN
A;Cross-references: EMBL:Z69086; PIDN:CAA93165.1; GSPDB:GN00066; SPDB:SPAC3H8.08c
A;Experimental source: strain 972h-; cosmid c3H8
C;Genetics:
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A; Accession: T38766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185
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                                                                                                                                                                                                                                                                     377 LILVDIEAKFYDPSNEDIQFRYIFLKMVFWTARVNLYQCFITLDSGILEDEE-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 DKEIIQMLLLRAYATKFRTRIRGVNTDLCRSIHVSTLVTPLF--QVTEKIGKNTSDLWFA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  573 VRNVQTLAEALLA 585
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                                                                                                            430 IİGN---LGESCİQCVRLL---ISQİTIL-----EKRGWLLVALLEIIHALMLAAFCR 476
                                                                                                                                                                                        278 LISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWML 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 ILEFFKNLLFVHLLSLSKNQREGCSTDM-----AVVSTPFFNRNLWYRLLSSRFSLWKS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 TLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                         ---LRCFFNDDISYN---FHLLLGR---LLDCGVSIYKSVHSLTVSKFIDKLESYESQLS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLFSTKIISDLSIFIKDRATAVNQECWDSVFDRSVLGYNPPVRFQSKRVPEQF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAFGL----LSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LC-----EIDGL------ECVLKY---RPPFIQHDTYGRLKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLLPIIAATIQLSDLPDVILNFYNSAGI-----TPLESSRLINLKLNEISEQEYKHLCLP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF-----INMGRLFTKVIEKVQALPSK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTIIQGKLTPQQYCELF----SLQKHWGHPVLYIDVALDKVKKHAQSVKILKPKVMFET 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KQRIQTLQSNLIA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LGQADFSL--NQILDFAEKLEYLA-PSYRNFSFSLKEKELNIGRTFGK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FCVFKFIVAKNHYHSQGSWYKTTMDLHLTPYLRQHIVSNSFPSQAEIYQHLWEWYFVEHE 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYILKIALKLROSLSLFFONSOSLORAYSTPYSYYRIILOKENKEKOALARHKCISILEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                 -----QTLQSNLIAIVRCFW-------FTVESGLIENHEGRKAYGAV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.4%; Score 102; DB 21.1%; Pred. No. 2.2; tive 56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 102;
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                      A;Molecule type: DNA
A,Residues: 1-1157 cBAL>
A,Residues: 1-1157 cBAL>
A,Residues: 1-1157 cBAL>
A,Cross-references: EMBL:Z28307; NID:g486562; PID:g486563; MIPS:YKR082w
A,Cross-references: EMBL:Z28307; NID:g486562; PID:g486563; MIPS:YKR082w
A,Experimental source: Brrain S288C
R;Garcia-Cantalejo, J.; Baladron, V.; Esteban, P.F.; Santos, M.A.; Bou, G.; Remacha
Yeast 10, 231-245, 1994
Yeast 10, 221-245, 1994
A,Title: The complete sequence of an 18,002 bp segment of Saccharomyces cerevisiae
A,Title: The complete sequence of an 18,002 bp segment of Saccharomyces cerevisiae
A,Reference number: S42009; MUID:94262327; PMID:8203164
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR3.
A;Reference number: A81500; MUID:20150255; PMID:10684935
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C;Accession: CB1624
R;Read, T.D.; Brunham, R.C.; Shen. C : Gill o no control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 
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$38160
NUP133 protein - yeast (Saccharomyces cerevisiae)
NUP133 protein - yeast (Saccharomyces cerevisiae)
NJAlternate names: protein YKR082w; protein YKR402
C;Spacies: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 21-Jul-2000
C;Accession: S38160; S42011; S51915; S39130
C;Accession: V.; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garcia-Cantal-
submitted to the Protein Sequence Database, March 1994
A;Reference number: S38158
A;Accession: S38160
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A;Experimental source: strain AR39, HL cells
C;Genetics:
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A; Residues: 1-1050 < REA>
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A; Molecule type: DNA
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 SYTQPISSYFSSRVERLEQISLWHQQIYNSLLEIPK----QVFLDQLTAHISGFKKQPFS 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 RLIHKKPALTHSQLVLHHITNYLKQDLWKNVLFQEQFHLLAVRYNVTSKHTSSLVDKLLA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 VRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 ----VVSTPFFNR-----NLWY-RLLSSRFSLWKSYCPRFFLDYLEA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VMRTLDKDNF-----SLTPDLIHDL-LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQAL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILDDL--HHFVDLLYTSETHSSLFSFFKIAETFNFKHRLA-----RYKPCAAFTVLENMS 305
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22.3%; Pred. No. 5;
7ative 51; Mismatches 116; Indels 104; Gaps
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19;

| Db 233 KYEGSMYQKLENVLRRASNTADDLE/OEVLORKDKADSTRNALAVLOAREK-FLFNL 286  Cy 79 LLSLSKNOREGCSTDWAVVSTPFNRNLWYRLLSSRFSLWKSYCPRFLDYLEAF 133   | RESULT 36 Deposes a campy/lobacter jejuni C;Species campy/lobacter jejuni C;Species campy/lobacter jejuni C;Species campy/lobacter jejuni C;Species campy/lobacter jejuni C;Species campy/lobacter jejuni C;Species campy/lobacter jejuni C;Species campy/lobacter jejuni C;Species campy/lobacter jejuni C;Species campylobacter jejuni C;Species campylobacter jejuni C;Species campylobacter jejuni reveals R;Perkhill, J i, Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C, W.; Quall, M.; Reajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel] Nature 403; 665-668, 2000 Nature 403; 665-668, 2000 Nature 403; 665-668, 2000 Nature 103, 665-668, 2000 Nature 103, 665-668, 2000 Nature 103, 665-668, 2000 Nature 103, 665-668, 2000 Nature 103, 665-668, 2000 Nature 103, 665-668, 2000 Nature 103, 665-668, 2000 Nature 103, 665-668, 2000 Nature 104, 665-668, 2000 Nature 105, 665-668, 2000 Nature 105, 665-668, 2000 Nature 105, 665-668, 2000 Nature 106, 665-668, 2000 Nature 1 | Oy 169 YLSLLODRYFPIASVMRTLDKONFSLTPDLIHDLLGHVPWLLHPSF 214   |
|---|--|---|
| A; Residues: 1-1157 cGAR> A; Cross-references: EMBL:227116; NID:g415899; PIDN:CAA81633.1; PID:g415902 A; Cross-references: EMBL:227116; NID:g415899; PIDN:CAA81633.1; PID:g415902 B; EMBD J. 13, 6062-6075, 1994 A; The control of the | Oy 143 QAVIKFPELETHFSYYPUSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDL 202  | Query Match 5.2%; Score 99; DB 2; Length 924; Best Local Similarity 19.9%; Pred. No. 7.4; Matches 90; Conservative 77; Mismatches 122; Indels 164; Gaps 27; |

-----SEFFINMGRLFTKVIE---KVQALPSKKQRIQTLQSNLIAIVRCFWFTVE 261

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19 KLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFVH 78

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A;Cross-references: GB:U39687; GB:L43967; NID:g1045744; PID:g1045751; TIGR:MG075A;Experimental source: strain G-37
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Science 270, 397-403, 1995
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium
A;Reference number: A64200; MUID:96026346; EMID:7569993
A;Accession: C64208
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                                                                                                                                                                                                                                                                                                                                                                           SLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFT-----KVIEKVQALPSKKQRIQT 244
                                                                                                                                                                                                                                                                                                                                                                                                           IKKVLFESENYKTLRKKYENEGFPGYHWAKFIVPGTFNSAENTFYSAI-----DKT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQTDSLKNLFSV----IGDILSETNVNKITLHAVKNNELLSLVETASTLKIKHL----- 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTIMYARCLEKLCKIASKVLFAPQSAMYEMFK--NQIKFLN 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSLQEANQHHAQFWQN----YAKYLEFNSNYQEAYHAYKKCLSLDSHATYQFDLAYLLMR
                                                                                                                                                                                                                                            ----HAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFD 324
                                                                                                                                                                                                                                                                              VNVNFHIDARLLTAELQNTVFSNPK-----PVIKSPVELSKSLFEVWKTIFENSVNQI
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Pred. No. 9.3;
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                                                                                                           C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; l F,295-458) Domain: cytochrome P450 homology <CYP> F,295-458) Domain: cytochrome P450 homology <CYP> F,436/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                              A; Gene: CYP2L1
C; Superfamily:
                                                                                                                                                                                             A;Accession: S74194
A;Molecule type: protein
A;Residues: 1-10,'X',12-39 <JAN>
C;Genetics:
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A;Experimental source: hepatopancreas
                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-492 < JAM>
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                                                                                                                                                                                                                                                                          Cross-references: EMBL:U44826; NID:g1304739;
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               56 KQALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRF 115
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                                                                Similarity
                                                 Conservative
                                                              5.1%; Score 97;
19.9%; Pred. No.
                                                 56;
                                                 Mismatches 106;
                                                                             DB 1;
                                                                                                                                                                                                                                                                              PIDN: AAB03106.1;
                                                                             Length 492;
                                               Indels 136; Gaps
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PID: g1304740

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A;Introns: 71/1; 165/3; 247/2; 335/2; 356/2; 389/3; 441/3; 497/3; 539/1; 607/3; 636/2 06/1; 1714/3; 1756/2 C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1846 < MUR>
A;Cross-references: EMBL:AF067217; PIDN:AAC17015.1; GSPDB:GN00019; CESP:F56A6.2
A;Cross-references: EMBL:AF067217; PIDN:AAC17015.1; GSPDB:GN00019; CESP:F56A6.2
A;Experimental source: strain Bristol N2; clone F56A6
C;Genetics:
C;Genetics:
A;Gene: CESP:F56A6.2
A;Map position: 1
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 DPKYILKIALKLRQSLSLFFQNSQSLQRAYSTP-----YSYYRIILQKENKEKQALA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGL 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----FVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLG 204
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W.C.; Greenberg, R.M.; Si
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ClSpecies: Chlamydophila pneumoniae, Chlamydia pneumoniae
ClSpecies: Chlamydophila pneumoniae, Chlamydia pneumoniae
ClDate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
ClAccesion: C72103
Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A,Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A,Recession: C72103
A,Recession: C72103
A,Molecule type: DNA
A,Residues: 1-512 <ARN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 5.1%; Score 96.5; DB 2; Length 512; Local Similarity 18.8%; Pred. No. 5.1%; Indels 177; Gaps es 83; Conservative 57; Mismatches 124; Indels 177; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVR- 294
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Best Local Similarity 22.1%; Pred. No. 13;
Marches 77; Conservative 51; Mismatches 117; Indels 104; Gaps
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79 KTALSKFECSDRPDFYTFKLF------113
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| PADVEDEHKAKIAARLSSVGFGSFFGA 249  | Qy 178 FPIASVMRTLDKDNFSLTPDLI-HDLLGH   |
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| FLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRY 177  | Qy 120 SYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYP  |
| B 2; Length 529;<br>1;<br>s 127; Indels 72; Gaps 11;   | N  |
| (Schizosaccharomyces pombe) -1997 #text_change 21-Jan-2000 Rajandream, M.A.; Walsh, S.V. 995 L/DDBJ pide (Spide Sp | RESULT 43 \$62468 grobable membrane transporter - fission yeast (Schi C;Species; Schizosaccharomyces pombe C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 C;Accession: T38579; \$62468 R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajan submitted to the EMBL Data Library, October 1995 A;Reference number; 221745 A;Accession: T38579 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-529 cBA2> A;Reperimental source: strain 972h-; cosmid c2G11 C;Genetics: 1-529 cBA2> A;Experimental source: strain 972h-; cosmid c2G11 C;Genetics: 1-529 cBA2> A;Gene: SPAC2G11.13 A;Map position: 1L |
|  | Qy 328 ELTSKLEWMLDQGLLESIPLY 348   |
| IGDRTLFTGGDEVMASWKLFTEVL 474   | G :  |
| KAYGAVLISSPQELGHAFIDNVR- 294 ::  | 1 K  |
| PSFSEFFINMGRLFTKVIEKVOAL 235   | Qy 186TLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQAL   |
| DRYFPIASVMR 185  | Qy 148FFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMR   |
| RFFLDYLEAFGLLSDFLDHQAVIK 147   | Qy 109RLLSSRFSLWKSYCPRFFLDYLE  |
| DSAKQLQQCINENLNENSVYHIDH 201   | SA   |
| STPYSYYRIILOKENKEKOALARHKCISILE 69   | Qy 20 LROSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQ   |
| DB 2; Length 512;<br>3;<br>8 124; Indels 177; Gaps 22;   | Query Match 5.1%; Score 96.5; DB Best Local Similarity 18.8%; Pred. No. 5.3; Matches 83; Conservative 57; Mismatches 1   |
| NID:94376502; PIDN:AAD18391.1; PID:9437651   | A;Cross-references: GB:AE001609; GB:AE001363; NID:<br>A;Experimental source: strain CWL029<br>C;Genetics:<br>A;Gene: zwf<br>C;Superfamily: glucose-6-phosphate dehydrogenase   |

| RESU<br>T419<br>larg<br>C;Sp<br>A;Va<br>C;Da<br>C;Da<br>C;Ni<br>R;Ni<br>subm<br>A;Re   | g S        | B 8        | 유 성        | B 8  | B 8       | B 8       | Mae Qu                          | RESULT H72041 H72041 C:Sobec C:Sobec C:Jate C:Jate C:Jate R;Kalm Nature A;Titl A;Refe A;Acce A;Acce A;Sobec A;Gene A;Gene   | Å Å        | ß 8   | å<br>Š  |
|--|------------|------------|------------|--|-----------|-----------|---------------------------------|---|------------|---|---|
| RESULT 45 T41933 T41933 Large tesume C;Species: h A;Varlety: g C;Date: 03-D C;Accession: R;Nicholas, submitted to A;Reference  | 293<br>390 | 236<br>355 | 183<br>306 | 135<br>253   | 96<br>197 | 46<br>137 | Query Ma<br>Best Loc<br>Matches | RESULT 44 H72041 H72041 C,Species C,Species C,Accessin R,Kalman, Nature G,A,Title: A,Fitle: A,Feferen A,Accessin A,Scatus: A,Scatus: A,Molecula A,Residues A,Experime C,Geneticc C,Geneticc A,Geneticc  | 320<br>362 | 271<br>303  | 219<br>250  |
| ESULT 45 41933 arge tegument protein - human herpesvirus 7 (strain JI) ;Species: human herpesvirus 7 ;Variety: strain JI ;Variety: strain JI ;Pate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-,Accession: T41933 ;Nicholas, J. ;Nicholas, J. ;Nicholas, J. ;Data Library, December 1995 ;Reference number: Z22022 | 9 9        | ப் ப்      | 0 00       | 35 LLSDFLDHQAVIKFFELETHFSYYPVS-GFVAPHQYLSLLQDRYFPIAS | 9         |           | O L.                            | RESULT 44 H72041 H72041 H72041 H72041 H72041 H72041 H72041 H72041 H72041 C;Species: Chlamydophila pneumoniae (strain CWL029) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May- C;Accession: H72041 R;Kalman, S; MtChell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, Rature Genet. 21, 385-389, 1999 A;Tile: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606; PMID:10192388 A;Accession: H72041 A;Status: preliminary A;Molecule type: DNA A;Cross-references: GB:AE001655; GB:AE001363; NID:g4377039; PIDN:AAD188 A;Ecross-references: GB:AE001655; GB:AE001363; NID:g4377039; PIDN:AAD188 A;Genetics: | e N        | 771 RKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFS | 119 -INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEG |
| :-2000<br>equence  |            | 389        | 354        | 182  | 252       | 196       | aps 1                           | 2000<br>L., G   | 358<br>421 | 319   | 302   |
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probable zinc proteinase [imported] - Arabidopsis thaliana (Gispecias: Arabidopsis thaliana (mouse-ear cress) (Cispecias: Arabidopsis thaliana (mouse-ear cress) (Cispecias: Arabidopsis thaliana (mouse-ear cress) (Cispecias: Arabidopsis thaliana (mouse-ear cress) (Cispecias: Arabidopsis thaliana (Cispecias: Arabidopsis Arabidopsis (Cispecias: Arabidopsis Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: Arabidopsis)) (Cispecias: A
A,Cross-references: GB:Z99122; GB:AL009126; NID:g2636029; PIDN:CAB15644.1; PID:g2636152 A,Experimental source: strain 168
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-970 cSTO>
A, Cross references: GB: AE002093; NID: 92335108; PIDN: AAC02769.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 WYRLLSSRFSLWKSYCPR-----FPLDYLEAF------GLLSDFLDHQAV---IKF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSDNGFELTLLGYNHKLRILLETVVGKIANFEVKPDRFAVIK----ETVTKEYQNYKFRQ 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 FELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRT------LDKDNFSLTPDL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 FTLIEAGKLNPEQDFYSLNPYVEQLMDTIYSSIDKLKTYALSFALDPFLDK----TPDV 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 IHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 TVESGLIENHEGRKAYGAVLISSPQELGHAFID----NVRVLPLELDQIIRLPFNTSTPQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 AREQEILKKEAGRR-----FSPELQFGRLHLEFLQKNDDVIFEBADQF------PP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 HKCISILEFFKNLLFVHL-----LSLSKNQREGCSTDMAVVSTPFFNRNLWYR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 ----TİQEWVQSAPDVHLHLPAPNVFIPTDLSL-KDADDKETVPVLLRKTPF--SRLWYK 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 LLSSRFSLWKSY-----CP----- 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.0%; Score 95; DB 2; Length 970;
21.7%; Pred. No. 17;
tive 48; Mismatches 128; Indels 174; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     93; Indels 81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 WLAFFDSEFSLWQARTPEGSQNMQGLYYGYLSALKKHAPNKPELKSLYQIHSAIAVCLRM 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 DPKYILKIALKIRQSLSEFFQNSQSLQRA-----YSTPYSYYRIILQKENKEKQALAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 NPAIVOKVVDELSPSNFRIFWESÖKFEGOTDKAEPWYNTAYSLEKITSS------
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                                                                                                                                                                                                                                                                                                               Query Match

5.1%; Score 95.5; DB 2; Length 536;
Best Local Similarity 21.8%; Pred. No. 6.8

Matches 57; Conservative 30; Mismatches 93; Indels 81
                                                                                                                                                                A,Gene: ywqB
C,Superfamily: Bacillus subtilis hypothetical protein ywqB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 ETLFSIRHFDELVELTSKLEW 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 EAL--PYTPQWLSEMTAKKDW 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Matches 97; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Map position: 2
C;Superfamily: insulysin
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: E70066
R;Kunst, F: Ogasawara, N: Moszer, I:, Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
R;Kunst, F:, Ogasawara, N:, Moszer, I:, Albertini, B.; Capuano, V:, Carter, N.M.; Chc
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harvood, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hasono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
Y, M.; Ogawara, R.; Odega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Potretelle
Y, M.; Gawara, R.; Odega, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sekiquchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toganon, A.; Tosato, V.; Voshida,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamanoto, K.; Yasumoto, K.; Yata, K.; Yata, K.; Yasumoto, M.; Tamakoshi, R.; Turpstra, P.; Tomptersin, Bacillus subtilis.
A;Afterence number A65580; MUID:98044033; PMID:9384377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1378 FD--LLDNIAHFRFAFDFNHQQNLİLKLKDKFKTLRTDİVFERFFNLDDTFVSSMNVENF 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1555 LTTLKSILSVVKSFWKBIINFDLTSYFQGKAEFTFQNVFPIINLKIFIYIITQAWSVTSD 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1324 NTDNIEKLSTLIKQIDPNRIAGGKQKFQDYLSKILTABTNQQ-----QTRYKEQLKKQY 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1496 TFFQVDSVFNTQLIVDEKG-IPVQFYNVFHNIVFKFFALNYKKIIVPDKVLNLVSTKYKI 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1615 ETQHSF-----GLPLEKFSLLIIANN----PEFLF-------GSLQCPVDLAINS 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1265 ILKWLIVFVKELNTFFVATMSEFGEVIPFDYKHFR-ALEYEINSKYIEIENKIICNBIIE 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.1%; Score 96; DB 2; Length 2059;
Best Local Similarity 20.6%; Pred. No. 37;
Matches 90; Conservative 62; Mismatches 164; Indels 120; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 CPRFFLDYLEAFGLLSDFLDHQAVI------KFFELETHFSYYP-----VSGF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LLQDRYFPI-ASVMRTLDKDNFSL----TP- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------DLIHDLLGHVPWLLHPSFSEFFINMGRL-FTKVI--EKVQALPSKKQRI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 QTLQSNLIAIVRCFW-FTVESGLIENHEGR------KAYGAVLIS----SPQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 ELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEMMLDQGLLE 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 FFKNL--LFVHLLSLSKNQREGCSTD----MAVVSTPFFNRNLWYRLLSSRF--SLWKSY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 ILKIALKLRQSLSLFFQNSQS-LQRAYSTPYSYYRIILQKENKEKQALARHK--CISILE 69
                                                                                                                                                                                                                                                                                                                                                         A;Note: U31
C;Superfamily: varicella-zoster virus 240K tegument protein
                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Modecule type: DNA
A;Rodecule type: DNA
A;Cross-references: BMBL:U43400; PIDN:AAC54693.1
A;Experimental source: strain JI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 SIPLYNQEKYLSGFEV 359
     Accession: T41933
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23;

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A;Molecule type: DNA
A;Residues: 1-133, 'RFV', 136-137, 'PDWS', 142, 'LASLYLTA' <JIM>A;Residues: 1-133, 'RFV', 136-137, 'PDWS', 142, 'LASLYLTA' <JIM>A;Cross-references: EMBL.X59720
R;Rodriguez-Cousino, N.; Lill, R.; Neupert, W.; Court, D.A.
Yeast 11, 581-585, 1995
A;Title: 1dentification and initial characterization of the
A;Reference number: S55867; MUID:95373282; PMID:7645349
A;Accession: S55868
A;Molecule type: DNA
A;Residues: 1-133, 'RFV', 136-137, 'FDWS', 142, 'LASLYLTA' <ROD>
                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X59720; MIPS:YCR080w R;Hengartner, C.J.; Thompson, C.M.; Zhang, J.; Chao, D.M.; Liao, S.M.; Koleske, Genes Dev. 9, 897-910, 1995
A;Title: Association of an activator with an RNA polymerase II holoenzyme. A;Reference number: A57062; MUID:95293223; PMID:7774808
A;Accession: C57062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Wedler, H.; Wambutt, R. submitted to the Protein Sequence Database, September 1996 A;Reference number: S74288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRB8 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: cyclin-dependent kinase 5 activator homolog; probable membrane C;Species: Saccharomyces cerevisiae
C;Date: 19-Mar-1997 #sequence revision 25-Apr-1997 #text change 20-Jun-2000
C;Accession: S74293; S19496; S19495; S19766; C57062; S53594; S55868; S68611; S5998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Feldmann, H.; Mannhaupt, G.; Vetter, I. submitted to the Protein Sequence Database, A;Reference number: S19429
A;Accession: S19766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-427 <WED>
A; Residues: 1-427 <WED>
A; Cross-references: EMBL:X59720; NID:g1907116; PID:g1907218; MIPS:YCR081w
A; Cross-references: EMBL:X59720; NID:g1907116; PID:g1907218; MIPS:YCR081w
A; Ballesta, J.P.G.; Franco, L.; Hoenicka, J.; Jimenez, A.; Remacha, M.; Sabubmitted to the Protein Sequence Database, March 1992
A; Reference number: S19486
A; Accession: S19496
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                                                                                                                                                                                                                                            R; Jinenez, A.
submitted to the EMBL Data Library,
A; Reference number: S53589
A; Accession: S53594
                                                                                                                                                                                                                                                                                                                                       A, Status: not compared with A, Molecule type: DNA A, Residues: 202-1427 <HEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 531-1427 < FEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 'MSFFGLENSGNARDGPLDFEESYKGYGEHELEENDYLNDETFGDNVQVGTDFDFGNPHSSGSS',4,'NAIGGNG
A;Cross-references: EMBL:X59720; MIPS:YCR080w
A;Note: this sequence has been revised in reference S55867
A;Note: YCR080w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 202-863 <BAL>
A;Cross-references: EMBL:X59720; MIPS:YCR080w
A;Accession: S19495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLP-FNTSTPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GEGMKYFYHQDGSNPSDENSALVHYIQVHRDDFSMNIKLQLFGLVAKQ
                                                                                                                                                                                                                                                                                                                                                                                        conceptual translation
                                                                                                                                                                                                                                                                                              December 1997
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                                                                                                     cytosolic protein Ycr77p
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A60026
     cell communication-mediating membrane protein pTra2A - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 03-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 C;Accession: A60026 R;Kuwabara, P.E.; Okkema, P.G.; Kimble, J. Mol. Biol. Cell 3, 461-473, 1992 Mol. Biol. Cell 3, 461-473, 1992
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A;Gene: SGD:SRBB
A;Gene: SGD:SRBB
A;Cross-references: SGD:S0000677; MIPS:YCR080w; MIPS:YCR081w
A;Map position: 3R
C;Superfamily: Saccharomyces cerevisiae SRBB protein
C;Keywords: nucleus; transmembrane protein
F;277-293/Domain: transmembrane #status predicted <TM1>
F;277-293/Domain: transmembrane #status predicted <TM2>
F;353-369/Domain: transmembrane #status predicted <TM3>
F;566-582/Domain: transmembrane #status predicted <TM3>
F;693-709/Domain: transmembrane #status predicted <TM5>
F;724-740/Domain: transmembrane #status predicted <TM6>
F;1081-108/Domain: transmembrane #status predicted <TM6>
F;1081-108/Domain: transmembrane #status predicted <TM7>
F;1169-1185/Domain: transmembrane #status predicted <TM7>
F;1169-1185/Domain: transmembrane #status predicted <TM8>
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R;Huang, O.O.; Lee, K.Y.; Wang, J.H.
FEBS Lett. 378, 48-50, 1996
A;Title: A novel yeast protein showing specific association
A;Reference number: $68611; MUID:96140706; PMID:8549800
A;Accession: $6861
A;Molecule type: protein
A;Residues: 701-1011,1013-1056 <HUA>
C;Genetics:
                                                                                                                                              605 LLINLKISPLMKSQYNMVLRNVMEYDVKFYEIFNFDQLVEITEQIKMRILSNDITNLQLS
                                                                                                                                                                                                                                                                                                                                                                           264 LIENHEGRK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 DFQLTIVTCKQFPKLSCIQLNCIDTQFTKLLD-DNPTEFDWPTYVDQNPLTMHKIIQLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 YILE---KLIFDMTNHYNDSOOL-RTWKROISYFLKLLGNCYSLRLINKE---IFHHWLV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 YILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRII-----LQKENKEKQALARHKCI 65
                                                                                                                                                                                                                   ---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HQYLSLLQDRYFPIASVM-----RTLDKDN-----FSLTPDLIHDLLGHVP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SILEFFKNLLF----VHLLSLSKNQREGCSTDMAVVST-----PFF----
KTPLSIKIMVAEWYLSHLCSGILSSV---NRTVLLKIFKIFC 703
                                                                -----EWMLD---QGLLESIPLYNQEKYLSGFEVLC 361
                                                                                                                                                                                                                                                                                         LAKNFSAQKRVVSYMMPSLYRLLNILITYGIIKVPTYIRKLISSGLLYLQDSNDKFVHVQ 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                WSIHPSRQFDHYESN-----QLVAKLLLL-----RINSTDEDLHEFQIEDAIWSLVFQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WLLHPS--FSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNL--IAIVRCFWFTVESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YYIVSSSKSMINDENYIINDIKKNNKIKLNILKILSSLILKIFQEQSLEVFIFPTSNWEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKPLLFEIVSNADTNONSDMKKKLELISYRNESLKNNSSIR-----NVIMSASNAN
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Similarity 18.8%; Pred. No. 28;
98; Conservative 65; Mismatches 155; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----WKS
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A; Reference number: A60026; MUID:92360913; PMID:1498366 A; Accession: A60026

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C.Species: Campylobacter jejuni
C.Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A.hitle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A.Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
!Nolecule type: DNA
| Residues: 1-699 < PPA>
| Cross-references: GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73415.1; PID:g696859
| Experimental source: serotype O2, strain NCTC 11168
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C,Superfamily: Thermotoga maritima P-type cation-transporting ATPase, ATPase nucleotide-
F,8-37/Domain: heavy-metal-associated homology <HMA>
F,8-37/Domain: ATPase nucleotide-binding domain homology <ATN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                          19;
A,Status: preliminary
A,Moctaule types: mRNA
A,Rocale types: mRNA
A,Rocale types: mRNA
A,Rocase references: GB.S42187; NID:9253436; PIDN:AAB22845.1; PID:9253437
A,Note: sequence extracted from NCBI backbone (NCBIN:110873, NCBIP:110874)
C,Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 EKPDYPNVVNQTCDKIFHDLNSTGIBFFDGSRSFSSTKSQFDTMQTEIVLLTPEMLLSAM 378
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Best Local Similarity 22.5%; Pred. No. 12;
Matches 76; Conservative 54; Mismatches 101; Indels 107; Gaps
                                                                                                                                                                                                                                                                                                                                                254 -----RCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDN-----VRVLPLE 299
                                                                                                                                                                                      Query Match
Best Local Similarity 16.7%; Pred. No. 29;
Matches 75; Conservative 65; Mismatches 120; Indels 188; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       49 LOKENKEKQALARHKCISILEFFKNLLFVH--LLSLSKNQREGCSTDMAVVSTPFFNRNL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 WYRLLSSRFSLWKSYCPRFFLDYLEAFG------LLSDFLDHQAVIKFFEL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 --RIRNS-----MFDL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 ETHFSYYPVSGF------VAPHQY-----LSLLQDRYFPIASV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 -----PSKSFTNSTKDALFQKIKLWLLSIEPRQKTCAASIHSCDTPLDSEHYFNICTD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 MRTLDK-------DNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVI 229
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                                                                                                                                                                                                                                                                                                          1 VHYCERTLDPKYILKIALKLROS-----LSLFFONSOSLORAYSTPYSYYRII 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 OHSDFVNGFESIW-TIEKAEELIHEFRLAL----
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| Q27712 panulirus a Q92797 chlamydia p Q92806 chlamydia p Q09812 schizosacch P52362 human herpe P41001 plasmodium P2548 saccharomyc P34709 caenorhabdi | P47711 mycoplasma P47711 mycoplasma P13783 kluvyeromyc P56784 arabidopsis P48190 zea mays (m P04114 homo sapten Q5775 methanococc P3575 measles vir P5775 methanococc P3575 measles vir P5776 methanocac P54747 butonnera ap | Q03660 saccharomyc<br>P31352 mabburg vir<br>P15736 simian 11 r<br>P3511 galdieria s<br>P46578 caenorhabdi<br>Q14517 homo saphen<br>P09975 marchantia<br>Q12496 saccharomyc<br>P58402 escherichia | P30855 escherichia Q12774 homo sapien P56105 helicobacte P5337 saccharomyc Q60260 methanococc Q13619 homo sapien P49309 saccharomyc P18458 berne virus Q924E rattus norv Q824E rattus perilia | Q960115 lactobact<br>Q06115 lactobact<br>Q06115 stamian 11 r<br>P30195 stamian 11 r<br>P30195 status norv<br>P40016 sactus norv<br>P40016 sactus conv<br>P40016 sactus conv<br>P58040 schizosacch<br>P58040 schizosacch<br>P58040 schizosacch<br>P58077 saccharomyc<br>Q57570 methanococc<br>P67570 methanococc<br>Q97544 streptococc<br>Q97744 areptococc<br>Q97740 arabidopsis<br>P5809 secherichia<br>P5728 buchnera ap<br>P3528 erysimum la<br>Q01500 p genome po<br>Q6730 aquifex aeo<br>P49025 lactococcus<br>P18544 saccharomyc<br>Q84405 oryctolagus<br>Q99mx1 mus musculu<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27815 escherichia<br>P27816 escherichia<br>P27816 escherichia<br>P27816 escherichia<br>P27817 escherichia  |
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Probable aromatic amino acid hyroxylass (EC 1.14.16.-).
CPN1046 OR CP0806 OR CP01046.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI TaxID=83559;
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STRAIN=CWILO29;

MEDLINE=99206606; PubMed=10192388;

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Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,

Colinger L., Grimwood J., Davis R.W., Stephens R.S.;

"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";

Nat. Genet. 21:385-389(1999).
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EMBL; AB002240; AAF73705.1; -.
EMBL; AP002548; BAA99253 1; -.
TIGR; CP0806; -.
TIGR; CP0806; -.
TIGR; CP0807173; Aaa hydroxylase.
Pfam; PF00351; biopterin_H; 1.
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Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CW1229 from USA.",
Nucleic Acids Res. 28:2311-2314(2000).
-!- COFACTOR: Binds 1 ferrous ion (By similarity).
-!- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO.
                                 361
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-!- PATHWAY: Catabolism of phenylalanine; first (rate-limiting) step.
-!- SUBUNIT: MONOMER.
-!- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
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STRAIGHARC 105692
STOWER C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Brody L.L., Coulter S.N., Folger K.R., Wastbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Was A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wonng G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen."
                                                                                  169 GAKATPKERSY-------LARLYWFTVEFGLVQEQGQTKIYGGILSSPGE 212
                                                 285 LGHAFIDNV-RVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSK----LEWM-LD 338
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SEQUENCE FROM N.A.

MEDIANE-94151319. PubMed-8108417;

Zhao G., Xia T., Song J., Roy R.A.;

Zhao G., Xia T., Song J., Roy R.A.;

"Pseudomonas aeruginosa possesses homologues of mammalian

"Phenylalanie hydroxylase and 4 alpha-carbinolamine dehydratase/DCOH
as part of a three-component gene cluster.";

Proc. Natl. Acad. Sci. U.S.A. 91:1366-1370(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: L-phenylalanine + tetrahydrobiopterin + O(2) L-tyrosine + dihydrobiopterin + H(2)O.
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InterPro: IPR001273, Aaa hydroxylase.
InterPro: IPR001213, blopterin H; 1.
PRINTS: PR00372; FVMHVDRXLASE.
IGRRAMS: TIGR01267; Phethydrox mono; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
Oxidoreductase; Monooxygenase; Phenylalanine catabolism; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
                                                                                                                                                                                                                                                                                                                                              262 AA
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EMBL; AE004522; AAG04261.1; -.
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273 DGLLP--PLFQPKE 284
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STRAINEEL TOR NIG661 / Serotype O1;
STRAINEEL TOR NIG661 / Serotype O1;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Ermolaeva M.D., Vamathevan J., Bass S., Oin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cholerae.";
Nature 406:177-483(2000).
Nature 406:177-483(2000).
-!- CATALYTIC ACTIVITY: L-phenylalanine + tetrahydrobiopterin + O(2) =
-!- COFACTOR: Binds I ferrous ion (By similarity).
-!- COFACTOR: Binds I ferrous ion (By similarity).
-!- PATHWAY: Catabolism of phenylalanine; first (rate-limiting) step.
-!- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 APHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 SFDRFFFALLADKKFPVATFLRRREEFDYLQEPDFFHEVYGHCAMLTHPDFAAFTHVYGQL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 FTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.6%; Score 256.5; DB 1; Length 289;
25.6%; Pred. NO.3.3-31; Indels 25; Gaps
tive 56; Mismatches 108; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 LWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVI-KFFELETHFSYYPVSGFV 164
                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR001273; Aaa hydroxylase.
Pfam; PR00151; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
TIGRFAMs; TIGR01267; Phedhydrox mono; 1.
PROSITE; PS00367; BIOPTERIN_HYDROXYL; 1.
Oxidoreductase; Monooxygenase; Phenylalanine catabolism; Iron; Complete proteome.
                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 149 IRON (POTENTIAL).
289 AA; 33445 MW; 2D68B31C6E31D521 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRON (POTENTIAL).
                                                                                                                                289 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004410; AAF96726.1; -. HSSP; P04177; 1TOH.
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Best Local Similarity 25.61
Matches 65; Conservative
                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                         monooxygenase).
PHHA OR VCA0828.
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VCA0828;
                                                                                                                                                                                                                                                                                                                                              cholerae
361 CQ 362
                                                                                                                          VIBCH
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Best Local :
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                                                                                                                                                                    "Molecular cloning of chick pineal tryptophan hydroxylase and clircadian oscillation of its mRNA levels.";

Brain Res. Mol. Brain Res. 42:25-20(1996).

1- CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + O(2) = 5-10 (1906).

1- COPACTOR: PERROUS ION.

1- COPACTOR: PERROUS ION.

1- PANTHWAY: THIS IS THE RATE-LIMITING ENZYME IN THE BIOSYNTHESIS OF SEROTORIN IN THE CENTRAL NERVOUS SYSTEM AND CATALYZES THE FIRST STEP OF THE SYNTHESIS OF MELATONIN IN THE PINEAL GLAND.

1- SUBLINIT: MULTIMER OF IDENTICAL SUBUNITS (BY SIMILARITY).

1- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neograthae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p70080;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tryptophan 5-monooxygenase (EC 1.14.16.4) (Tryptophan 5-hydroxylase)
                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=White leghorn; TISSUE=Pineal gland; MEDLINE=97072811; PubMed=8915576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHICK
                                                                                                                                                                                                                                                                                                                                                                         Takahashi J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TR5H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DELVELTSK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHEGRKAYGAVLISSPQELGHAFID---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHF 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVLQATTGWRVARVPALIPFQTFFELLASQQFPVATFIRTPEELDYLQEPDIFHEIFGHC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRLFQLAQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDQGKRIYGGGILSSPKETVYSLSDEPLHQAFNPLE---AMRTPYRIDILQPLYFVLPDL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLLTNPWFAEFTHTYGKLGLKA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----THFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNGFIHYPETEHQVWNTLITROLKVIEGRACQEYLDGIEQLG-----LPHERIPQLDEIN 67
 U26428; AAC60036.1;
P04176; 1PHZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
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126
135
262 1
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126
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IRON (BY SIMILARITY).
F -> L (IN REF. 1).
MW; A5665839C5961A45 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 235.5; DB 1;
Pred. No. 1.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                        Barrett R.K., Sangoram A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SKEER--
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RESULTION RESULTION RESULTION REPORT TO PORT OF THE RESULTION REPORT OF THE RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RES
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Best Local S
Matches 65
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MOD RES 58
METAL 273
METAL 278
METAL 318
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PROSITE; I
TR5H_HUMAN STANDARD;
P17752; Q16736; O95188;
O1-AUG-1990 (Rel. 15, Created)
16-CCT-2001 (Rel. 40, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
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InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF00351; biopterin_H; 1.
Pfam; PF01842; ACT; 1.
PRINTS; PR00372; FYWHYDRXLASE.
                                                                                                                                                                                                                                        Tipper J.P., Citron B.A., Ribbiro P., Kauf "Cloning and expression of rabbit and huma hydroxylase cDNA in Escherichia coli.", Arch. Biochem. Biophys. 315:445-453 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90332431; PubMed=2377472;
Boulalard S., Darmon M.C., Ganear Y., Launay J.M., Mallet concluded to the coding sequence of human tryptophan hydroxylase.
Nucleic Acids Res. 18:4257-4257(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                        MEDLINE=98421834; PubMed=9751214;
Wang G.A., Coon S.L., Kaufman S.;
"Alternative splicing at the 3'-cDNA
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                       SEQUENCE OF 388-444 FROM N.A. WEDLINE=98421834; PubMed=975121
                                                                                                                                                                                                                                                                                                                                           MEDLINE=95077422; PubMed=7986090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 YRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYYP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAGYLSPRDFLAGLAFRVFHCTQYVRHSSDPLYTPEPDTCHELLGHVPLLAEPSFAQFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRELN-----KLYPTHACREYLKNLPLLTKYCGYREDNIPQLEDVSRFLKERTGFTIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSISELKHSLSGSAKVKPFDPKVTCKQECLITTFQEVYFVSESFEEAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE
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BIOPTERIN_HYDROXYL;
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annotation update)
(EC 1.14.16.4) (Tr
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IRON
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Pred. No. 5.9e-11;
L; Mismatches 93;
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                                                                                                                                                                                                  (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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human brain
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COFACTOR: FERROUS ION.

219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278

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Phasianidae sp. (Quail)
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                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9006;
                                                                                                                                                                                                     PHASP
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                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Broopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licensedib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 PVAGYLSPRDFLSGLAFRVFHCTQYVRHSSDPFYTPEPDTCHELLGHVPLLAEPSFAQFS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 WGTVFRELNKLYPTHACR----BYLKNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLNEDVLQVSVFALLLFLPSLHGECHPDT
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             -i- PATHWAY: THIS IS THE RATE-LIMITING ENZYME IN THE BIOSYNTHESIS OF SEROTONIN IN THE CENTRAL MERVOUS SYSTEM AND CATALYZES THE FIRST STEP OF THE SYNTHESIS OF MELLAPOINI IN THE PINEAL GLAND.
-i- SUBDNIT: MULTIMER OF IDENTICAL SUBUNITS.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- TISSUE SPECIFICITY: ISOFORM 2 SEEMS TO BE LESS WIDELY EXPRESSED THAN ISOFORM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY PKA) (POTENTIAL)
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FRINTS, TIGROL270; TTP 5 monoox; 1.

PROSITE; PS00367; BIOPERIM HYDROXYL; 1.

Oxidoreductase; Monooxygenase; Serotonin biosynthesis; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S -> N (IN REF. 2).

Q -> R (IN REF. 2).

A -> G (IN REF. 2).

; 86C398869ABR120A CRC64;
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-> I (IN REF. 1).
P -> NL (IN REF. 1
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43; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MINI JAJUON, IPRO02912; ACT.
IINEEPEPO, IPRO01273; Aaa hydroxylase.
Pffan; PF00351; Abopterin_H; 1.
Pfan; PF01842; ACT; 1.
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EMBL; L29306; AAA67050.1; -.
EMBL; AF097280; AAC69459.1; -.
PIR; S10489; S10489.
HSSP; P04177; 1TOH.
Genew; HGNC:12008; TPH.
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444 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydroxy-L-phenylalanine + dihydropteridine + H(2)O.
-!- COPACTOR: FERROUS ION.
-!- ENZYME REGULATION: PHOSPHORYLATION LEADS TO AN INCREASE IN THE CATALYTIC ACTIVITY.
-!- PATHAMY: Catecholanine biosynthesis; first step.
-!- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGRO1269; Tyr3 monoox; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron;
Neurotransmitter biosynthesis; Phosphorylation.
MOD_RES 40 HOSPHORYLATION (BY PKA) (BX SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

TISSUB-Adrenal gland,
MEDLINE-88089590; PubMed-2447231;
MEDLINE-88089590; PubMed-2447231;
REUQUEC M., Grina B., Lamouroux A., Mallet J.;
"Cloning of quail tyrosine hydroxylase: amino acid homology with other hydroxylases discloses functional domains.";
J. Neurochem. S0:142-148[198].
--- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE PHYSIOLOGY OF ADRENERGIC
                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-UNN-2002 (Rel. 41, Last amotation update)
Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 WKEVYSTLKSLYPTHACK---EYLEAFNLLEKFCGYNENNIPQLEEVSRFLKERTGFQLR 282
291 QEIG------LASLGASEEAVQKLAT------CYFFTVEFGLCKQDGQLRVFGAGL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 491;
                                                                                                   279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                                                   335 LSSISELKHALSGHAKVKPPDPKITCKQECLITTPQDVYFVSESFEDAKE 384
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IRON (BY SIMILARITY).
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Pred. No. 8.7e-11;
                                                                                                                                                                                                                                                                                                                                                            491 AA
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PRINTS; PR00372; FYWHYDRXLASE.
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29.1%;
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                                                                                                                                                                                                               P098LU;
01-MAR-1989 (Rel. 10, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tryptophan 5-monooxygenase (EC 1.14.16.4) (Tryptophan 5-hydroxylase)
                                    EMBL; M28000; AAA42262.1; -.
EMBL; X53501; CAA37579.1; -.
EIR; JL0034; WHRTW.
PIR; A24367; A24367.
                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-91245924; PubMed=1645430; Kim K.S., Wessel T.C., Stone D.M., Carver C.H., Joh T.H., Park D.H.; "Molecular cloning and characterization of cDNA encoding tryptophan hydroxylase from rat central serotonergic neurons."; Brain Res. Mol. Brain Res. 9:277-283(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-Wistar; TISSUE-Pineal gland;
MEDLINE-88244702; PubMede-3379411;
Darmon M.C., Guibert B., Leviel V.,
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Mammalia; Eutheria;
NCBI_TaxID=10116;
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"Sequence of two mRNAs encoding active
J. Neurochem. 51:312-316(1988).
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87005247; PubMed=2875901;
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yptophan hydroxylase.";
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Best Local
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MOD RES 58
METAL 272
METAL 277
METAL 277
METAL 317
SEQUENCE 444 AA
                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=90243261; PubMed=2110547;

Stoll J., Kozak C.A., Goldman D.;

Stoll J., Kozak C.A., Goldman D.;

Characterization and chromosomal mapping of a cDNA encoding tryptophan hydroxylase from a mouse mastocytoma cell line.";

Genomics 7:88-96(1990).

-I-CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + O(2)

-I-CATALYTIC ACTIVITY: L-tryptophan + dihydropteridine + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TR5H_MOUSE
P17532;
01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
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PROSITE; PS00367; BIOPTERIN_HYDROXYL; 1.

Oxidoreductase; Monooxygenase; Serotonin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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Pfam; PF00351; biopterin_H; 1.
Pfam; PF01842; ACT; 1.
PRINTS; PR00372; FYWHYDRXLASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159
                                                                                                                          hydroxy-L-tryptophan + dihydropteridine + H(2)0.

COFACTOR: PERROUS ION.

PATHWAY: THIS IS THE RATE-LIMITING ENZYME IN THE BIOSYNTHESIS OF SEROTONIN IN THE CENTRAL MERVOUS SYSTEM AND CATALYZES THE FIRST STEP OF THE SYNTHESIS OF MELATONIN IN THE PINEAL GLAND.

SUBUNIT: MULTIMER OF IDENTICAL SUBUNITS.

SIMILARITY: BELONGS TO THE BIOFTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                     _TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSSISELRHALSGHAKVKPFDPKVACKQECLITSFQDVYFVSESFEDAKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL
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(Rel. 15, Last
(Rel. 41, Last
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                                                                                                                                                                                                                                                                                                                                                                                               (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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272
277
317
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27.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
annotation update)
(EC 1.14.16.4) (Tryptophan 5-hydroxylase)
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IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
; C3CF5245727CC825 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 227.5; DB 1;
Pred. No. 1.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447
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collaboration -

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PRT;
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NCBI_TaxID=7936;
[1]
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272
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
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MEDLINE=95077422; PubMed=7986090;
Tipper J D., Citron B.A., Ribeiro P., Kaufman S.;
"Cloning and expression of rabbit and human brain tryptophan hydroxylase cDNA in Escherichia coli.";
Ach. Biocham. Biophys. 315:445-453 (1994).
-!- CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + O(2) = 5 hydroxy-L-tryptophan + dihydropteridine + H(2)O.
-!- COPACTOR: FERROUS ION.
-!- COPACTOR: FERROUS ION.
-!- CATHWAY: THIS IS THE RATE-LIMITING ENZYME IN THE BIOSYNTHESIS OF SEROTONIN IN THE CENTRAL NERVOUS SYSTEM AND CATALYZES THE FIRST
                                                                                                                                                                                                                                                                                                                                                                                                                                       97; Indels 27; Gaps
                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY PKA) (POTENTIAL).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IGO839F22A1138BCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87289638; PubMed=3475690; Grentt H.E., Ledley F.D., Reed L.L., Woo S.L.C.; "Full-length cDNA for rabbit tryptophan hydroxylase: functional domains and evolution of aromatic amino acid hydroxylases."; Proc. Natl. Acad. Sci. U.S.A. 84:5530-5534(1987).
                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 447;
                                                                                                                                                                 PRINTS; PR00372; FYMHYDRXLASE.
TGRRAMs; TIGRO1270; TTP 5 monoox; 1.
PROSTTE; PS00367; BIOPPERIN HYDROXTL; 1.
Oxidoreductase; Monooxygenase; Serotonin biosynthesis; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 LSSISELKHALSGHAKVKPPDPKIACKQECLITSFQDVYFVSESFEDAKE 387
                                                                                                                                                                                                                                                                                                                                                                                                                    1.3e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               12.0%; Score 226.5; 27.4%; Pred. No. 1.3
                                                                MGD; MGI:98796; Tph.
InterPro; IPR002912; ACT.
InterPro; IPR001273; Aaa_hydroxylase.
Pfam; PF00351; blopterin_H; 1.
Pfam; PF01842; ACT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                     61 61 PHI
275 275 IRC
280 280 IRC
320 320 IRC
447 AA; 51343 MW; ...
EMBL, J04758; AAA63401.1;
PIR, A34582; A34582.
HSSP; P04177; 1TOH.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                     Phosphorylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RABIT
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                            SUBUNIT: MULTIMER OF IDENTICAL SUBUNITS.
SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 WYRLLSSRFSLWKSYCPRFFLDYLBAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 WGTVFRELNKLYPTHACR---EYLKNLPLLSKYCGYREDNIPQLEDISNFLKERTGFSIR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygli; Neopterygli; Teleostei; Anguilliformes; Anguillidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (BY PKA) (POTENTIAL).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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TGRRAMs; TIGRO1270; Trp 5 monoox; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
Oxidoreductase, Monooxygenase; Serotonin biosynthesis; Iron; Phosphorylation.
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STEP OF THE SYNTHESIS OF MELATONIN IN THE PINEAL GLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 PHOSPHORYLATION (BY PKA) (PO 277 IRON (BY SIMILARITY). 317 IRON (BY SIMILARITY). 102 M -> L (IN REF. 1). 151 L -> S (IN REF. 1). 203 KY -> ND (IN REF. 1). 203 KY -> ND (IN REF. 1). 203 TY -> K (IN REF. 1). 207 R -> Q (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (IN REF. 1). 203 T -> K (I
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INTERPO; IPRO02912; ACT.
INTERPO; IPRO01273; Asa hydroxylase.
Pfam; PF00351; biopterin H; 1.
Pfam; PF01842; ACT; 1.
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JAH MOUSE STANDARD.

D TY3H MOUSE STANDARD.

C P24529;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

Tvrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosin
               RESULT
TY3H_MC
AC P2
DT 01
DT 15
DT 15
DT 15
CGN TF
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MEDITUR=98344760; PubMed=9681435;

NA MEDITUR=98344760; PubMed=9681435;

NA VINCENT J.D., Biguet N.F., Vidal B., Veron M., Mallet J.,

Vincent J.D., Dufour S., Vernier P.;

Vincent J.D., Dufour S., Vernier P.;

Vincent J.D., Dufour S., Vernier P.;

Tourion Pydroxylase in the european eel (Anguilla anguilla): cDNA

Cloning, brain distribution, and phylogenetic analysis.";

J. Neurochem. 71:460-470(1998)

T. J. Neurochem. 71:460-470(1998)

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Best Local S
Matches 65
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PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P04177; 1TOH.
InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF00351; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WYRLLSSRFSLWKSY-CPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSY 157
                                                                                                                                                                                                                                                                                                                                                          LLSSYGELVHSLSDEPERREFDPEAAAAEPYQDQNYQSVYFVSESFTDAKE
                                                                                                                                                                                                                                                                                                                                                                                                          LISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPOETLFSIRHFDELVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCVHELLGHVPMLADRTFAQF 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEF 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ransmitter biosynthesis; Phosphorylation.

S 38 38 PHOSPHORYLATION (BY PKA)

321 321 IRON (BY SIMILARITY).

326 326 IRON (BY SIMILARITY).

366 366 IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
65; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                LASIGASEEDIEKLST-----LYWFTVEFGLCKQGDGVKAYGAG
               Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55490 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 225.5; DB 1;
Pred. No. 1.8e-10;
8; Mismatches 99;
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                                                                                          (Tyrosine 3-hydroxylase)
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                  Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Matches 66
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SEQUENCE
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Submitted (APR-1992) to
-i- FUNCTION: PLAYS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREAMs; TIGR01269; Tyr 3 monoox; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
Catecholamine blosynthesis; Oxidoreductase; Monooxygenase; Iron;
Neurotransmitter blosynthesis; Phosphorylation.
MOD_RES 19 PHOSPHORYLATION (BY CAMK2) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P04177; 1TOH.

MGD, MGI.98735; Th.

InterPro; IPR001273; Aaa_hydroxylase.

Pfam; PF00351; blopterin H; 1.

PRINTS; PR00372; FYWHYDRXLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M69200; AAA40434.1; -.
EMBL; X53503; CAA37580.1; -.
PIR; JN00669; JN0068.
HSSP, P04177; 1TOH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91248263; PubMed=1674869;
IChikawa S., Sasaoka T., Nagatsu T.;
"Primary structure of mouse tyrosine hydroxylase deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
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                                             279
                                                                                             350
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                                                                                                                                                                                                                                                      159
                                                                                                                                                                                                                                                                                                      233
                                                                                                                                                                                                                                                                                                                                                       107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydroxy-L-phenylalanine + dihydropteridine + H(2)O.
COFACTOR: FERROUS ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENZYME REGULATION: PHOSPHORYLATION LEADS TO AN INCREASE CATALYTIC ACTIVITY.

PATHWAY: Catecholamine biosynthesis; first step.

SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYDROXYLASES FAMILY
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               PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF
                                                                                             QDIG-----
                                                                                                                                          INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL
                                                                                                                                                                                                                                                                                                      WKEVYATLKGLYATHACR---EHLEAFQLLERYCGYREDSIPQLEDVSHFLKERTGFQLR 289
                                                                                                                                                                                                   PVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFAQFS
                                                                                                                                                                                                                                                                                                                                                                                                          66; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                498 AA;
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51
331
336
376
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PR-1992) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYWHYDRXLASE.
                                                                                             ·LASIGASDEEIEKLST------VYWFTVEFGLCKQNGELKAYGAGL
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59
331
336
376
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o the EMBL/GenBank/DDBJ databases.
IMPORTANT ROLE IN THE PHYSIOLOGY OF ADRENERGIC
                                                                                                                                                                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 225.5; DB 1
Pred. No. 1.8e-10;
2; Mismatches 101
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IRON
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PHOSPHORYLATION
PHOSPHORYLATION
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RON (BY SIMILARITY).

RON (BY SIMILARITY).

62790179664F6DC6 CRC64;
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PKA) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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31;

Gaps

<u>ن</u>

218

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334

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Green C.B., Beehars Funded 19743;
"Tryptophan hydroxylase expression is regulated by a circadian clock in Xenopus laevis retina.";
In Xenopus laevis retina.";
In Xenopus laevis retina.";
In Xenopus laevis retina.";
In Xenopus laevis retina.";
In Xenopus laevis retina.";
In Xenopus laevis retina.";
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In Xenopus laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis laevis 
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394 LSSYGELLHSLSEEPEVRAFDPDTAAVQPYQDQTYQPVYFVSESFSDAKDKLRNYASRIQ 453
                                                                                                                                                                                                                ÎS-JUL-1998 (Rel. 36, Created)
15-UL-1998 (Rel. 36, Last sequence update)
15-UL-1998 (Rel. 36, Last annotation update)
Tryptophan 5-monooxygenase (EC 1.14.16.4) (Tryptophan 5-hydroxylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia: Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Monooxygenase; Serotonin biosynthesis; Iron. METAL 309 309 IRON (BY SIMILARITY). METAL 314 314 IRON (BY SIMILARITY). METAL 354 354 IRON (BY SIMILARITY). SEQUENCE 481 AA; 55406 MW; 6852C33EFFBDEBAO CRC64;
                                                                                                                                                     481 AA
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TIGREAMS; TIGR01270; Trp 5 monoox; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002912; ACT.
InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF00351; biopterin_H; 1.
Pfam; PF01842; ACT; 1.
                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94246419; PubMed=8189245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L20679; AAA21306.1; -.
HSSP; P04177; 1TOH.
                                                                                                                                                     STANDARD;
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es 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IISSUE=Retina;
                                                                                                                                                         TRSH XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Catecholamine biosynthesis, first step.
-!- SUBINIT: HOMOTETAARE.
-!- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
HYDROXYLASES FAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anton X.X., Manaster J.S., Kordower X.X., Markham X.X., Bredesen D.E.; Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydroxy-L-phenylalanine + dihydropteridine + H(2)O.
-!- COFACTOR: FERROUS ION.
-!- ENZYME REGULATION: PHOSPHORYLATION LEADS TO AN INCREASE IN THE CATALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Crystal structure of tyrosine hydroxylase at 2.3 A and its implications for inherited neurodegenerative diseases."; Nat. Struct. Biol. 4:578-588(1987).
-- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE PHYSIOLOGY OF ADRENERGIC
                                                                                                                                                                               20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Tyrosine 3-monoxygense (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH)
                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
278 LISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLE 334
                               371 LLSSISELKHSLSGNAKVKPFD------PMVTCN-QECI--ITSFQELYFVSESFE 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-498.
MEDINE_973896; PubMed=9228951;
GOOGWill KE., Sabatier C., Marks C., Raag R., Fitzpatrick P.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haycock J.W., Haycock D.A.;
"Tyrosine hydroxylase in rat brain dopaminergic nerve terminals.
Whitiple-site phosphorylation in vivo and in synaptosomes.";
J. Biol. Chem. 266:5650-5657(1991).
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDIINE-85111249; PubMed=2857492;
Grimm B., Lamouroux A., Blancor F., Faucon Biguet N., Mallet J.;
"Complete coding sequence of rat tyrosine hydroxylase mRNA.";
Proc. Natl. Acad. Sci. U.S.A. 82:617-621(1985).
                                                                                                                                           498 AA
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InterProx; IRROD1273; Aaa hydroxylase.
Pfam; PF00351; biopterin H; 1.
PRINTS; PR00372; PYWHYDKIAMSH.
IIGREMA; IIGR01269; Tyr 3 monoox; 1.
PROSITE; P$00367; BIOPTERIN HYDROXYL; 1.
                                                                                                                                           PRT;
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                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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01-FEB-1996
15-JUN-2002
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Neurotransmitter biosynthesis; Phosphorylation; 3D-structure.
MOD_RES 19 19 PHOSPHORYLATION (BY CAMKZ).
MOD_RES 31 31 PHOSPHORYLATION.
MOD_RES 40 40 PHOSPHORYLATION (BY PKA).
DOMAIN 51 59 POLY-ALA.
                                                                                             SEQUENCE FROM N.A.

MEDILINE=88274405; PubMed=2899135;

Saadat S., Stehle A.D., Lamouroux A., Mallet J., Thoenen "predicted amino acid sequence of bovine tyrosine hydroxy similarity to tyrosine hydroxylases from other species.";

J. Neurochem. 51:572-578(1988).
                         SEQUENCE OF 153-169.
MEDLINE=88183482; PubMed=2895648;
Abate C., Smith J.A., Joh T.H.;
Characterization of the catalytic domain of bovine
                                                                                                                                                                                         "Isolation and nucleotide sequence of a cDNA clone encoding bovine adrenal tyrosine hydroxylase: comparative analysis of tyrosine hydroxylase gene products."

J. Neurosci. Res. 19:440-449(1988).
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=88259287; PubMed=2898537;
D'Mello S.R., Weisberg E.P., Stachowiak M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TY3H_BO
P17289;
 Biochem Biophys Res.
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
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65; Conserv
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(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH).
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55965 MW;
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26.7%;
   Commun. 151:1446-1453(1988)
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Pred. No. 2
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                            tyrosine
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SEQUENCE OF 1-27
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 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTSKLE
                                                    INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL
                                                                                PAAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPECCHELLGHVPMLADRTFAQFS
                                                                                                          PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF
                                                                                                                                     WKEVYSTLRGLYPTHACR---EHLEAFELLERFCGYREDRIPQLEDVSRFLKERTGFQLR
                                                                                                                                                                                                         Similarity
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                            -LASIGVSDEEIEKLST----
                                                                                                                                                                                                       11.7%;
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Score 221.5; DB: Pred. No. 3.7e-10

DB 1;

Length Indels

490;

Gaps

'n

281 218

Mismatches

---LYWFTVEFGLCKQNGEVKAYGAGL

334 385 278 341

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EMBL; M36704; AAA30779.1; -.
EMBL; M36705; AAA30798.1; -.
PIR; A27687; A27687.
PIR; JL0033; JL0039.
HSSP; P04177; ITCH.
InterPro; IPR001273; Aaa hydroxylase.
Pfam: PF00351; biopterin_H; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Biochim, Biophys, Acta 953:142-156(1988).

-i- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE PHYSIOLOGY OF ADRENERGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINB=88163736; PubMed=2894860;
Haavik J., Andersson K.K., Petersson L., Flatmark T.;
"Soluble tyrosine hydroxylase (tyrosine 3-monooxygenase) from bovine adrenal medulla: large-scale purification and physicochemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00351; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
TIGRFAM6; TIGR01269; Tyr 3 monoox; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; FALSE NEG.
Catecholamine biosynthesis; Oxidoreductase; Monk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) dihydroxy-L-phenylalanine + dihydropteridine + H(2)O. COFACTOR: FERROUS ION. ENZYME REGULATION: PHOSPHORYLATION LEADS TO AN INCREASE IN CATALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROXYLASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: Catecholamine biosynthesis; first step SIMILARITY; BELONGS TO THE BIOPTERIN-DEPENDENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biosynthesis;
              54992 MW;
PHOSPHORYLATION (BY PKA).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
AAMI -> GSLV (IN REF. 2).
P -> K (IN REF. 2).
P -> K (IN REF. 2).
R -> V (IN REF. 2).
R -> V (IN REF. 2).
B -> D (IN REF. 2).
GHV -> AHG (IN REF. 2).
K -> N (IN REF. 2).
K -> N (IN REF. 2).
K -> N (IN REF. 2).
K -> N (IN REF. 2).
K -> N (IN REF. 2).
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-!- CATALYTIC ACTIVITY: L-phenylalanine + tetrahydrobiopterin + O(2) =
-Ltyrosine + dihydrobiopterin + H(2)O.
-!- COFACTOR: Binds 1 ferrous ion (By similarity).
-!- COFACTOR: Binds 1 ferrous ion (By similarity).
-!- PATHWAY: Catabolism of phenylalanine; first (rate-limiting) step.
-!- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
HYDROXYLASES FAMILY. [1]
SEQUENCE FROM N.A.
SEGUENCE FROM N.A.
SEGUENCE PROM N.A.
MEDINE-2108099;
MEDINE-2108090;
PubMed=11214968;
MEDINE-2108090;
Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Mateumoto M., Mateumo A.,
Kishida Y., Kiyokawa C., Nakaza M., Mateumoto M., Mateumo A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti:" | : | | : : | | : : | | : : | | | : 14 IPDFEDVSTKLRKLIGWEIIAVPGLIPAAPFFDHLANRRFPVTNWLRTRQELDYIVEPDM 133 90 CSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPR------FFLDYLEAFGLLSD 138 139 FLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDL 198 199 IHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWF 258 386 ISSYGELLHSLSEEPEIRAFDPDAAAVQPYQDQTYQPVYFVSESPSDAKDKLRSYASRIQ 445 40; Mismatches 109; Indels 36; Gaps 22 CRADFTVAQD-----YDYSDEEQAVWRTLCDRQTKLTRKLAHHSYLDGVEKLGLLDR 73 Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NGBI\_TaxID=381; TRIRIA, FANCIS, TIGRO1267; Phe44hydrox mono; 1.
PROSITE; PS00367; BIOPTERIN\_HYDROXYL; 1.
Oxidoreductase; Monooxygenase; Phenylalanine catabolism; Iron; 11.7%; Score 221; DB 1; Length 275; 26.0%; Pred. No. 2e-10; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-140 140 IRON (POTENTIAL). 275 AA; 31347 MW; BC29D255534BC215 CRC64; IRON (POTENTIAL) EMBL; AP003005; BAB51399.1; ... InterPro; IPR001273; Aaa hydroxylase. PRT; Pfam; PF00351; biopterin H; 1. PRINTS; PR00372; FYWHYDRXLASE. Best Local Similarity 26.03 Matches 65; Conservative STANDARD; 135 Complete proteome. nonooxygenase). PHHA OR MLR4831. 15-JUN-2002 15-JUN-2002 PH4H RHILO Q98D72: SEQUENCE Query Match ò 셤 셤 ઠે ò

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TY3H HUMAN STANDARD; PRT; 528 AA.
P07101, 015589; 015585;
01-APR-1988 (Rel. 07, Created)
01-APR-1989 (Rel. 11, Last sequence update)
15-UIN-2002 (Rel. 41, Last annotation update)
Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH).
259 TVESGLI-ENHEGRKAYGAVLISSPOELGHAFI-DNVRVLPLELDQIIRLPFNTSTPQET 316
                                     SEQUENCE OF 1-30 FROM N.A.

SEQUENCE OF 1-30 FROM N.A.

Ginns E.I., FubMed=2296667;

Lamarca M.E., McAllister C.G., Paul S.M.;

"Expression of human tyrosine hydroxylase cDNA in invertebrate cells
"Expression of human tyrosine hydroxylase cDNA in invertebrate cells
J. Blol. Chem. 263:7406-7410(1988).
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MEDLINE-88117543; PubMed=2892893;
MEDLINE-88117543; PubMed=2892893;
Grima B., Mallet J.;
Ranalysis of the S' region of the human tyrosine hydroxylase gene:
combinatorial patterns of exon splicing generate multiple regulated
tyrosine hydroxylase isoforms.";
J. Neurochem. 50:988-991(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A single human gene encoding multiple tyrosine hydroxylases with different predicted functional characteristics."; Nature 326:707-711(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (TYPES 1 TO 4).
MEDILINE=89008200; PubMed=2902075;
KOBAYASHI K., Kaneda N., Ichinose H., Kishi F., Nakazawa A.,
Kurosawa Y., Fujita K., Nagatsu T.;
"Structure of the human tyrosine hydroxylase gene: alternative splicing from a single gene accounts for generation of four mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87298614; PubMed=2887169; Kaneda N., Kobayashi K., Ichinose H., Kishi F., Nakazawa A., Kurosawa Y., Fujita K., Nagatsu T.; Fislation of a novel cDha clone for human tyrosine hydroxylase: alternative RNA splicing produces four kinds of mRNA from a sinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (TYPE 3).
MEDILINE-87316931; PubMed=2888085;
Kobayashi K., Kaneda N., Ichinose H., Kishi F., Nakazawa A.,
Kurosawa Y., Fujita K., Nagatsu T.;
"Isolation of a full-length cDNA clone encoding human tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grima B., Lamouroux A., Boni C., Julien J.-F., Javoy-Agid F., Mallet J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene.";
Biochem. Biophys. Res. Commun. 146:971-975(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hydroxylase type 3.";
Nucleic Acids Res. 15:6733-6733(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-94 FROM N.A. (TYPE 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (TYPES 1 TO 4).
MEDLINE=87173064; PubMed=2882428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. 103:907-912(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                          317 LFSIRHFDEL 326
                                                                                                                                                                                                              239 YFVLPSFDAL 248
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                                                                                                                                                                                                                      TAUSITE; PS00367; BIOPTERIN HYDROXYL; 1.

Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron;

MOD_RES 71

TOMAIN 85

90

POLY-ALA.

NETAL 361

361

IRON (BY SIMILARITY).

METAL 366

METAL 366

MISSING (IN ISOFORM 4).

VARSPLIC 1

VARSPLIC 31

VARSPLIC 31

VARSPLIC 31

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MISSING (IN ISOFORM 1).

VARSPLIC 35

MISSING (IN ISOFORM 1).

VARSPLIC 35

MISSING (IN ISOFORM 1).
                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y00414; CAA68472.1; ALT_SEQ.
EMBL; M17589; AAA61179.1; --
EMBL; M25290; CAA28908.1; --
EMBL; M24791; AAA61173.1; JOINED.
EMBL; M24789; AAA61173.1; JOINED.
EMBL; M24789; AAA61170.1; --
EMBL; M24789; AAA61170.1; --
EMBL; M24789; AAA61170.1; JOINED.
EMBL; M24789; AAA61170.1; JOINED.
EMBL; M24789; AAA61170.1; --
EMBL; M24789; AAA61167.1; --
EMBL; M27991; WHHUY1.
PIR; A27791; WHHUY2.
PIR; B27791; WHHUY3.
PIR; B27791; WHHUY3.
PIR; B26825; WHHUY4.
PIR; JE0012; JE0013.
PIR; JE0014; JE0013.
PIR; JE0014; JE0014.
HSSP; P04177; 1704.
HSSP; P04177; 1704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF00351; biopterin H; 1.
PRINTS; PR00372; FYWHYDRXIASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:
MIM; 191290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: Catecholamine biosynthesis; first step.
ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1, 2, 3 (SHOWN HERE)
ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: PLAYS AN IMPORTANT ROLE IN THE PHYSIOLOGY OF A NEURONBS.

CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + C dihydroxy-L-phenylalanine + dihydropteridine + H(2)O. COFACTOR: FERROUS ION.

ENZYME REGULATION: PHOSPHORYLATION LEADS TO AN INCREASE CATALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                     SSRFSLWKS-----YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHF 155
                        EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG
                                                     QLRPVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFA
                                                                               SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                            AEEIATWKEVYTTLKGLYATHACGEHLEÄFALLERFSGYREDNIPQLEDVSRFLKERTGF 316
                                                                                                                                                               65; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGNC:11782; TH.
                                                                                                                                                                 Conservative
 -LASLGASDEEIEKLSTLS-
                                                                                                                                                                          11.6%;
                                                                                                                                                                 38;
                                                                                                                                                               Score 220; DB 1; Length 52
Pred. No. 5.3e-10;
Mismatches 104; Indels
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 WFTVEFGLCKONGEVKAYG
                                                                                                                                                                                         Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL outstation
                                                                                                                                                                 36;
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                                                     Query Match
Best Local S
Matches 74
                                                                                                                                                                                                                   EMBL; U14395; AAA62877.1; -.
EMBL; X76209; CAA53802.1; -.
PIR; UN0010; UN0010.
HISSP; P04177; 1TOH.
P1yBase; PEBP10005626; ple.
InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF000351; biopterin H; 1
PRINTS; PR00372; FYHHYDRXIASE.
                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        +
                                                                                                                                                  Neurotransmitter biosynthesis.
METAL 338 338 I
                                                                                                                                                                          TIGRFAMS; TIGRO1269; TYr 3 monoox; 1.
PROSITE; P800367; BIOPTERIM, HYDROXYL; 1.
Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron;
258 EYRAAFQKLQDEQIFVETRLPQLQEMSDFLRKNTGFSLRPAAGLLTARDFLASLAFRIFQ 317
                         128 DYLEAFGLLSD---FLDH-----QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421
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Similarity 508 AA;

11.6%; llarity 28.6%; Conservative 3

37;

Score 219; DB 1; Length 508; Pred. No. 6.1e-10; Mismatches 94; Indels

Gaps

8

57861 MW;

2D194E0E8495E66F CRC64; (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).

IRON IRON

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Neuron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapor Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TY3H DROME STANDARD; PRT; 508 AA.

118459;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UU-1998 (Rel. 36, Last annotation update)
Tyrogine 3-monooxygenase (EC 1.14.16.2) (Tyrogrecine Pale).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neckameyer W.S., Quinn W.G., "Isolation and characterization of the gene for Drosophila tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=90166583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276
                                                                                                                                                                                                                                             CAPALYTIC ACTIVITY: 1-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydroxy-L-phenylalanine + dihydropteridine + H(2)O. COPACTOR: FERROUS ION. PERFOUS ION. PATHWAY: Carecholamine biosynthesis; first step. SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: PLAYS AN I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVLISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=2483109;
Quinn W.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT ROLE IN THE PHYSIOLOGY OF ADRENERGIC
                                moved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Tyrosine 3-hydroxylase) (TH)
                                                                                                                                                                collaboration
                                                                                                                                                            outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNĀ clones.";
Biochemistry 23:5671-5675(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 12-21 FROM N.A.
                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       monooxygenase).
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                                                                                                                                                                                                                                                                                                                                                                                                               Hamdan F.F., Ribeiro P.,
"Cloning and characterization of a novel form of tyrosine hydroxylase from the human parasite, Schistosoma mansoni.";
-! CATALWITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydroxy-L-phenylalanine + dihydropteridine + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: Catecholamine biosynthesis; first step.
-!- SMILMAITY: BELODOGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
HYDROXYIASES PAMILY.
                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH).
               180 IASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKK 239
                                                             292 --NVRVLPLE-----ELVELT 330
                                                                                                                      422 PASTAVQPYQDQEYQPIYYVAESFEDAKDKFRRWVSTMSRPFBVRFN-PHTERVEVLDSV 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 DYLEAFGLLSDFLDH-----QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Platyhelminthes, Trematoda, Digenea, Strigeidida,
Schistosomatoidea, Schistosomatidae, Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88; Indels 41; Gaps
                                             240 QRIQTLOSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFID-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001273; Aaa hydroxylase.
Pfam; PP00321; biopterin H; 1.
TIGRPAMs; TIGR01269; Tyr 3.
PROSTIR; PS00367; BIOPTERIN HYDROXY1; 1.
Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 216.5; DB 1; Length 465; 24.9%; Pred. No. 8.6e-10;
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IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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                                                                                                                                                                                                                                   465 AA.
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                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                      Schistosoma mansoni (Blood fluke).
                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9751167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurotransmitter biosynthesis
                                                                                                                                               331 SKLEWMLDQGLLESIPLYN 349
                                                                                                                                                             481 DKLETLVHQMNTEILHLTN 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 24.9
les 59; Conservative
                                                                                                                                                                                                                                  STANDARD;
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MEDLINE=98421787; Pul
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6183;
                                                                                                                                                                                                                                  TY3H SCHMA
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X-RX CRYSTALLOGRAPHY (2.2 ANGSTROMS).

X-RX CRYSTALLOGRAPHY (2.2 ANGSTROMS).

X-RX CRYSTALLOGRAPHY (2.2 ANGSTROMS).

X-RX CRYSTALLOGRAPHY (2.2 ANGSTROMS).

X-RX CRAINTES I.G., House C.M., Michell B.J., Goodwill K.E.,

X-TANCHIAL Biol. 6:442-446 (1999).

X-TANCHIAL Biol. 6:442-446 (1999).

X-TANCHIAL ACTIVITY. L-phenylalanine + tetrahydrobiopterin + O(2) =

X-TANCHIAL ACTIVITY. L-phenylalanine + tetrahydrobiopterin + O(2) =

X-TANCHIAL ACTIVITY. L-phenylalanine + tetrahydrobiopterin + O(2) =

X-TANCHIAL ACTIVITY. CATANINAL FOR THE MOLECULE.

X-1- COPACTOR: FERRONS ION.

X-1- CATANINAL STEES FOR PHENYLALANINE AND TO CONTAIN

X-1- CATANINAL CATABOLISM OF PHENYLALANINE AND TO CONSTITUTE AN

X-1- CATANINAL CATABOLISM OF PHENYLALANINE AND TO CONSTITUTE AN

X-1- CATANINAL CATABOLISM OF PHENYLALANINE AND TO CONSTITUTE AN

X-1- CATANINITY. BOMONIMER.

X-1- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID

X-1- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID

X-1- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
                                                                                                                                                  274 CTQXIRHHSRPMHTPEPDCIHELIGHMPMLVNRQFADFSQELG-----LASLGASEEEI 327
                                                                                                                                                                                                                                                                                         240 QRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLE 299
                                                                                                                                                                                                                                                                                                                                            180 IASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKK 239
214 EYIDGFQLLEKYCNYNSESIPQLQTICEFMHRTSGFRIRPVAGLVSPKDFLASLAFRVFQ 273
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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MEDLINE-85122617; PubMed=6098294;
Robson K.J.H., Beattie W., James R.J., Cotton R.C.H., Morgan F.J.,
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13-MGC1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
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RESULT 20
PH4H HUMAN
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R PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.

V Oxidoreductase; Monooxygenase; Phosphorylation;
Phenylalanine catabolism; Iron; 3D-structure.

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Matches 61
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EMBL; K02599; AAA41794.1; -.
PIR; A00509; MRRTF.
PIR; A14970; A14970.
PIR; A25321; A25321.
PDB; 1PR7; 30-APR-99.
PDB; 2PHM; 30-APR-99.
InterPro; IPR002912; ACT.
InterPro; IPR001273; Asa_hydroxylase.
Pfam; PF01842; ACT; 1.
Pfam; PF01842; ACT; 1.
Pfam; PF01842; ACT; 1.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH)
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MEDLINE=85199778; PubMed=2986678; Kwok S.C.M., Ledley F.D., Dilella A.G., Robson K.J.H., Woo S.L. "Nucleotide sequence of a full-length complementary DNA clone a mino acid sequence of human phenylalanine hydroxylase.";
                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                   TISSUE=Liver;
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7; Mismatches
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VARIANT PRO-311.

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MEDLINE=88294030; PubMed=2840952;

Lichter-Konecki U., Konecki D.S., Dilella A.G., Brayton K., Maritan T.M., Trefz F.K., Woo S.L.C.;

Hahn T.M., Trefz F.K., Woo S.L.C.;

"Phenylalanine hydroxylase deficiency caused by a single base

"Phenylalanine hydroxylase deficiency phenylalanine hydroxylase
Lyonnet S., Caillaud C., Rey F., BETTHELOH M., LICHLE T. Munnich A.; Munnich A.; "Molecular genetics of phenylketonuria in Mediterranean mutation associated with partial phenylalanine hydroxyla
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Konecki D.S., Lichter-Konecki U.;
"The phenyletonuria locus: current knowledge about
mutations of the phenylalanine hydroxylase gene in v
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Erlandsen H., Flatmark T., Stevens R.C., Hough E.;
"Crystallographic analysis of the human phenylalanine hydroxylase
catalytic domain with bound catechol inhibitors at 2.0-A resolution of the catalytic domain with bound catechol inhibitors at 2.0-A resolution of the catalytic domain with bound catechol inhibitors at 2.0-A resolution of the catalytic domain with bound catechol inhibitors at 2.0-A resolution of the catalytic domain with bound catechol inhibitors at 2.0-A resolution of the category of the catalytic domain with bound catechol inhibitors at 2.0-A resolution of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the category of the categ
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MEDLINE=96174613; PubMed=8594560;
HOANG L., Byck S., Prevost L., Scriver
HOANG L., Byck S., Prevost L., Scriver
"PAH Mutation Analysis Consortium Data
producing and other allelic variation
Nucleic Acids Res. 24:127-131(1996).
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REVIEW ON PKU VARIANTS
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"Structure of tetrameric human phenylalanine hydroxylase implications for phenylketonuria.";
J. Biol. Chem. 273:16962-16967(1998).
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Stevens R.C.;
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MEDLINE-93052278; PubMed-1358789;
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VARIANT LEU-364 DEL.
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Svenstions within the coding sequence of the phenylalanine
"Two muticins within the coding sequence of the phenylalanine
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MEDLINE=92380641; Pubmed=1355066;
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Conservative 44; Mismatches 100; Indels 27; Gaps
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Lin C.H., Hsiao K.J., Tsai T.F., Chao H.K., Su T.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                           VARIANT 364-LEUT-GLUT-368 DEL.
MEDLINE-39258321, PubMed-1363837,
Jarlzelska J., Mell D., Mauuszak R., Borski K., Munnich A.;
"A new 15 bp deletion in exon 11 of the phenylalanine hydroxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guldberg P., Henriksen K.F., Guettler F.;
"Molecular analysis of phenylketonuria in Denmark: 99% of the
mutations detected by denaturing gradient gel electrophoresis.";
Genomics 17:141-146(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 AVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 AGLLSSFGELQYCLSEKPKILPLELEKTAIQNYTVTEFQPLYYVAESFNDAKE 397
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01-AUG-1990 (Rel. 15, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
                                                                                                                                                                                                                                                                                           MEDLINE=93258323; PubMed=1363838;
Desviat L.R., Perez B., Ugarte M.;
"A new FKU mutation associated with haplotype 12.";
Hum. Mol. Genet. 1:765-766(1992).
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MEDLINE=94172999; Pubmed=8068076;
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94010878; PubMed=8406445;
                                                                                                                                                                                                       gene in phenylketonuria.";
Hum. Mol. Genet. 1:763-764(1992)
                                    in Chinese.";
Hum. Genet. 89:593-596(1992).
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     deficiency.";
Am. J. Hum. Genet. 44:511-517(1989).
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DB 1;

Length

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EMBL; X51942; CAA36205.1; -.
PIR; S15758; S15758.
HSSP; P00439; PPAH.
MGD; MGI:97473; Pah.
InterPro; IPR002912; ACT.
InterPro; IPR001273; Aaa_hydroxylase.
Pfam; PF00351; biopterin_H; 1.
Pfam; PF01842; ACT; 1.
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TIGRPAMS; TIGRO1268; Phe4hydrox tetr; 1.
TIGRPAMS; TIGRO1268; Phe4hydrox tetr; 1.
PROSITE; P800367; BIOPTERIM HUDROXYL; 1.
Oxidoreductase; Monooxygenase; Phosphorylation;
Phenylalanine catabolism; Iron; Disease mutation.
Phenylalanine catabolism; Iron; Disease mutation.
Phenylalanine catabolism; Iron; Disease mutation.
Phenylalanine catabolism; Iron; Disease mutation.
Phenylalanine catabolism; Iron; Disease mutation;
Oxidoreductase; Monooxygenase; Phosphorylation;
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MEDLINE=90241147; PubMed=2334400;
Ledley F.D., Grenett H.E., Dunbar B.S., Woo S.L.C.;
"Mouse phenylalanine hydroxylase. Homology and divergence from phenylalanine hydroxylase.";
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MEDLINE=97224471; PubMed=9119379;
MCDOnald JD., Charlton C.K.;
"Characterization of mutations at the mouse phenylalanine hydroxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 277-294.
MEDLINE=85122617; PubMed=6098294;
Robson K.J.H., Beattie W., James
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MEDLINE=80220293; PubMed=7387651;

Wretborn M., Humble E., Ragnasson U., Engstroem L.;

"Amino acid sequence at the phosphorylated site of rat liver phenylalanine hydroxylase and phosphorylation of a corresponding synthetic peptide.";
SEQUENCE
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DNA clones.";
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FA1CD4D0A598E8D9 CRC64
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RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

RA Arlat M., Billault A., Brottier P., Camus J.C., Cunnac S., Demange N.,

RA Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,

RA Gaspin C., Tabbault P., Whalen M., Wincker P., Evy M.,

RA Siguier P., Thabault P., Whalen M., Wincker P., Levy M.,

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RA Weissenbach J., Weissenbach J., Weissenbach J., Weissenbach J., Weissenbach J., Weissenbach J., Weissenbach J., Weissenbach J., Weissenbach J., Weissenbach J., Weissenbach J., Weissenbach J., Weissenbach J., 
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Matches 61
                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                Complete
METAL
                                                                                              EMBL; AL646074; CAD17143.1; -.
InterPro; IPR001273; Aaa_hydroxylase.
Pfam; PF00351; biopterin H; 1.
TIGRPAMs; TIGR01267; Phe4hydrox mono;
PR051TE; PS00367; BIOPTERN HYDROXYL;
Oxidoreductase; Monooxygenase; Phenyla
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PHHA OR RSC3355 OR RS02630.
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IS-JUN-2002 (Rel. 41, Last sequence update)
IS-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
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STRAIN=GMI1000;
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Ralstonia.
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                                                                                                    Monooxygenase; Phenylalanine catabolism;
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Pred. No. 1.7e-09;
5; Mismatches 87
IRON (POTENTIAL).
IRON (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- PATHWAY: Catabolism of phenylalanine; first (rate-limiting) step.
-i- SUBDNT: MONOMER.
-i- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
HYDROXYLASES FAMILY.
-i- CAUTION: Ref.1 sequence differs from that shown due to a
frameshift in position 172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Volner A., Nersissian A.M., Abu-Omar M.M.;
"Expression, isolation, and metal-dependent catalysis of phenylalanine hydroxylase from Chromobacterium diaceum "; submitted (APR-1999) to the EMBL/GenBank/DDBU databases.
-!-CATALYTIC ACTIVITY: L-phenylalanine + tetrahydrobiopterin + O(2) = L-tyrosine + dihydropiopterin + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 12540;
MDDLINE=202011593; PubMed=1655752;
Onishi A., Liotta L.J., Benkovic S.J.;
"Cloning and expression of Chromobacterium violaceum phenylalanine
"Mydroxylases in Escherichia coli and comparison of amino acid sequence
with mammalian aromatic amino acid hydroxylases.";
J. Biol. Chem. 266:18454-18459(1991).
                                                                                                                                                                                                                                                                                        153 --THFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLL 210
                                                                                                                                                            211 HPSFSEFF--INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENH 268
                                                                                                                                                                                                                           108 YRLLSSRFSLWKSYCPR-----FFLDYLEAFGLLSDFLDHQAVIKFFELE---- 152
                                                                                                       50 HRYTAADHATWRTLYDRQEALLPGRACDEFLQGLSTLG-----MSREGVPSFDRLNETLM 104
                                                                                                                                                                                                                                                                     269 BGRKAYGAVLISSPQELGHAFIDNV--RVLPLELDQIIRLPFNTSTPQETLFSIRHFDEL 326
                                             Gaps
                                         95; Indels 44;
         10.6%; Score 201; DB 1; Length 313; 26.2%; Pred. No. 8.6e-09; ive 41; Mismatches 95; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               P30967; Q9XC88; Q9R634;
01-UUL-1993 (Rel. 26, Created)
15-UNN-2002 (Rel. 41, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 1-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromobacterium violaceum.
Query Match
Best Local Similarity 26.2%
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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NCBI_TaxID=536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monooxygenase).
                                                                                                                                                                                                                                                                                                                                     327 VELT 330
                                                                                                                                                                                                                                                                                                                                                                     267 FDAT 270
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PH4H DROME STANDARD; PRT; 452 AA.
PH4H DROME STANDARD; 046110;
P107576; 027599; 0277600; 046110;
16-OCT-2001 (Rel. 15, Created)
15-OCT-2001 (Rel. 40, Last sequence update)
15-UND-2002 (Rel. 41, Last annotation update)
Protein henna [Includes: Phenylalanine-4-hydroxylase (EC 1.14.16.1)
(PAH) (Phe-4-monoxygenase); Tryptophan 5-monoxygenase (EC 1.14.16.4)
(TRH) (Tryptophan 5-hydroxylase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Canton-S, and Oregon-R; TISSUE=Embryo, and Head; 
BRDILNE=25156168, PubMed 1, 
Neckameyer W.S., White K.; 
Neckameyer W.S., white K.; 
"A single locus encodes both phenylalanine hydroxylase and tryptophan 
hydroxylase activities in Drosophila."; 
J. Biol. Chem. 267:4199-44066 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 FLDYLEAFGLLSDFL-DHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 LQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQE----LGHAFIDNVRVLPLEL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 FLEGLERLEVDADRVPDFNKLNEKLMAATGWKIVAVPGLIPDDVFFEHLANKRFPVTWWL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQT 244
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endoperygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Sequence and expression of the Drosophila phenylalanine hydroxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 -----MLARLYWYTVEFGLINTPAGMRIYGAGILSSKSESIYCLDSASPNRV---GPDL
                                                       PPR, averse,
HSSP, P00439; 4PM.
INTERPRO, IPR001273; Aaa_hydroxylase.
InterPro, IPR001273; Aaa_hydroxylase.
Fram, PF00331; biopterin H; 1.
PRINTS, PR00331; PYNHYDRXINE.
TIGRFAMS; TIGR01267; Phethydrox mono; 1.
PR0SITE; PS00367; BIOPTERIN HYDRXINGXVII. 1.
Oxidoreductase; Monoxygenase; Phenylalanine catabolism; Copper.
METAL COPPER (POTENTIAL).
COPPER (POTENTIAL).
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Morales G., Requena J.M., Jimenez-Ruiz A., Lopez M.C., Ugarte M.
                                                                                                                                                                                                                                                                                                                                                                                      33;
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Ruiz-Vazquez P., Moulard M., Silva F.J.;
"Structure of the phenylalanine hydroxylase gene in Drosophila
                                                                                                                                                                                                                                                                                                                                 Query Match 10.4%; Score 196.5; DB 1; Length 297; Best Local Similarity 27.4%; Pred. No. 1.8e-08; Matches 63; Conservative 40; Mismatches 94; Indels 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 DQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQ 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 MRİMNTRYRIDİFQKİYFVİDSFKQLFDAİAP------DFAPLYLQ 264
                                                                                                                                                                                                                                                                                  SEQUENCE 297 AA; 33594 MW; AAA67B6097171FB0 CRC64;
EMBL; M55915; AAA23115.1; ALT_FRAME.
EMBL; AF146711; AAD37774.1; -.
PIR; A40996; A40996.
HSSP; P00439; 4PAH.
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Lih P.W., Hoskins R.A., Galle R.F.,
RA Addams M.D., Celniker S.E., Kichards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pefeiffer B.D.,
RA Man K.H., Doyle C., Baxer E.G., Helt G., Nelson C.R., Miklos G.I.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Bocchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Bocchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Perriara S., Pleischann W.,
RA Fooler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gozrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kinmel B.E. Kodlra C.D., Kraft C. Kravitz S., Kulp D., Lai Z.,
Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Siden-Klamo G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palaska R.
melanogaster and evidence of alternative promoter usage.", Biochem. Biophys. Res. Commun. 225:238-242(1996).
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Matches 73
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EMBL; M32802; AAA699513.1; -.
EMBL; V98116; CAA66797.1; -.
EMBL; X98116; CAA66798.1; -.
EMBL; AJ001718; CAA66798.1; -.
EMBL; AJ001719; CAB51601.1; -.
EMBL; AJ001719; CAB51601.1; -.
EMBL; AJ001720; CAB51601.1; -.
EMBL; AJ001720; CAB51601.1; -.
EMBL; AJ001722; CAB51599.1; -.
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InterPro; IPR002912; ACT.
InterPro; IPR001273; Aaa_hydroxylase.
Pfam; PF00351; biopterin_H; 1.
Ffam; PF01842; ACT; 1.
                                                                                         303
                                     279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD
                                                                                                                                                                                                                                                                                                                                         107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSD---FLDH-----QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                        WGIIFRNLTKLYKTHACR---EYNHVFPLLVDNCGFREDNIPQLEDVSNFLRDCTGFTLR
                                                                                         QEIG------LASLGAPDDYIEKLST-----IFWFTVEYGVCRQEGELKAYGAGL
                                                                                                                                       INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL
                                                                                                                                                                                                                                         PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                     PVAGLLSSRDFLAGLAFRVFHSTQYIRHPSKPMYTPEPDVCHELMGHVPLFADPAFAQFS
                                                                                                                                                                                                                                                                                                                                                                                          Similarity 27.: 73; Conservative
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164
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                                                                                                                                                                                                                                                                                                                                                                                                                 10.3%;
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FK -> LR (IN REF. 2).

YHIESRSSL -> CILSRILAPWF (IN REF. 2).

PGYEFFVEADGKSGALGKAIEDVKEQCSYFNIISRDYKDNA
-> SSCFWRRMENRSLGKSHRGCEGAMLATLTSSCRELQGV
MP (IN REF. 2).
A -> G (IN REF. 2).
A -> G (IN REF. 2).
S -> C (IN REF. 2).
S -> C (IN REF. 2).
CRQ -> LAK (IN REF. 2).
CRQ -> LAK (IN REF. 2).
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Pred. No. 4.9e-08;
9; Mismatches 111;
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990F554150056867 CRC64;
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302

338 346 242

10;

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84 WIVVAVPGLVPDDVFFDHLANRRFPAGGFIRKPHELDYLQEPDIFHDVFGHVPMLTDPVF 143
                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                               331 ----SKLEWMLDQGLLESIP 346
                                                                                                                                                                   : | : | : | : | 249 FGAIYERLASVSDIGVAEIVP 269
                                                                                                                                                                                                                                                     STANDARD;
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P90986;
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SEQUENCE FROM N.A.

STRAIN-ATCC 19089 / CB15;

MEDLINE-21173698; PubMed=11259647;

Nierman W.C., Feldblyuw T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Risen J., Heidelberg J.F., Alley W.R.K., Ohta N., Maddock J.R.,

Potcoka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

A. Rolnay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A. Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

A. Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulboacter crescentus";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

-! CATTVITY. L.-bhenylalanine + tetrahydrobiopterin + O(2) =

-! CATTVITY. Exposine + dihydrobiopterin + H(2)O.

-! CATANINY. BELONGS TO THE BIOPTERIN-DEPENDENT AROWATIC AMINO ACID

HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensegibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
347 LSSYGELEYCLTDKPQLKDFE-----PEVTGV---TKYPITQFQPLYYVADSFETAKE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 ----VSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSF 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caulobacter crescentus.
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
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PRINTS; PR00372; PYWHYDRXLASE.
TIGRPAMs; TIGR01267; PH644bydrax mono; 1.
PROSITE; P800367; BIOPTERIN HYDROXYL; 1.
Oxidoreductase; Monooxygenase; Phenylalanine catabolism; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 10.0%; Score 189.5; DB 1; Length 294; 1 Similarity 24.1%; Pred. No. 6.4e-08; 63; Conservative 43; Mismatches 108; Indels 47;
                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 WKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFE----LETHFSYYP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 134 IRON (POTENTIAL).
294 AA; 32761 MW; A623276FD0506720 CRC64;
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..
                                                                                                                                 294 AA.
                         339 QGL--LESIP----LYNQEKYLSGFEVL 360
                                                      397 KTIKFANSIPRPFGVRYN--AYTQSVEVL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001273; Aaa hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE005836; AAK23591.1; -.
HSSP; P04176; 1PHZ.
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::
                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                           Caulobacter.
NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                                       monooxygenase).
PHHA OR CC1612.
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                                                                                                                                PH4H_CAUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydroxy-L-phenylalanine + dihydropteridine + H(2)O.
-!- COFACTOR: FERROUS ION.
-!- PATHWAY: Catecholamine biosynthesis; first step.
-!- PATHWAY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH).
                                                 275 GAVLISSPQELGHAFID-NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELT--- 330
                                                                                                                                                                                                           :| | | | :| | | :| | 152 QLIHSAELLTQNHVAL----TKFSIFAKKLSDEKNQSQIWFPRHISELDQCSKCITKYE 206
215 SEPPINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Mismatches 114; Indels 85; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Sukaryote, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 KLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQA-LARH-----KCISILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormPep; B0432.5; CE29946.
InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF0031; biopterin_H; Depterin_H; PR0031; PWHYDRXIASE.
PROSTE; PR00367; BT0PTERIN HYDROXYL; 1.
Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.4%; Score 178.5; DB 1; Length 524; Best Local Similarity 24.3%; Pred. No. 9.8e-07; Matches 77; Conservative 41; Mismatches 114; Indels 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Henkhaus J., Wohldmann P.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
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357 351 IRON (BY SIMILARITY).
397 397 IRON (BY SIMILARITY).
524 AA; 59593 MW; 32B106950A629802 CRC64;
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RESULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT PHABULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smye R.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: L-phenylalanine + tetrahydrobiopterin + O(2) =
-:- COFACTOR: FERROUS ION (BY SIMILARITY)
-:- COFACTOR: FERROUS ION (BY SIMILARITY)
-:- PATHWAY: Catabolism of phenylalanine; first (rate-limiting) step.
-:- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
HYDROXYLASES FAMILY.
   TIGRFAMS; TIGRO1268; Phe4hydrox tetr; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYI; 1.
HYDROXTEAL PROCESSE; Monooxygenase; Phenylalanine catabolism; Iron.
METAL 28 28 IRON (BY SIMILARITY).
METAL 290 290 IRON (BY SIMILARITY).
METAL 30 30 IRON (BY SIMILARITY).
SEQUENCE 457 AA; 52129 MW; 68365836DFEC8D4F CRC6
                                                                                                                                                                                                                                                                           EMBL; Z66497; CAA91286.1; -.
HSSP; P04176; LPHZ.
Wormbep; KO8F8 4; CE21050.
InterPro; IPR002912; ACT.
InterPro; IPR001273; Aaa_hydroxylase.
Pfam; PF00151; hopterin_H; 1.
Pfam; PF001842; ACT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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P909252
15-ULL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat.)
Putative phenylalanine-4-hydroxylase (EC 1.
monooxygenase).
K08F8.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELRPCSGLLSARDFLASLAFRVFQTTTYLRHHKSPHHSPEPDLIHELLGHVPMFSDPLL
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                                                                                                                                                                                                                                                      PR00372;
285
290
330
457
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                                                                                                                                                                                                                                                      FYWHYDRXLASE.
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       IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
; 68365836DFEC8D4F CRC64;
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(EC 1.14.16.1)
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EMBL; J03131; AAA28718 1; -.
EMBL; J03131; AAA28719 1; -.
EMBL; M20230; AAA28721 1; -.
EMBL; M20231; AAA28720 1; -.
EMBL; M20331; AAA28720 1; -.
PIR; A29813; A29813
PIR; A29813; B29813
PIR; B29813; B29813
HSSP; P08799; IMND.
FlyBase; FPBP0000719; Euk\_pkinase.
InterPro; IPR000719; Euk\_pkinase.

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Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING. MEDLINE=88151067; PubMed=2449973; Montell C., Rubin G.M.; Wontell C., Rubin G.M.; "The Drosophila minaC locus encodes two photoreceptor c proteins with domains homologous to protein kinases and heavy chain head."; Cell 52:757-772(1988).
                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NINC_DROME STANDARD; PRT; 1501 AA.
P10676; P10677;
01-CCT-1989 (Rel. 12, Created)
01-CCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neither inactivation nor afterpotential protein C (EC 2.7.1.37).
NINAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228
                                                                                                                                                                                                                                                                                                                                                         ACTIVITIES.

CATALYTIC ACTIVITY: ATP + a protein = ADP + a phospho SUBCELLULAR LOCATION: CYTOSKELETON.

ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown short form, are produced by alternative splicing. SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                             SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL FUNCTION. THE NINAC PROTEINS JOIN PUTATIVE SERINE/THREONINE-PROTEIN KINASE AND MYOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVSDFLKDCTGYTIRPVAGLLSSRDFLAGLAFRVFHSTQYIRHHSAPKYTPEPDICHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAESFASAKNKLKSWAATINRPFQIRYNAYTQRVEILDKV 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLE--LDQIIRLPFNTSTPQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGHVPLFADVEFAQFSQEIGLASLGAPDDVIEKLATL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGHVPWLLHPSFSEFFINMGRLF----TKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIEFGICQQDGEKKAYGAGLLSSFGELQYALSDKPEVVDFDPAVCCVTKYPITEYQPKYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 25.5
56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -FSIRH--FDELVELTSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 175.5; DB
Pred. No. 1.4e-06
5; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 two photoreceptor cell specific protein kinases and the myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                             ONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                             THE MYOSIN
                                                                                                                                                                                                                                                                                                                                                                                                            here) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----YWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287
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Schizosaccharomyces pombe (Fission yeast).
                                Marburg virus
                                                                                                                                                                                                                                     RNA (N)
      (L protein).
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Q10144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAS8 SCHPO
ID YAS8 SC
AC 010174,
DT 01-0CT-
DT 15-UUN-
DT 15-UUN-
GN SPACSHI
OS SCHIZO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                            SWART; SMOULD; 149;
PROSITE; PSS0096; 107;
PROSITE; PSS00109; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
Cytoskeleton; Actin-binding; ATP-binding; Myosin; Transferase; Vision;
Serine/threonine-protein kinase; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFRGFRDPVRLPPLVNEKSGQLNENTADFIRPFAKKWREKS
IFQVLLHYRAARF -> GKKTQVDRLREYDEEHIDISETPS
EAEEMFLEARMDEALAAVRIAKIEQASAEE (IN SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1083 FRGFRDPVRLPPLVNEKSGQLNENTADFIRPFAKKWREKSIFQVLLHYRAARFQDFVNLS 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 22.4%; Fred. No. 1.8;
Matches 85; Conservative 58; Mismatches 130; Indels 107; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 GHAFIDNVRVLPLELDQIIRL-----PFNTSTPQETLFSI-----RHFDELVELT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       943 SFHSDVVQQQMKALGVLDTVIARQ---KGFS----SRLPFDEFLRRYQFLAFDFBE--P 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 IASVMRTLDKDNFSLTPDLIHDL-----LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 ALPSKKQRIQTLQSNLIAIVRCFWFTVESGLI-----ENHEGRKAYGAVLISSPQEL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      839 PEMIETFRSSLDESIMLMFTWQLTKAGNLTMP---FEAVQHKDESERKSYALNTLSAGĆI 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 SILEFFKULLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSS-RFSLWKSYCPR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 FF----LDYLEAFGILSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 PKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHK----CI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
15-UNN-2002 (Rel. 41, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (Large structural protein)
                                                                                                                                                                                                                                                                                                                                                                    1136 1501 MISSING (IN SHORT ISOFORM).
253 253 K -> Q (IN REF. 1; AAA28720,AAA28721).
189 1089 P -> R (IN REF. 1; AAA28721).
1501 AA; 174269 MW; D167EABC82A3933A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       896 SQVN-----NLRTLAANFRFTCLTLLKMLSQ---NANLGVHFVRCIRADL--EYKPR
                                                                                                                                                                                                                                                NON ALPHA-HELICAL, C-TERMINAL DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 106.5; DB 1; Length 1501; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                  ACTIN-BINDING (BY SIMILARITY)
                                                                                                                                                                                                                                                              (BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2331 AA
                                                                                                                                                                                                                                                                                         BY SIMILARITY
InterPro; IPR000048; IQ_region.
InterPro; IPR001245; TyT_pkinase.
InterPro; IPR001609; myosin_head.
Pfam; PF00063; myosin_head.
Pfam; PF00069; pkinase; 1.
Pfam; PF000612; IQ; 2.
ProDom; PD000001; Euk pkinase; 1.
ProDom; PD000001; Euk pkinase; 1.
SWART; SM00015; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1143 ------0QVHIYNQ 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 SKLEWMLDQGLLESIPLYNQ 350
                                                                                                                                                                                                                                                                                                                                                                                                                                        5.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRPL MABVP
P35262;
                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                            NP BIND
BINDING
                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 29
RRPL_MABVP
   셤
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                                                                                                                                                                                                                                     MEDLINE=96028047; PubMed=7487490;
Bukreyev A.A., Volchkov V.E., Blinov V.M., Dryga S.A., Netesov S.V.;
Bukreyev A.A., Volchkov V.E., Blinov V.M., Dryga S.A., Netesov S.V.;
"The complete nucleotide sequence of the Popp (1967) strain of Marburg
virus: a comparison with the Musoke (1980) strain.";
Arch. Virol. 140:1589-1600(1995).
-i. PUNCTION: THIS PROFEIN IS PROBABLY A COMPONENT OF THE ACTIVE
POLYMERSAB. IT MAY FUNCTION IN RNA SYNTHESIS,
METHYLATION OF CARBS, AND POLIVE, A) SYNTHESIS.
-i. CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 FCVFKFIVAKNHYHSQGSWYKTTMDLHLTPYLRQHIVSNSFPSQAEIXQHLWEWYFVEHE 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           524 -LGQADFSL--NQILDFAEKLEYLA-PSYRNFSFSLKEKELNIGRTFGK-----LPYR 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 TLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF-----INMGRLFTKVIEKVQALPSK 238
                   ruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
rburg-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 KTIIQGKLTPQQYCELF----SLOKHWGHPVLYIDVALDKVKKHAQSVKILKPKVMFET 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 FKNILLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 EAFGL----LSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMTLARITY: PRIMARILY WITH THE N-TERMINAL HALF OF THE L PROTEINS OF RHABDOVIRUSES AND PARAMYXOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 KYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  471 PLFSTKIISDLSIFIKDRATAVNQECWDSVFDRSVLGYNPPVRFQSKRVPEQF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

5.5%; Score 104.5; DB 1; Length
Best Local Similarity 23.4%; Pred. No. 44.4;
Matches 59; Conservative 42; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; $32776; $32776.
PIR; $44054; $44054.
InterPro; IPRO10105; Viral RNA pol L.
Pfan, PPO0946; Paramyx RNA pol; 1.
Transferase; RNA-directed RNA polymerase.
SEQUENCE 2331 AA, 266635 MW; 7EDID61DDEEF9B8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
15-UTM-2002 (Rel. 41, Last annotation update)
Putative transcriptional regulatory protein C3H8.08c.
8PAC3H8.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X68494; CAA48508.1; -. EMBL; Z29337; CAA82542.1; -.
(strain Popp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                NCBI_TaxID=33728;
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                                                                                                                                                                                                                                                                                                                                                                                   RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Goolins M., Commor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Commor R., Cronin A., Davis P., Feltwell T., Praser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Larris D., Hidalgo J., Hodgson G.,
RA Gentles S., Wones L., Jones M., Leather S., McDonald S., McLean J.,
RA Gentles S., Wolke S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Goliver K., O'Neil S., Pearson D., Ouail M.A., Rabbinowitsch E.,
RA Gliver K., Jones L., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Goliver K., Taylor R.G., Tivey A., Malsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volkaert G., Aert R., Robben J., Grymonprez B.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Galibert F., Aves S. J., Xiang Z., Hunt C., Moore K., Hurst S. M.,
RA Galibert F., Aves S. J., Xiang Z., Hunt C., Moore K., Hurst S. M.,
RA Galibert F., Aves S. J., Xiang Z., Hunt C., Moore K., Hurst S. M.,
RA Galibert F., Aves S. J., Moreno S., Armstrong J., Forsburg S.L.,
RA Gerrutti L., Lowe T., McCombie W.R., Pallsen I., Potashkin J.,
RA Gerrontti L., Lowe T., McCombie W.R., Pallsen I., Potashkin J.,
RA Gerrontti L., Lowe T., McCombie W.R., Pallsen I., Potashkin J.,
RA Grynti L., Lowe T., McCombie W.R., Pallsen I., Potashkin J.,
RA Grynti L., Lowe T., McCombie W.R., Pallsen I., Potashkin J.,
RA Grynti L., Lowe T., McCombie W.R., Pallsen I., Potashkin J.,
RA Grynti L., Lowe T., McCombie W.R., Pallsen J., Potashkin J.,
RA Grynti L., Lowe T., McCombie W.R., Pallsen D., Potashkin J.,
RA Grynti L., 
                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z69086; CAA93165.1; -.
HSSP; P12351; 1PYC.
InterPro, IPRO01138; Fungi_TrN.
Pfam; PF00172; Zn_clus; 1.
SMART; SM00066; GAL4; 1.
PROSITE; PS00463; ZN2_CY6_FUNGAL_1; 1.
PROSITE; PS00468; ZN2_CY2_FUNGAL_2; 1.
Hypothetical protein; Transcription regulation; DNA-binding; Nuclear protein; Zinc; Metal-binding.
DNA BIND 19 45 ZN(2)-CYS(6), FUNGAL-TYPE.
SEQUENCE 563 AA; 64690 MM; C32CDBEA4F84D358 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=972;
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                                            121
                                                                                                                                        67
                                            YCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPI
                                                                                         DKEIIQMLLLRAYATKFRTRIRGVNTDLCRSIHVSTLVTPLF--QVTEKIGKNTSDLWFA
                                                                                                                                      ILEFFKNLLFVHLLSLSKNQREGCSTDM-----AVVSTPFFNRNLWYRLLSSRFSLWKS 120
                                                                                                                                                                                        TLLPIIAATIQLSDLPDVILNFYNSAGI-----TPLESSRLINLKLNEISEQEYKHLCLP 239
                                                                                                                                                                                                                                       TLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCIS 66
                                                                                                                                                                                                                                                                                       80;
                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                       Conservative
·EIDGL-----ECVLKY---RPPFIQHDTYGRLKP-
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                                                                                                                                                                                                                                                                                                        5.4%;
                                                                                                                                                                                                                                                                                       56;
                                                                                                                                                                                                                                                                                                             Score 102; DB 1; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                       142;
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                                            180
                                                                                         297
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Query Match Best Local

Similarity

5.3%;

Score 100.5; DB Pred. No. 3.7;

DB 1;

Length 1157;

CRC64;

Nuclear F TRANSMEM SIMILAR

protein; Transport; M 217 233 98 420

33 POTENTIAL. 20 TO NUP120 (AA 434-763) 133319 MW; C8BDBB7D709C5C08 C Transmembrane.

SEQUENCE

98 1157 ΑĀ,

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RESULT 31
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                                                               EMBL; X80066; CAA56372.1; -.
EMBL; Z27116; CAA81633.1; -.
EMBL; Z28307; CAA82161.1; -.
PIR; S38160; S38160.
PIR; S39123; S39123.
SGD; S0001790; NUP133.
                                                                                                                                                                                                                                                                                                                                           MEDLINE=94262327; PubMed=8203164; Garcia-Cantalejo J., Baladron V., Esteban P.F., Santos M.A., Bou Garcia-Cantalejo J., Baladron V., Esteban P.F., Santos M.A., del Remacha M.A., Revuelta J.L., Ballesta J.P.G., Jimenez A., del Re "The complete sequence of an 18,002 bp segment of Saccharomyces cerevisiae chromosome XI contains the HBS1, MRP-L20 and PRP16 ge and six new open reading frames."; Yeast 10:331-245(1994).

'-- FUNCTION: INVOLVED IN POLY(A) + RNA TRANSPORT AND NUCLEAR POINTED BUTTON.
                                                                                                                                                                                       This SWISS-PROY entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=JUXUR;
MEDLINE=95112817; PubMed=7813444;
Doye V. Wepf R., Hurt E.C.;
"A novel nuclear pore protein Nup133p with distinct roles in poly(A)+
RNA transport and nuclear pore distribution.";
ENBO J. 13:6062-6075(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation update)
Nucleoporin NUP133 (Nuclear pore protein NUP133).
NUP133 OR YKR082W OR YKR402.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
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S K D R B B R S
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MEDLINE=94055391, PubMed=8237108;
MEDLINE=94055391, PubMed=8237108;
MEDLINE=94055391, PubMed=8237108;
Sanchez A., Kiley M.P., Holloway B.P., Auperin D.D.;
Sanchez analyzis of the Ebola virus genome: organization, genetic elements, and comparison with the genome of Marburg virus.";
Virus Res. 29:315-340(1993)
Virus Res. 29:315-340(1993)
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Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
Ebola-like viruses.
                                                                                                  926 ---STIVSLYET-FFNE-----FPKEFSF-----TLFEYLIKHKKLNDLIFRFPQQH 868
                                                                                                                                                                                                                                                                                                               143 QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDL 202
                                                                                                                                                                                                                                                                                                                                                                         DVLIQFFQESA-----PKYGHVAWIQ--QILDGSYADAMNTLKNITVDDSKKGESL---- 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 GLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              957 E--KNISNKLKKGEVQICKRFKNGS-----IREVFVILVEELKSTTVVN 998
   83; Gaps
                                                                                                                                                                                      EGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFL-----DH 142
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                                                              30 NSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNL--LFVHLLSLSKNQR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRPL BBOZM STANDARD; PRT; 2212 AA.

O305316; 039794;
01-FBB-1994 (Rel. 28, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UNM-2002 (Rel. 41, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (Large structural protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       203 LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              918 -----SECELHLINVAKLSSLLVEK------DULDINTLRKIQYNLDTIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99171703; PubMed=10073695; Volchkov V.B., Volchkova V.B., Chepurnov A.A., Blinov V.M., Netesov S.V., Feldmann H.; "Characterization of the L gene and 5' trailer region of Ebola
52; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                999 LSDLVELYSMLD--DEESLFIPLRLLSVDGNLLNFEV 1033
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72; Conservative
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 FFLDYLEAFGL----LSDFLDHQAVI-----KFFELETHFSYYPVSGFVAPHQYLSL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      515 RVPEQF-----LEQENFS-----IENVLSYAQKLEYLLPQYRNFSFSLKEKELNVGR 561
                                                                                                                                                                                                                                                                                                                                                 35 LIRLEMTPQQLCELF----SIQKHWGHPVLHSETAIQKVKKHATVLKALRPIVIFETY- 408
                                                                                                                                                                                                                                                                                                                                                                                                  73 NLLFVHLLSLSKNQREGCSTDMAVVS----TP----FFNRNLWYRLLSSRFSLWKSYCPR 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               463 -HLDHPPLFSTKIISDLSIFIKDRATAVERTCWDAVFEPN-----VLGYNPPHKFSTK 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 LQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWL--LHPSFSEFF-----INMGR 223
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                13 ILKIALKLRQSLSEFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma genitalium.
Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                 DB 1; Length 2212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-156; 269-402; 643-736 AND 808-947 FROM N.A. STRAIN-ANCC 33530 / G-37; SPEDINE-94075230; Pubmed-8253680; Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III; A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                  Indels
EMBL; X67110; CAA47483.1; -.
EMBL, AP086833, AAD14899.1; -.
EMBL, L11365; AABHO07.1; -.
InterPro; IPR001016; Viral_RNA_pol_L.
Pfam; PR00946; Paramyx RNA_pol, 1.
Transferase; RNA-directed RNA polymerase.
SEQUENCE 2212 AA, 252722 WW; SB07EDDC370E2934 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P473<u>7</u>1, Q49190;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                  ch
1 Similarity 23.1%; Pred. No. 8.5;
62; Conservative 42; Mismatchem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 LFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                562 TFGK-----LPYPTRNVQTLCEALLA 582

    Bacteriol. 175:7918-7930(1993).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein MG075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYCGE
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                             CPL1 PANAR
Q27712;
15-DEC-1998
15-DEC-1998
15-JUN-2002
                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Hepatopancreas;
MEDLINE=96201120; PubMed=8619632;
James M.O., Boyle S.M., Trapido-Rosenthal H.G., Smith W.C.,
Greenberg R.M., Shiverick K.T.;
"CDNA and protein sequence of a major form of P450, CYP2L, in
hepatopancreas of the spiny lobster, Panulirus argus.";
Arch. Biochem. Biophys. 329:31-38(1996).
-i- FUNCTION: EFFICIENT IN CATALYZING THE MONOOXYGENATION OF
BENZPHETANINE, AMINOPYRINE, BENZO(A) PYRENE, PROGESTERONE,
TESTOGREFONE
                                                                                                                                                                                                                                                                                                                                                                                                                                   PANAR
 similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
TIGR;
                                                                                                                                                                                                                                                                         Panulirus argus (Spiny lobster).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
Malacostraca; Eumalacostraca; Bucarida; Decapoda; Pleocyemata;
Palinura; Palinuroidea; Palinuridae; Panulirus.
                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 2L1 (EC 1.14.14.1) (CYPIIL1).
                                                                                                                                                                                                                                                          NCBI_TaxID=6737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Transmembrane; Complete proteome TRANSMEM 11 31 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 QNSQSLQRAYSTPYSYYRIILQKENKEK---QALARHKCISILEFFKNLLFVHLLSLSKN 85
                                          TESTOSTERONE.
CATALYTIC ACTIVITY: RH + reduced flav
oxidized flavoprotein + H(2)O.
SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKKEYTFKDNLKFFPFKADGSSRLEFDLSKPDQRVIPFAFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSIRDLFADML-FGKSLESVNDSDSFIKINGSFTLKYHGDNLNLLPNYHSLITKNVGYQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFT-----KVIEKVQALPSKKQRIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQTDSLKNLFSV----IGDILSETNVNKITLHAVKNNELLSLVETASTLKIKHL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----HAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFD 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNVNFHIDARLLTAELQNTVFSNPK-----PVIKSPVELSKSLFEVWKTIFENSVNQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELG-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKKVLFESENYKTLRKKYENEGFPGYHWAKFIVPGTFNSAENTFYSAI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IK--FFELETH-----FSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U39688; AAC71293.1; ALT_INIT.
U01715; AAC43189.1; ALT_INIT.
U02751; AAD12514.1; -.
U01749; AAD10562.1; -.
U01775; AAD10595.1; -.
MG075; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  951 9
1024 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.2%;
ilarity 19.9%;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NVQYKVLVDKFELKNSFIK-----ELLNFFPDTKDITPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116424 MW; 5B1540E6855CB554 CRC64
               TO THE CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 4.6;
41; Mismatches 134; Indels
                                                                      reduced flavoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 98.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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               P450
                                          Endoplasmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               852
                                                                      + 0(2)
                                          reticulum
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                                          (B)
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EXSB\_CHLP 35 EXSB\_CHLP 1D EXSB AC 0927/2 DT 30-M2 DT 16-OC DT 16-OC DE EXODE GN RECB OC Chlan OC NCBI CN [1] RN [1] RN [1] RX MEDLI RX MEDLI RX KALMB RA Oling RA Oling RA Oling RA Oling RA Comp

NCBI\_TaxID=83558;

Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila

SEQUENCE FROM N.A. STRAIN=CWL029;

MEDLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).

EX5B\_CHLPN STANDARD; PRT; 1050 AA. 0927G7; Q952B1; Q9K2F2; 30-MAY-2000 (Rel. 39, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Exodeoxyribonuclease V beta chain (EC 3.1.11.5). RECB OR CEN0738 OR CF0007.

CHLPN

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Best Local S
Matches 74
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Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450; 1.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Electron transport Microsome; Endoplasmic reticulum.
BINDING 436 436 HEME (BY SIMILARITY)
SEQUENCE 492 AA; 56767 MW; F27EE702DD09D5EE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U44826; AAB03106.1; -. HSSP; P00179; 1DT6.
                                                                      313
                                                                                                                                                                                                                                                                                                                     162
                                                                                                                                                                             274
                                                                                                                                                                                                                                                 214
                                                                                                                                                                                                                                                                                                                                                      114 -MWQTH-RRFILRQLRDLGMGKSRLEAAIQHEAACLVQELKKHTDQPMPLPKSINLAVLN
                                                                                                                                                                                                                                                                                                                                                                                     116 SLWKSYCPRFFLDYLEAFGL----LSDFLDHQAVIKFFELETHFSY---YPVS-----
                                                                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 KQALARHKÇISILEFFKNILFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRF 115
  INODTELACYRL 382
                                   YNOEKYLSGFEV
                                                                                                                                                                                                                                                                                  VIWKLVADHRY--SLOOQEGQYFTQLLTTTTDNMQGFAL-----NLFNYLPWLLMITPD
                                                                                                                                                                                                                                                                                                                   ---GFVAPHQYLSLLQD----RYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLL--HPS
                                                                                                                                                                                                                                                                                                                                                                                                                          KTALSKFECSDRPDFYTFKLF------GEGNDVGVV----FSNGV----
                                                                      YLMKYPEVQAKIQREIDAAVPRGTLPSLEHKDKLAYFEATIHEV--HRIVSLVPLGVSHY
                                                                                                                                          -ATLDPSNPKDLLDAYLIDLQERKEDPLSTMNIETVRAVIMDLFGAGTETTSTMIRWTIL
                                                                                                                                                                           YGAVLISSPQELGHAF-----IDNVRVLPL----
                                                                                                                                                                                                              FVKNWMGVRVLRDGVCE-----LKDYMKT---
                                                                                                                                                                                                                                             PSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                     ELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 97;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Electron transport; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
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                                                                                                                                                                                                              ---FIKEHQ----
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SEQUENCE FROM N.A.

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STRAIN=AR39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000212; UwrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
DNA repair; Complete proteome.
NP BIND 21 28
CONFLICT 142 N - V'C'ENTIAL).
CONFLICT 182 142 N - V'C'ENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 LLSDFLDHQAVIKFFELETH---FSYYPVS-GFVAPHQYLSLLQDRYFPIAS------ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 ILDDL--HHFVDLLYTSETHSSLFSFKIAETFNFKHRLA----RYKPCAAFTVLENMS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 -VMRTLDKDNF----SLTPDLIHDL-LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQAL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 WVERTLEFCNLDRIFNTLLVDLQEYLKQNYTPW-LSPDESVF-----ALEKLLSS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 RLIHKNPALTHSQLVLHHITNYLKQDLWKNVLFQEQFHLLAVRYNVTSKHTSSLVDKLLA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 ----VVSTPFFNR-----FG 134
                      MEDIJINE=20150255; PubMed=10684935; MEDIJINE=20150255; PubMed=10684935; Mead T.D., Brunham R.C., Shen C., Glll S.R., Heidelberg J.F., Wated T.D., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gainn M., Nelson M., DeBoy R., Kolonay J., McClarty G., Salzberg S.L. Eisen J., Fraser C.M.; Rollamydia trachomatis Mopn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.1%; Score 97; DB 1; Length 1050;
22.1%; Pred. No. 6.2;
tive 51; Mismatches 117; Indels 104; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 RIILQKENKEKQALARHKCISIL--EFFKNILF---VHILSLSKNOREGCSTDMA---- 95
                                                                                                                                                                                                                                                                                                                                                                      -1- CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5- to 3'-or 3'- to 5'-direction to yield 5'- phosphooligonucleotides.
-1- SUBUNIT: CONSIST OF THREE SUBUNITS; RECE AND RECD (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. UVRD SUBFAMILY.
                                                                                                                                                                                                                  Shiral M., Hirakaw H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiral M., Hirakaw H., Kimoto M., Tabuchi M., Kushi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWLO29 from USA.", Nucleic. Acids Res. 28:2311-2314 (2000).

-!- PUNCTION: REQUIRED FOR EFFICIENT DNA REPAIR; IT CATALYZES THE UNWINDING OF DOUBLE-STRANDED DNA AND THE CLEAVAGE OF SINGLE-STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION.

ALL OF THESE ACTIVITIES REQUIRE CONCOMITANT HYDROLYSIS OF ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 142 N -> K (IN REF. 2).
182 182 V -> I (IN REF. 1).
1050 AA; 121056 MW, 6E2CD03C2AEB83B7 CRC64;
                                                                                                                                  pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                        MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001655; AAD18877.1; -. EMBL; AE002164; AAF37903.1; -. EMBL; AP002547; BAA98945.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 22:1
nes 77; Conservative
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                     236 PSKKORIQTLOSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPOELGH---AFIDN 292
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-1. CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-gluconolistic Christian Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAMY Companies of the CRAM
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MEDLINE=99206666; PubMed=10192388;

MEDLINE=99206666; W., Marathe R., Lammel C., Fan J., Hyman R.W.,

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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
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MEDLINE=20330349; PubMed=10871362;
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Pfam; PF00479; G6PD; 1.
Pfam; PF02781; G6PD_C; 1.
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DT 15-JUN
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ProDom; PD001129; G6PD; 1.

TIGRFAMS; TIGR00871; zwf; 1.

PROSITE; P800069; G6P DEHYDROGENASE; 1.

PROSITE; P800069; G6P DEHYDROGENASE; 1.

OXIGOREGUCTASE; NADP; Glucose metabolism; Complete proteome.

ACT SITE 205 BY SIMILARITY.

SEQUENCE 512 AA; 58739 MW; EABC8DBFRC940FCF COCCA.
MEDLINE-21848401; PubMed=11859360;
MEDLINE-21848401; PubMed=11859360;
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
https://doi.org/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.
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STRAIN=972;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKKS-----PYNLFAAEECSRCPIENDLL-----IIRIQPDE-GVALKFNCKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EW--DQDSSPSFPNY
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18.8%; Pred. No. 2
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Mismatches 124; Indels 177;
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                                                                                                                                                                                                                       RESULT 38
       TEGU_HSV7J
P52362;
01-OCT-1996
01-OCT-1996
16-OCT-2001
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RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

A Taylor K., Taylor R.G., Tivey A., Waish S.V., Warren T., Whitehead S.,

A Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Babel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

A Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

A Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Goffeau A., Cadleu E., Dreano S., Gloux S., Lehaure V., Mottler S.,

A Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Daga R.R., Cruzado I., Jimenez J., Sanchez M., del Rey F., Benito J.,

Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,

"The genome sequence of Schizosaccharomyces pombe.",

"Nature 415:871-880(2002)."
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Best Local
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TRANSMEM 25 42 92
TRANSMEM 72 92
TRANSMEM 130 150
TRANSMEM 241 241
TRANSMEM 269 289
TRANSMEM 365 385
TRANSMEM 365 385
TRANSMEM 39 449
TRANSMEM 429 449
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TRANSMEM 467 487
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 SYCPRFFLDYLEAFGLLSD--FLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRY 177
362 NFQLTLLGMGISSFALLGTVIÍPYLTEYFQLNSLQVVMIISILLPMAÞLÝGLLGÝIPGFE
                                                                                                                                                                                                                                                                                                                                                DDLDSYITNTTIDSSEEEPYLLEHSLILNESAPPADVEDEHKAKIAARLSSVGFGSFFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWSPSSFLLGKIVFLILVDLNFIISOSCYDSF-LPIFLRFYPITR--GPITLESALODET 189
                                                                                                                                                                                                                                                                                                                                                                                                     FPIASVMRTLDKDNFSLTPDLI-HDLLGH-----
                                                                                                                                                                      RKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFN----TSTPQETLFS-----
                                                                                                                                                                                                                               AILFQIIFTPILYKTNNNP-----IILPITVTVCSCWWLILSTPLCTIVTLPVENHSS
                                                                                                                                                                                                                                                                                    -INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGL-----IENHEG
                                                                                                             -DAILTLLYNSVKESYHSFKHAMSISSIRLFLFSRLFINCGIQTSLSSAVIFGKARLNLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 529 AA;
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                                                     -----irhfdelveltsklemmidgelesiplyndekylsgfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58641 MW;
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Pred. No. 3.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F., Benito J., Forsburg S.L., shkin J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72;
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                                                                                                                                                                                                                                                                                                                                                249
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   421
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(Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)

STANDARD;

2059 AA

Page 27

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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
         NCBI_TaxID=5839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87;
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1555 LTTLKSILSVVKSFWKEIINFDLTSYPQGKAEFTFQNVFPIINLKIFIYIITQAMSVTSD 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1324 NTDNIEKLSTLIKQIDPNRIAGGKQKFQDYLSKILTAETNQQ------OTRYKEQLKKQY 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1378 FD--LLDNIAHFRPAFDFNHQQNLILKLKDKFKTLRTDTVFERFPNLDDTFVSSMNVENF 1435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 FFKNL--LFVHLLSLSKNQREGCSTD----MAVVSTPFFNRNLWYRLLSSRF--SLWKSY 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 ELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLE 343
                                                                                                                                                                                                                                                                                                                                                                  r Match
5.1%; Score 96; DB 1; Length 2059;
Local Similarity 20.6%; Pred. No. 18;
les 90; Conservative 62; Mismatches 164; Indels 120; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              13 ILKIALKLRQSLSLFFQNSQS-LQRAYSTPYSYYRIILQKENKEKQALARHK--CISILE 69
                                                                                                                                   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRGUMENT PROTRIN.
-!- SIMILARITY: BELONGS TO PAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLFI, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOP2.
Plasmodium falciparum (isolate K1 / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                            EMBL; U43400; AAC54693.1; -.
SEQUENCE 2059 AA; 239476 WW; AAE6CA6DEDC5D316 CRC64;
                                  Human herpesvirus (type 7 / strain JI) (HHV7).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-FKA-2000 (Rel. 39, Last annotation update)
DNA topotsomerase II (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1398 AA.
                                              Viruses; dsDNA viruses, no RNA st
Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=57278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1654 LİPLLEKKKYFTAFTI 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344 SIPLYNQEKYLSGFEV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
Large tegument protein.
U31.
                                                                                                          SEQUENCE FROM N.A.
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P41001;
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TOP2_PLAFK
TOP2_PLAFK
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DT 01-FEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAKES DOUBLE-STRAND BREAKS.
-!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
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ACT SITE 830 830 DNA CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -: MISCELLANBOUS: EUTATO TOPOISOMERASE I AND II CAN RELAX BOY NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES RELAX ONLY NEGATIVE SUPERCOILS.

-: SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
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161029 MW; BAAD7BEE88FE5BE9 CRC64;
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20.8%; Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of double-stranded DNA.
SUBUNIT: HOMODIMER (BY SIMILARITY).
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Interpro; IPR003597; CBPA MYPB topis.
Interpro; IPR001951; DNA topoisoll.
Interpro; IPR001205; DNA topoisoll.
Pfam; PF00204; DNA GYTASBB; 1.
Pfam; PF00218; DNA topoisolv.
Pfam; PF02518; HATPBAGE c; 1.
PRINTS; PR00518; TPIZFAMILY.
PRINTS; PR00418; TPIZFAMILY.
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POLY-ASN.
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ProDom; PD000742; DNA_topoisoIV; 1.
SWART; SM00433; TOP2c; 1.
SWART; SM00434; TOP4c; 1.
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HSSP; P06786; 1BGW.
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-!- SUBCELLULAR LOCATION: Nuclear.
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Best Local :
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PIR; 319496; S19495.
PIR; S19495; S19495.
TRANSFAC; T02152; -.
SGD; S000677; SRBB.
InterPro; IPR000651; RasGBFN.
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15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Suppressor of RNA polymerase B SRB8.
SRB8 OR YCR081W OR YCR81W/YCR80W.
Saccharomycee cerevisiae (Baker's yeast).
Saccharomycee Cerevisiae (Baker's yeast).
Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Hengartner C.J., Thompson C.M., Zhang J., Chao D.M.,
Koleske A.J., Okamura S., Young R.A.;
"Association of an activator with an RNA polymerase
Genes Dev. 9:897-910(1995).
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P25648; P2
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Feldmann H., Mannhaupt G., Vetter I.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-530 FROM N.A. Ballesta J.P.G., Franco L.,
                                                                                                                                                                                                         SEQUENCE
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                                   12
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FUNCTION: COMPONENT OF THE RNA POLYMERASE
MEDIATOR OF ACTIVATION SUBCOMPLEX.
SUBCELLULAR LOCATION: Nuclear (Probable).
   YILKIALKLROSLSLFFQNSQSLQRAYSTPYSYYRII-----LQKENKEKQALARHKCI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFKGRIESNGKTGYETIGIINKIDNDTLEITELPIK-KWTQDYKEFLEE--LLTDEKH 973
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                                                                                       l Similarity 18.8
98; Conservative
                                                                                                                                                                                                      protein.
E 1427
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                                                                                                              18.8%;
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                                                                                                                 Score 95;
Pred. No.
                                                                                          Mismatches
                                                                                                                                                                                                         776A2A9D82E331FE CRC64;
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II HOLOENZYME
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                                                                                                                                           Length 1427;
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Rhabditidae; Pelode
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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
fining transformer protein 2 precursor.
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EMBL; U39690; AAC71314.1; -. EMBL; U01713; AAC43186.1; -. EMBL; U01762; AAD10577.1; -.
                                              Hypothetical protein MG096.
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Pfam; PF03086; DUF240; 1
                                                                                       NCBI_TaxID=2097;
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SEQUENCE 65
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                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIMILARITY: TO MEMBRANE PROTEIN PATCHED OF D.MELANOGASTER.
                                                                                                                                                                                                                                                                                                                                                        1475 AA; 170352 MW; F8C6456B3D3654BE CRC64;
                                                                                                                                                                      Transmembrane; Receptor; Signal.
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POTENTIAL.
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                                                                                                               EMBL; M91371; AAA28150.1; -.
EMBL; S42187; AAB22845.1; -.
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SEQUENCE FROM N.A.

MEDLINE=96026346, PubMed=7569993;

MEDLINE=96026346, PubMed=7569993;

MEDLINE=96026346, PubMed=7569993;

Flatesc C.M., Googyne J.D., White O., Adams M.D., Clayton R.A.,

Flateschmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Roydon D.T., Utcherback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Boct K.F., Hu P.-C., Lucier T.S.,

Fleterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D. Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchmann R.D. Bult C.J., Kerlavage A.R., Satton G., Kehley J.M., Fritchman J.L., Weidman J.F., Saudek D.M., Phillips C.A., Merrick J.L., Nouyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Pererson S.N., Smith H.O., Hutchison C.A., III, Venter J.C.; Lucier T.S., Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
4.9%; Score 93.5; DB 1; Length 650;
Best Local Similarity 18.6%; Pred. No. 6.4;
Marches 59; Conservative 53; Mismatches 128; Indels 77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TPFFNRNLWY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 LEKETDYDQNFKSFTEKFKDEKITNNQLGIVDIYNLFSGF--HKSVKSTVDLMNQLQKQV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 ETHFSYYPV-SGFV----APHQYLSLLQDRYFP------IASV-----MRTLDK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wycoplasma genitalium.Bacteria; Firmicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A. STRAIN-ATC 33530 / G-37; MEDLINE-94075230; PUNMED-8253680; Hutchison C.A. III; Peterson S.N., H P.-C., Bott K.F., Hutchison C.A. III; "A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequencing.";
J. Bacteriol. 175:7918-7930(1993).
J. Bacteriol. 175:7918-7930(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 protein, Complete proteome.
650 AA; 74802 MW; 30539DDC6F69DDC3 CRC64;
P47342; Q49188;
01-FEB-1996 (Rel. 33, Created)
30-MAX-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 ILEFFKNLLFVHLLSLSKNQREGCSTDMAVVS-----
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InterPro; IPR004306; MG032/096/288_1.
InterPro; IPR004319; MG032/096/288_2.
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SOURCE STORY OF STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET 
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Best Local Similarity
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Praser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherry B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
"The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
                                                                                                                                                      CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U39686; AAC71283.1; -.
EMBL; U02154; AAD12436.1; -.
TIGR; MG065; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing.";
J. Bacteriol. 175:7918-7930(1993).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94075230; PubMed=8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison
"A survey of the Mycoplasma genitalium genome
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                               SEQUENCE
                                                                                                                                                                                         PROSITE; PS00211; ABC TRANSPORTER; 1.

Hypothetical protein; ATP-binding; Transport; Complete NP_BIND 269 276 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 393-466 FROM N.A. STRAIN=ATCC 33530 / G-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCBI_TaxID=2097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSNLIAI-----VRCFWFTVESGLIEN-----HEGRKAYGAVLISSPQELGHAFIDNVR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNFDLAFLRKADVIIKDKVRYNFEMQMQFQTVYVGGGNTVINLDFTLKAQTVNFANLQDL
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                                                                                                                                                                                                                                                                                                SM00382; AAA;
                                                                                                               466 AA;
                                                                                                           399 (
54009 MW;
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    4.9%;
                                                                                                               GDEPTG -> WWWTYW (IN REF. A585044B8A90391C CRC64;
    Score 92.5;
Pred. No. 5
                                      DB 1; Length 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.A. III;
by using random
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FILE III 44

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Best Local S
Matches 54
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    72
                                                                             18
                                                                                                                                                  13
        K-----PILFVHLLSLSKN-----QREGCSTDMAVVSTPFFNRNLWYRLL--
                                                                             IIKFTVRLRK-----TESLOKDIESALPSYKVVVSPFKNQEVSLFDRYE----ETH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61,
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FLP KLULA
P13783;
01-JAN-1990
01-JAN-1990
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDILINE=68232585; PubMed=3520486;
Chen X.J., Saliola M., Falcone C., Bianchi M.M., Fukuhara H.;
Chen X.J., Saliola M., Falcone C., Bianchi M.M., Fukuhara H.;
Requence organization of the circular plasmid pXD1 from the yeast
Kluyveromyces drosophilarum.";
Nucleic Acids Res. 14:4471-4481(1986).
Nucleic Acids Res. 14:4471-4481 (1986).
                                                                                                                                                                                                              PIR; S28086; S28086
DNA recombination;
ACT_SITE 336
                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             riasmid pKD1.
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinase
                                                                                                                                                                                                                                                                                         EMBL; X03961; CAA27591.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPETITIONS OF THE PLASMID.
SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GITTNAVLKGVDLAIKSHDFIVILGPSGSGKTTLLNI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLIENHEGR-----KAYGAVLISSPQELGHAFIDNV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKKQEILLNNWENSNERLFLKNEVKKVNWLNSPRQKQQAAQIDDQNIIELKNVYKY-ITN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFEKKLFEATOOFNNLEK-NTAISDDLPLOFKVRTTOLKAORERELKNLLNKIK-LKNLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYYDRFFITKYNHYSLSLLFSFINEQ-----IETVIASY--NSFLNEHNKLAFNKVSF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWK-----
ILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQK-ENKEKQALARHKCISILEFF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----FSEFFINMGRIFTK-VIEKVQALPSKKQRIQTLQ---SULIAIVRCFWFTVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYCPRFFLDYLE--AFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSL----- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEESQNYLQKGLKQLKKEYKRSI------IYNPNLEYK----RFVKWKENFTETFE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LQDRYFPIASVMRTLDKDNFSLTPDL----
                                                                       Similarity
                                                                                                                                               447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 13, Created)
(Rel. 13, Last sequence update)
(Rel. 40, Last annotation update)
FLP protein.
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                                                 Conservative
                                                                                                                                                                                                                                                                   S28086.
                                                                                                                                            ΑA,
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                                                                                                                                                                                      DNA integration; Plasmid.
TRANSIENT COVALENT LINKAGE
STRAND CLEAVAGE AND REJOINI
                                                                                                                                               51110 MW;
                                                                       4.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                 37;
                                              Score 92; DB 1;
Pred. No. 5.2;
7; Mismatches 8
                                                                                                                                                                  STRAND CLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                               89D08AB52718A104 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                 82;
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                                                                                             Length 447
                                                                                                                                                                                              REJOINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                 DNA DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                 Gaps
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                                                 12;
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-SS 113

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EMBL; X86563; CAA60266.1; -.
MaizeDB; 118213; -.
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                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast; mRNA F
SEQUENCE 544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays (Maize).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chloroplast
                                                                                                                                                                                                                                                                                            MATK MAIZE
P48190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                |:| |: || |: || | :: : |
185 RYSDLKNLDPRTFEIYNNSF--LGPIVRATVTETKSRTERYVNFYPVNGDCDLLISLYDY 242
114 RFSLWKSYCPRPFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSG----FVAPHQY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Bassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 YRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELFTHFSYYPVSGFVAPH 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 QCYFSVWFQSQKVNINQLSKDNLEFLGYLSSLRLNPLVVRSQMLE-----NSFLIDN 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 HKCISILBFFKNLL--FVHLLSLSKNQ-----REGCSTDMAVVSTP-----FFNRNLW 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 ----IHHFFKVFVNNFPAILGLLKDPFIHYVRYHGRCILATKDTPLLMNKWKYYFVNLW 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 HVCE------YESIFFFLRKRSHLRSTSYEVLFERIVFYGK------ 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 HYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SINTLARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thalfana.";
DNA Res. 6:283-290(1999).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Columbia;
MEDLINE=20039611; PubMed=10574454;
Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
"Complete structure of the chloroplast genome of Arabidopsis
                                                                                                                                                                                                                    243 L-----RVCSPIEKTVSSNRPTNQTHQFL---PESLARTFSRF 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.9%; Score 92; DB 1; Length 526; Best Local Similarity 22.1%; Pred. No. 6.4; Matches 65; Conservative 35; Mismatches 118; Indels
                                                                                                                                                                                  170 LSLLODRYFPIASVMRTLDKDNFSLTP-DLIHDLLGHVPWLLHPSFSEF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chloroplast; mRNA processing.
SEQUENCE 526 AA; 63038 MW; 4798486C56ACC011 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        526 AA.
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Chloroplast.
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InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; Mark N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; Mark N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                 168 QYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGH----VPWLLHPSFSEFFINMGR 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 LEYRSQDVPSLHLLRFFLYYYSNWNSFITSMKSI-------FLLKKENKRLFRFL 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 MDPLMHYVRYQGKAILASKGTLLIKKKWKSYLVNFSQYFFSFWTQPQRIRLNQLTNSCFD 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-95395841; PubMed=7666415; MEDLINE-95395841; PubMed=7666415; Maier R.M., Neckermann K., Igloi G.L., Koessel H.; Maier equence of the maize chloroplast genome: gene content, hotspots of divergence and fine tuning of genetic information by
                                                                                                                                                     224 LFTKVIEKVOALPSKKOR-----IQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                  429 ICRNISHYYSGSSKKKNLYRIKYILRLCCVKTLARKHKSTVRTFLKRLGSGLLE 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcript editing.";
J. Mol. Biol. 251:614-628(1995).
-i- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
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18.6%; Pred. No. 6.7;
Live 64; Mismatches 140; Indels 116;
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01-FEB-1996 (Rel. 33, Last sequence update)
115-JUN-2002 (Rel. 41, Last annocation update)
Probable intron maturase (Maturase K).
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InterPro; IPR002865; Matk N.
Pfam; PP01348; Intron_maturas2; 1.
Pfam; PP01824; Matk N; 1.
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Cladaras C., Hadzopoulou-Cladaras
Zannis V.I.;
"The complete sequence and structuments of the complete sequence and structuments of the complete sequence and structuments."
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Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
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B-100.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-88003974; PubMed=3652907;
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Deeb S.S., Motuls
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MEDLINE=87041416; PubM
Law S.W., Grant S.M., I
Lee N., Brewer H.B. Jr
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[3]
SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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MEDLINE=88003974;
                                                                                               apolipoprotein
forms.";
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"Human liver apolipoprotein B-100
"Aderived amino acid sequence.";
" c a 83;
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                                         OF 709-906
F 709-906 FROM N.A.
270450; PubMed=3860836;
Motulsky A.G., Albers
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Yang C.-Y., Chen P.-F.,
Jr., Chan L.;
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.M., Higuchi K.,
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Sci. U.S.A.
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Primates;
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ionship between
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Catarrhini; Hominidae;
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CHYLOMICTON'S ADOLIC PROPORTEN BY THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY APOLLEPPROPIEN B-100 (FDB). IT IS A DOMINANTLY INHERITED DISRABER OF LICEPARTICLES BY DEFECTIVE AND INTERNALIZATION AND INCREASED PRONENESS TO CORONARY ARTERY DISEASE (CAD).

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McCarthy B.J.;
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MARIANTS FDB GLN-3527 AND CYS-3558.
MEDLINE=97403938; PubMed=9259199;
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Hum. Genet. 102:44-49
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                             12;
                                                                                                                             4211 YTREELCTMFIREVGTVLSQVYSKVHNGSEIL-----FSYFQDLVITLPFE----L 4257
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STRAIN=JAL.1 / DSM 2661 / ATCC 43067;

STRAANN=JAL.1 / DSM 2661 / ATCC 43067;

Bult C.J. White O., Olsen G.J., Zhou L., Fleischmann R.D., Mante O., Olsen G.J., Zhou L., Fleischmann R.D., Raich C.J., White O., Olsen G.J., Firzderald L.M., Clayton R.A., Gocayne J.D., Serlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A., Stott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberte K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- CAPLYTIC ACTIVITY: S-adenosylmethioninamine + putrescine = 5'-methylthioadenosine + spermidine.
--- PATHWAY: FIETH (LAST) SIEP IN THE BIOSYNTHESIS OF SPERMIDINE FROM ARGININE AND METHIONINE.
--- SIMILARITY: BELONGS TO THE SPERMIDINE/SPERMINE SYNTHASES FAMILY.
                                                                                                                                                                                60 ARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                             68; Gaps
                                                                             3 YCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYR---IILQKENKEKQAL 59
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20.7%; Pred. No. 99; ive 48; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                        167 -----HQYLSLLQDRYFPIASVMRT----LDKDNFSLTPDLI-----
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01-NOV-1997 (Rel. 35, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Probable spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase) (SPDSY).
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Archaea; Euryarchaecta; Methanococci; Methanococcales;
Methanacaldococcaees; Methanocaldococcus.
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InterPro; IPR001045; Sprmine synthase.
Pfam: PF01564; Spermine_synth; 1.
TIGRPAMS; TIGR00417; speE; 1.
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Best Local S
Matches 46
                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=93227570; PubMed=8470368;

MOTI T. Sasaki K., Hashimoto H., Makino S.;

MOTI T. Sasaki K., Hashimoto H., Makino S.;

"Molecular cloning and complete nucleotide sequence of genomic RNA

"Molecular cloning and complete nucleotide sequence of genomic RNA

"the AIK-C strain of attenuated measles virus.";

Virus Genes 7:67-81(1993).

-i- PUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY

FUNCTION IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A)

SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAS, RNA EDITING OF THE

GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.

-i- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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P35975;
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Spermidine |
DOMAIN
EMBL; S58435; AAB26147.1; -.
PIR; G48556; G48556.
InterPro; IPR001016; Viral RNA pol L.
Pfam; PF00946; Paramyx_RNA_pol; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994
01-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                    Paramyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                     Measles virus (strain AIK-C) (Subacute sclerose panencephalitis
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=36408;
                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA negative-strand viruses; Mononegavirales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 -- PAKGLPEKEFYKNVFKCLN-----DDGIMVQQSESPLYNLDLIQNICRYLKDAGFKI 221
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                                                                                                                                                               SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES
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46; Conserv
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biosynthesis; Transferase; Complete proteome.
B5 126 BINDING TO DECARBOXYLATED SAM
(POTENTIAL)
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(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
ase beta subunit (EC 2.7.7.48) (Large
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Pred. No. 3
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P12576; 01-OCT-1989 01-OCT-1989

MEASE

MEASE

STANDARD;

PRT;

2183

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01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-OTN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)

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Query Match
Best Local
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SEQUENCE 2
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726 PNDQIFIKYPMGGIEGYCQ 744
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                                    -NQE--
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                                                                                                                                             GPVLKTYSRSPVHTSTRNVRAAKGFIGFPQVIRQDQDTDHPENMEAYETVSAFITTDLKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; RNA-directed RNA polymerase.
2183 AA; 247754 MW; 12A6686F4CA62199 CRC64;
                                  KY-LSGFEVLCQ 362
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Pred. No.
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Gattaneo R., Schmid A., Spielhofer P., Kaelin K., Baczko K., Meulen V., Pardowitz J., Flanagan S., Rima B.K., Udem S.A.; "Mutated and hypermutated genes of persistent measles viruses which caused lethal human brain diseases.";
Virology 173.415-425(1989).
-i- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY FUNCTION IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A) SYNTHESIS OF MEMLY SYNTHESIS OF THE ACTIVITY.

GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.
-i- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + {RNA}(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dowling P.C.;
"Measles virus L protein evidences elements of ancestral polymerase.";
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Blumberg B.M., Crowley J.C., Silverman J.I., Menonna J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virusės; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
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                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90085790; PubMed=2596022;
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                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Inestitute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

4.8%; Score 91; DB 1; Length 2183;
Best Local Similarity 20.6%; Pred. No. 47;
Matches 78; Conservative 46; Mismatches 119; Indels 136; Gaps
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EMBL; K01711; AAA75501.1; -.
PIR; A28919; ZLNZMV.
PIR; A28919; ZLNZMV.
PICEPPC; IPRO01016; Viral_RNA_pol_L.
Pfam; PF00946; Paramyx, RNA_pol; 1.
Transferase; RNA-directed RNA polymerase.
SEQUENCE 2183 AA; 247646 MW; IBOB03CA2E2B6EA5 CRC64;
-!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
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Drosophila melanog Phenylalanine hydr

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Chlamydia pneumoni
Chlamydia pneumoni
Protein encoded by
phhAB fusion prote
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Neurone specific t
Rat tyrosine hydro
Rat tyrosine hydro
Human tyrosine hydro
                                                                                                       January 9, 2003, 11:51:03 ; Search time 65 Seconds (without alignments) 742.103 Million cell updates/sec
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Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes

Claim 1; Page 134; 364pp; English.

WPI; 2002-154726/20. N-PSDB; ABL91284.

Ratti G,

Grandi G;

(CHIR-) CHIRON SPA.

03-JUL-2000; 2000GB-0016363. 11-JUL-2000; 2000GB-0017047. 21-JUL-2000; 2000GB-0017983. 07-AUG-2000; 2000GB-0019368. 18-AUG-2000; 2000GB-0020440. 14-SEP-2000; 2000GB-0027549. 10-NOV-2000; 2000GB-0031706.

W0200202606-A2 Chlamydia pneumoniae.

10-JAN-2002.

03-JUL-2001; 2001WO-IB01445

Chlamydial infection; antigen; immunogen; vaccine; diagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; cardoid artery stenosis; myocardial infarction; cerebrovascular disease; aortic aneurysm; claudication; stroke;

Chlamydia pneumoniae cp7380 protein, SEQ ID NO:201.

29-JUL-2002 ABB90626;

(first entry)

ABB90626 standard; Protein; 362

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AB890626 AB990626 AB890626 AB890626 AB890626 AB990626 AB890626 AB9 Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia Cpneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia commoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as commonial infarction, cerebrovascular disease, carotid artery stenosis, composition, cerebrovascular disease, aortic aneurysm, calcular disease and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydia linfections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of Chlamydia pneumoniae proteins dispersent sequence represents a pneumoniae gene expression. The present sequence represents a composition of the invention composition of compositions of the probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a composition of the invention. Query Match Best Local S Matches 362 Sequence itch 100.0%; Score 1889; DB 23; Length 362; sal Similarity 100.0%; Pred. No. 8.6e-182; 362; Conservative 0; Mismatches 0; Indels 0; 362 AA; 0,

ALIGNMENTS

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1 VHYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALA 60

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                                                                                                                                                                                      173 AVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEW 232
                                                                                                                                                               156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
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                                                                                  96 VVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHF 155
                                          11; Gaps
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                                                                                                              4 WYSTPFLIVFSMEKLLS------KIFLDYLEAFGLLSDFLDHQAVIKFFELETHF
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Query Match 66.2%; Score 1250.5; DB 20; Length 259; Best Local Similarity 91.8%; Pred. No. 1.3e-117; Matches 245; Conservative 3; Mismatches 8; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by pFUSAB vector DNA insert sequence.
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/label= Junction_peptide
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/label= Linker_peptide
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/label= phhB protein
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/label= phhA protein
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/label= Lacz_peptide
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Chimeric - Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory diseases such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent critis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae specially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                            240
61 RHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFPNRNLWYRLLSSRFSLWKS 120
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                                                                                                                                                                                                                                               241 RIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL 300
                                                                                                                                                                                                                                                                                                                              301 DQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL 360
                                                          121 YCPRFFLDYLEAFGILSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSILQDRYFPI 180
                                                                                                                                                                                                                          RIQTLOSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL 300
                                                                                                                                                                                                                                                                                                       DQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEXYLSGFEVL 360
                                                                                                                                                                    181 ASVARTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ
                                                                                                                                          ASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae transmembrane protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 1410-1411; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY35703 standard; Protein; 259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-IB01890.
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97FR-0014673,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia pneumoniae.
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21-NOV-1997;
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Griffais R;

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses novel cells comprising a nucleic acid encoding CC a gene product having phenylalanine hydroxylase (PAH) activity such CC as phenylalanine hydroxylase (phhA). 4-carbinolamine debydratase (phhB) and aromatic aminotransferase (phhC), which are derived CC from a prokaryotic organism. The patent also relates to fusion proteins comprising a protein enhancing and/or stabilising the proteins comprising a protein enhancing and/or stabilising the PAH activity in addition to PAH activity. The cells are useful CC for preparing a protein derived from casein, globulin or a whey protein CC as a milk protein derived from casein, globulin or a whey protein CC as a milk protein derived from casein, globulin or a whey protein having reduced content of phenylalanine. The method involves contacting the food product starting material with the cells or fusion proteins CC such that at least part of the phenylalanine content of the starting material is converted into compounds that do not cause phenylated for methodic disorder resulting in an accumulation in the body of methodic disorder resulting in an accumulation in the body of function. The present sequence is a protein encoded by pFUSAB vector DNA insert sequence. This sequence comprises a lacz peptide from CC Escherichia coli, a linker peptide and phhA and phhB proteins.
                                                      Phenylalanine hydroxylase; PAH; phhA; 4a-carbinolamine dehydratase; ph aromatic aminotransferase; phhC; milk protein; animal protein; casein; proteinaceous food product; globulin; whey protein; phenylketonuria; PKU; inherited metabolic disorder; impaired brain function; nootropic; cell therapy; phhAB fusion protein.
                       Unidentified
                                                                                                                                                                                                                                                                                                             AAE11161 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product having phenylalanine hydroxylase activity, that is derived a prokaryotic organism, is useful for treating phenylketonuria in
                                                                                                                                                                                   phhAB fusion protein fragment.
                                                                                                                                                                                                                              18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 5; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                               232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 SILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRF 125
                                                                                                                                                                                                                                                                                                                                                                                                               PLE---AMRTPYRIDILQPLYFVLPDLKRLFQLAQE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ER---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFID---NVRVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLDGIEQLG-----LPHERIPQLDEINRVLQATTGWRVARVPALIPFQTFFELLASQQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLDYLEAFGLLSDFLDHQAVIKFFELE-----THFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVLEFGFKLKTTQYVARQPD------DNGFIHYPETEHQVWNTLITRQLKVIEGRACQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VFLARLYWMTIEFGLVETDQGKRIYGGGILSSPKETVYSLSDEPLHQAFN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        429 AA;
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                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                             Protein;
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Pred. No. 4.4e-15;
6; Mismatches 114;
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153 81

RVLQATTGWRVARVPALIPFQTFFELLASQQFPVATFIRTPEELDYLQEPDIFHEIFGHC 140

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DMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELE 152 DIGFIHYPETEHQVWNTLITRQLKVIEGRACQEVLDGIEQLG-----LPHERIPQLDBIN ----THESYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV 206

Query Match Best Local S Matches 61

Similarity 24.9 51; Conservative

12.5%;

52;

Score 235.5; DB 22; Pred. No. 5.9e-15; 2; Mismatches 103;

Indels Length 415;

33;

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80

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The patent discloses novel cells comprising a nucleic acid encoding a gene product having phenylalanine hydroxylase (pAH) activity such as phenylalanine hydroxylase (phAH), 4a-carbinolanine dehydratase (phAH) and product having phenylalanine hydroxylase (phAH), 4a-carbinolanine dehydratase (phAH) and product and protein comprising a protein enhancing and/or stabilising the pAH activity in addition to pAH activity. The cells are useful for producing pAH. The sequences of the invention are also useful for producing a protein access food product (animal protein such as a milk protein derived from casein, globulin or a whey protein for a manufacturing material with the cells or fusion protein such hat at least part of the phenylalanine content of the starting material is converted into compounds that do not cause phenylatering material is converted into compounds that do not cause phenylatering material is converted into compounds that do not cause phenylatering material is converted into compounds that on the susful for manufacturing a medicament for treating PKU, which is an inherited metabolic disorder resulting in an accumulation in the body of Lybenylalanine and metaboliting in an accumulation protein fragment.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel recombinant cells comprising a nucleic acid encoding a gene product having phenylalanine hydroxylase activity, that is derived from a prokaryotic organism, is useful for treating phenylketonuria in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-590055/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-2000; 2000US-0525116.
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Fig 18; 91pp; English.
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Jensen SH,
  415 AA;
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295..336
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353..380
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228..2
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55..90
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...415
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Gjetting
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F, Nielsen
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
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                                                                                                                                                                                                                                                                                                                  107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                               174 WGTVPQELNKLYPTHACR----EYLKNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR 230
                                                                                                                                                                                                                                                                                    159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                               219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                       27; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Yang Y, Wejhrman T, Goodrich R;
                                                                                  Query Match
12.3%; Score 231.5; DB 22; Length 444;
Best Local Similarity 27.8%; Pred. No. 1.6e-14;
Matches 64; Conservative 43; Mismatches 96; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 LSSISELKHALSGHAKVKPFDPKITCKQECLITTFQDVYPVSESPEDAKE 384
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were missing at the time of publication
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27-APR-2000; 2000US-0560875.
20-UTM-2000; 2000US-0598075.
19-UTU-2000; 2000US-0620325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0654936.
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30-NOV-2000; 2000US-0728422
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                                              444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAK52341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM79208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SXS
                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
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                                                                                                                                                                                                                                                                                                                                셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynecleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissum growth factor activity, immunomodilatory activity and activity, tissum growth factor activity, immunomodilatory activity and activity, tissum growth factor activity, immunomodilatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                      PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIB 266
                                                    267 NHEGRKAYGAVLISSPQELGHAFID---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHF 323
                                                                                                                                            : | : : | : : | | : | | : | | : | | 106GKIYGGILSSPKETVYSLSDEPLHQAFNPLE---AMRTPYRIDILQPLYFVLPDL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cao Y,
ng ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Ca
Wang D, Wang J, Zhang J, Ren F, Chen R, Wang
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 446-447; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                               AAM80192 standard; Protein; 444 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
20-UNN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0620325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-065351.
20-OCT-2000; 2000US-063325.
30-NOV-2000; 2000US-059325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein SEQ ID NO 3838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-FEB-2001; 2001WO-US04098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-476283/51.
                                                                                                                                                                                                            324 DELVELTSK 332
                                                                                                                                                                                                                                                        242 KRLFOLAGE 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAK53325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157190-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAM80192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xue AJ,
                                                                                                                                                                                                                                                                                                                                RESULT 5
AAM80192
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CCCCCCCCCCCCX8X414X8X1111X4X8888888X6X6X8X8X8X8X8X8X8X8X8

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PRODUCTION OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE O
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Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. Stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activity. Infinity in activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuronal tryptophane hydroxylase; nFPH; neuronal disease; primary haemostasis deficiency; allergy; transplantation; serotonin; antiarteriosclerosis; thrombolytic; anticoagulant; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiallergic; gynaecological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurone specific tryptophane hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                         Claim 21; Fig 9; 21pp; German
                                                                                                and treating primary hemostatic des
activity of tryptophan hydroxylase
                                                                                                                                                            Regulating levels of serotonin, useful for diagnosing neuronal disease and treating primary hemostatic deficiency, comprises controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-AUG-2000; 2000DE-1043124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-2001; 2001WO-DE03178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200217891-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO17329 standard; Protein; 434 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 LSSISELKHVLSGHAKVKPFDPKITCKQECLITTFQDVYFVSESFEDAKE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                    2002-281015/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEIG-----LASLGASEEAVOKLAT-----CYFFTVEFGLCKQDGQLRVFGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVAGYLSPRDFLSGLAFRVFHCTQYVRHSSDPFYTPEPDTCHELLGHVPLLAEPSFAQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WGTVFQELNKLYPTHACR---EYLKNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity 27.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 AA;
                                                                                                                                                                                                                                                                                                                                                              Bader M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 227.5; DB 22; 
Pred. No. 4.2e-14; 
3; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Best Local 9
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method of influencing the level of serotonin, which involves the specific regularion of TPH (tryptophan hydroxylase) and/or neurona-specific TPH (nTPH) activity. The method is used for the diagnosis of neuronal diseases and for treating deficient primary haemostasis. Also reducing production of serotonin is used to treat arteriosclerosis and thrombosis, particularly where associated with diabetes mellitus, and to treat excessive (or normal but unwanted) immune system responses, e.g. allergy, (auto) immune diseases, risks associated with pregnancy, particularly pre-eclampsia, and transplant rejection. The present sequence is a neurone-specific TPH protein.
                                                                                                                                                                                                                                                                                                                                                          Sequence
      279
                                              281
                                                                                  219
                                                                                                                        221
                                                                                                                                                              159
                                                                                                                                                                                                  164 WGTIFRELNKLYPTHACR---EYLRNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR 220
                                                                                                                                                                                                                                        107 WYRLLSSRPSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                             Local
                                                                                INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL
                                                                                                                        PVAGYLSPRDFLSGLAFRVFHCTQYVRHSSDPLYTPEPDTCHELLGHVPLLAEPSFAQFS
                                                                                                                                                            PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
      ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE
                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                          434 AA;
                                                                                                                                                                                                                                                                                Conservative
                                                 -LASIGASEETVOKLAT-----CYFFTVEFGLCKQDGQLRVFGAGL
                                                                                                                                                                                                                                                                                                12.0%;
                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                              Score 226.5;
Pred. No. 5.1e
43; Mismatches
                                                                                                                                                                                                                                                                              1e-14;
1es 97;
                                                                                                                                                                                                                                                                                                               DB 23; Length
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                      434;
                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                Gaps
                                                                                    278
                                                                                                                          280
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RESULT 8
Human; rat; tyrosine hydroxylase; TH; substitution; N-termina enhanced enzymatic activity; wild-type; transformation; dopam Parkinsons disease, Alzheimers disease; brain; encapsulation; selectively permeable; polymer capsule; antibody.
                                                                                                                                                                                                                                                                    04-NOV-1994
                                                                                                                 13-MAR-1991;
26-JAN-1993;
                                                                                                                                                          05-APR-1994.
                                                                                                                                                                           US5300436-A.
                                                                                                                                                                                          Rattus rattus.
                                                                                                                                                                                                                                                  Rat tyrosine hydroxylase
                                                                                                                                                                                                                                                                                    AAR50185;
                                                                                                                                                                                                                                                                                                    AAR50185 standard; Protein;
                                                               WPI; 1994-125849/15.
                                                                                Filer D,
                                                                                                (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                          13-MAR-1991;
                                                                                Friedhoff AJ,
                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                 91US-0669446
93US-0009075
                                                                                                                                          91US-0669446
                                                                                Goldstein M,
                                                                                                                                                                                                                                                                                                      498
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                                                                                 ū
                                                                                                                                                                                                                                  N-terminal;
                                                                                                                                                                                                                           dopamine;
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Modified DNA encoding variant tyrosine hydroxylase with N-terminal amino acid substn. and cells contg. it - can to treat diseases associated with defective function of enzyme, e.g. Parkinson's disease or Alzheimer's disease

used

Disclosure; Fiig 5; 27pp; English

91US-0669446.

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This sequence represents rat tyrosine hydroxylase (TH) and may be used in the production of the varient TH molecules of the invention. These varients contain amino acid substitutions in the N-terminal portion of the molecule, and in the rat molecule these substitutions.

These varients contain amino acid substitutions in the N-terminal portion of the molecule, and in the rat molecule these substitutions.

Arg46. Varients containing one or more of these amino acid substitutions, have substantially enhanced enzymatic activity compared to the wild-type enzyme. The most pref. substitution being Ser40 for Tyr or Leu. DNA encoding the TH varients, and cells card for Tyr or Leu. DNA may be used for treating diseases associated with defective function of TH, or dopamine, eg. Parkinsons disease.

The implanted into the brain or encapsulated in a selectively permeable polymer capsule which allows release of the cells products but protects them from attack by the hosts antibodies or cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 QLRPVAGLLSAKDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 QFSQDIG------LASLGASDESIEKLST------VYWFTVEFGLCKQNGELKAYG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 SSRFSLWKS------YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 SYYPYSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGIJENHEGRKAYG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 AVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, rat; tyrosine hydroxylase; substitution; N-terminal; dopamine;
neurological disorder; antibody; varient.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.7%; Pred. No. 1.8e-13;
Matches 65; Conservative 39; Mismatches 103; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 AEEIATWKEVYVTLKGLYATHACREHLEGPOLLERYCGYREDSIPOLEDVSRFLKERTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Phosphorylation site"
153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR36741 standard; protein; 498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-0669446.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat tyrosine hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                             498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus rattus.
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451 RIQ 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 KLE 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-SEP-1993
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353 G-----LASLGASDEEIEKLST-----VYWFTVEFGLCKQNGELKAYGAGLLSS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 WKS-----YCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHFSYYPVS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAR36740-41 represent the human and rat tyrosine hydroxylase protien respectively. These sequences may be used in the construction of a varient tyrosine hydroxylase which contains at least one amino acid substitution in the N-terminal 55 amino acids. The substitution of cresponds to an amino acid selected from SerB, SerB, Arg37, Arg38, Gln39, Ser40, Leu42, 11e42, Glu43, Asg44, Ala45, Arg46 or Lys47. The enzymatic activity of the varient protein: as at least 3-fold greater than that for the wild type protein. Cells transfected with the DNA encoding these proteins may be used for treating neurological disorders associated with a deficiency in tyrosine hydroxylase or dopamine. These proteins may be used to generate antibodies specific for the varient tyrosine hydroxylases to monitor the enzyme during a treatment regimen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 WKEVYVTLKGLYATHACREHLEGFOLLERYCGYREDSIPOLEDVSRFLKERTGFOLRPVA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 GRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 GEVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSBFFINM 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 POELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTSKLE 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 YGELLHSLSEEPEVRAFDPDTAAVQPYQDQTYQPVYFVSESFNDAKDKLRNYASRIQ 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, rat, tyrosine hydroxylase, TH, substitution; N-terminal; enhanced enzymatic activity; wild-type, transformation; dopamine; Parkinsons disease; Alzheimers disease; brain; encapsulation; selectively permeable; polymer capsule; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99; Indels 36;
                                                                                                                                                                           Genetically modified tyrosine hydroxylase having increased activity - used for treating neurological disorders e.g. parkinsy - used Alzheimer's diseases and affective disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%; Score 221; DB 14; Length 498;
llarity 27.4%; Pred. No. 2.2e-13;
Conservative 37; Mismatches 99; Indels 36
                                                                                                Wu J;
                                                                                                Filer D, Friedhoff AJ, Goldstein M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR50184 standard; Protein; 497 AA.
                                                                                                                                                                                                                                                             Disclosure; Fig 5; 20pp; English.
                                                        (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tyrosine hydroxylase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 65; Conserva
                                                                                                                                        WPI; 1993-175456/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498 AA;
                  13-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1994
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents human tyrosine hydroxylase (TH) and may be CC used in the production of the varient TH molecules of the invention. These varients contain amino acid substitutions in the N-terminal CC portion of the molecule, and in the human molecule these substitutions are pref. at positions Ser19, Ser31, Arg37, Arg38, Ser40, Leu41, Glu43, Asg94, Al445, Arg46 or Lya47. Varients CC substantially enhanced enzymatic activity compared to the wild-type CC enzyme. The most pref. substitutions being Ser40 for Tyr or Leu. DNA encoding the TH varients, and cells transformed with this DNA can be used for treating diseases associated with defective function CC of TH, or dopamine, eg. Parkinsons disease and Alzheimers disease, Cand effective disorders. The cells can then be implanted into the CC which allows release of the cells products but protects them from CC which allows release of the cells products but protects them from CC attack by the hosts antibodies or cells.
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified DNA encoding variant tyrosine hydroxylase with N-terminal amino acid substn. and cells contg. it - can to treat diseases associated with defective function of enzyme, e.g. Parkinson's disease or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 21-24; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-1991;
26-JAN-1993;
           Human tyrosine hydroxylase
                                                       AAR36740;
                                                                           AAR36740 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Filer D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-1991;
                                  20-SEP-1993
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                                                                                                                                                                                                                          346
                                                                                                                                                                                                                                              216
                                                                                                                                                                                                    276
                                                                                                                                                                                                                                                                                                                                      112 SSRFSLWKS------YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHF 155
                                                                                                                                   450
                                                                                                                                                        332
                                                                                                                                                                               390
                                                                                                                                                                                                                                                                    286 QLRPVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFA
                                                                                                                                                                                                                                                                                          156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                                                                                                                                                                                 226 AEEIATWKEVYTTLKGLÝATHACGEHLÉÁFALLERFSGYREDNIPQLEDVSRFLKERTGF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1994-125849/15.
                                                                                                                                                                                                                                       RIQ 452
                                                                                                                                                        KLE 334
                                                                                                                                                                                                                         QFSQDIG-----LASLGASDEEIEKLSTLS-
                                                                                                                                                                              AGLLSSYGELLHCLSEEPEIRAFDPEAAAVQPYQDQTYQSVYFVSESFSDAKDKLRSYAS
                                                                                                                                                                                                 AVLISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTS
                                                                                                                                                                                                                                                                                                                                                            1 Similarity
65; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Friedhoff AJ,
                                                                                                                                                                                                                                                                                                                                                                                                       497
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                (first entry)
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93US-0009075
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                                                                                                                                                                                                                                                                                                                                                                      11.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldstein M,
                                                                                                                                                                                                                                                                                                                                                            38;
                                                                              497
                                                                                                                                                                                                                                                                                                                                                                       Score 220; DB 15;
Pred. No. 2.8e-13;
                                                                                                                                                                                                                                                                                                                                                            Mismatches 104;
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                                                                                                                                                                                                                           -WFTVEFGLCKQNGEVKAYG
                                                                                                                                                                                                                                                                                                                                                                                Length 497;
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                                                                                                                                                                                                                                                                                                                                                             36;
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Best Local
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Homo sapiens Human; rat; tyrosine hydroxylase; substitution; N-terminal; dopamine; neurological disorder; antibody; varient.

Modified-site Modified-site Key Modified-site 13-MAR-1991; 13-MAR-1991; US5212082-A. Modified-site 91US-0669446 91US-0669446 /note= 222 /note= 152 Location/Qualifiers /note= "Phosphorylation site" note= "Phosphorylation site" "Phosphorylation site" "Phosphorylation site"

18-MAY-1993.

Filer D, (UYNY ) UNIV NEW YORK STATE Friedhoff AJ, Goldstein Σ, ž

N-PSDB; AAQ41886. 1993-175456/21.

Genetically modified tyrosine hydroxylase having increased activity - used for treating neurological disorders e.g. Parkinson's and Alzheimer's diseases and affective disorder s e.g. disorders

Disclosure, Fig 6; 20pp; English.

tyrosine hydroxylase protien respectively. These sequences may be used in the construction of a varient tyrosine hydroxylase which contains at least one amino acid substitution in the N-terminal 55 amino acids. The substitution corresponds to an amino acid selected from Ser8 Ser31, Arg37, Arg37, The enzymatic activity of the varient proteins is at least 3-fold greater than that for the wild type protein. Cells transfected with the DNA encoding these proteins may be used for treating neurological disorders associated with a deficiency in tyrosine hydroxylase or dopamine. These proteins may be used to generate antibodies specific for the varient tyrosine hydroxylases to monitor the enzyme during a treatment regimen. The sequences given in AAR36740-41 represent the human and rat

Sequence 497 AA;

Similarity

Length 497;

332 390 346 276 156 226 112 SSRFSLWKS------YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHF 155 KLE 334 QLRPVAGLLSAKDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFA AEEIATWKEVYTTLKGLYATHACGEHLEAFALLERFSGYREDNIPQLEDVSRFLKERTGF AGLLSSYGELLHCLSEEPEIRAFDPEAAAVQPYQDQTYQSVYFVSESFSDAKDKLRSYAS AVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTS QFSQDIG-----LASLGASDEEIEKLSTLS---EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG SYYPVSGEVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS Conservative 11.6%; Score 219; DB 14; 26.7%; Pred. No. 3.5e-13; tive 38; Mismatches 104; 104; WFTVEFGLCKQNGEVKAYG Indels 36; Gaps 331 275 345 215 285 389 ა --

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493 PASTAVQPYQDQEYQPIYYVAESFEDAKDKFRRWVSTMSRPFEVRFN-PHTERVEVLDSV 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 213.5; DB 12; Length 452; Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 13(1-3); 59pp; English
                                                                                                           AAR13119 standard; Protein; 452 AA.
                        331 SKLEWMLDQGLLESIPLYN 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%;
26.6%;
                                     552 DKLETLVHQMNTEILHLTN 570
                                                                                                                                                                                                                                                                                                                                                              90WO-US07619.
                                                                                                                                                                                                                                                                                                                                                                                       90US-0538276
                                                                                                                                                                                                                                                                                                                                                                                                   89US-0456095
                                                                                                                                                                                     Phenylalanine hydroxylase.
                                                                                                                                                           (first entry)
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N-PSDB; AAQ12712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 AA
                                                                                                                                                                                                                                                                                      Vibrio cholera.
                                                                                                                                                                                                                                                                                                                                                              21-DEC-1990;
                                                                                                                                                           08-OCT-1991
                                                                                                                                                                                                                                                                                                             WO9109871-A.
                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1989;
                                                                                                                                                                                                                                                                                                                                       11-JUL-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murphy JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                   AAR13119;
                                                                                    RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 STQYVRHVNSPYHTPEPDSIHELLGHMPLLADPSFAQFSQEIG------LASLGASD 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 DYLEAFGLLSD---FLDH-----QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 EYRAAFQKLQDEQIFVETRLPQLQEMSDFLRKNTGFSLRPAAGLLTARDFLASLAFRIFQ 388
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                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 21438; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 11.6%; Score 219; DB 22; Length 579; Local Similarity 28.6%; Pred No. 4.4e-13; Dedit 17; Conservative 37; Mismatches 94; Indels Score
                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 21438.
                                                                                                                                                                                                                                                                                                                                                                           Myers EW;
                                                                    ABB64882 standard; Protein; 579 AA
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11-JUL-2000; 2000US-0614150.
                                                                                                                     (first entry)
                                                                                                                                                                                                          Drosophila melanogaster,
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Hybrid, fusion, membrane translocation, binding region; HIV; infection; toxin; steroid; hormone; monoclonal antibody; antigen; diphtheria; exotoxin; phenylketonuria; cholera; interleukin; IL-2; protease; epidermal growth factor; ricin; tetanus; haxosaminidase; Shiga-like toxin A; SLT-A; PH; ligand; insulin; nuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hybrid molecules for targetting chemical entity to cell - have membrane trans-locating and cell binding-regions and used to treat HIV infection, genetic enzyme-deficiency disorders etc.
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This protein comprises for human phenylalanine hydroxylase (PH). A DNA molecule (see AAT91638) encoding PH was used to construct a PH-diphtheria toxin B' gene that was expressed in E. coli. The resulting hybrid protein can be used in the treatment of phenylketonuria. The active PH enzyme is targeted to, and incorporated into, the broad range of cells which native diphtheria normally attacks, achieving the widespread therapy that is needed for this inherited disorder. Claimed hybrid proteins comprise a translocation domain and a cell binding domain. They can be used for the delivery of agents (e.g. therapeutic genes, toxins, detectable labels) into cells. The use of a translocation
                                                                                                                                                                                                                                                                                                                                                                           New hybrid molecules for delivery of agents to cells - comprise a binding domain of a cell binding ligand and a portion of a translocation domain of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phenylalanine hydroxylase; human; hybrid protein; cell delivery; cell binding ligand; translocation domain; diphtheria toxin B';
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                                                                                                                                                                                                                                                                                                                             Example 5; Fig 13A-C; 30pp; English.
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DB; AAT91639.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
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84US-0618199.
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85US-0742554.
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90US-0538276.
93US-0102387.
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07-JUN-1984;
27-JUN-1991;
25-APR-1985;
07-JUN-1985;
22-DEC-1989;
14-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            shiga-like toxin; p
cytosol; therapy; q
adipocyte; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria; translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus; shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV; cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poiso; adipocyte; cancer; virus; infection; antibody.
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                                                             Recombinant DNA molecule encoding a three part hybrid protein used the treatment of Aids and genetic deficiency diseases - \,
                                                                                                                                                WPI; 1999-632431/54.
N-PSDB; AAZ30664.
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         Example 5; Fig 13; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
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91US-0722484.
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pred. No. 1.1e-12;
4; Mismatches 100;
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25-APR-1985; 07-JUN-1985; 27-JUN-1991; 07-JUN-1984;

Murphy

(SERA-)

SERAGEN

07-JUN-1984;

16-SEP-1997 US5668255-A. Homo sapiens phenylketonuria;

The invention relates to a recombinant DNA molecule encoding a hybrid protein comprising three parts: (a) the first part comprises a portion of a ranalocation domain of a naturally cocurring protein of the binding domain of a naturally cocurring protein of a ranalocation domain of a naturally cocurring protein of a portion of a translocation domain of a naturally cocurring protein correct from diphtheria toxin, botulinum neurotoxin, ricin, cholera toxin, which translocate the third part of the across the cytoplasmic committee from diphtheria toxin, shiga-like toxin, pertussis toxin and tetanus toxin, which translocate the third part of the across the cytoplasmic membrane into the cytosol of the cell; and (c) the third part comprises a polypeptide entity to be introduced into the cell, which is non-native to the naturally occurring protein of (b). This sequence represents the invention. The hybrid molecule enables the direction of appropriate invention. The hybrid molecule enables the direction of appropriate invention. The hybrid molecule enables the direction of appropriate alleviate or cure the disease. The hybrid is especially used in treating energing the missing function, to supplying the missing function, to supplying the missing function, to supplying cellular levels of a particular enayme or a scarce precursor or cofector, to directing or appropriate and proteins such as adipocytes, cancer cell, or virus infected-cells), to counteracting viral infections such as lively by introducing appropriate antibodies to viral proteins. It is also involved in the process of getting non-therapeutic substances such as detectable labels into cells. 

452 AA; Sequence

4 241 RLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFA 300 104 RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHF 155 156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215 216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275 301 QFSQEIG-----LASLGAPDEYIEKLAT-----IYWFTVEFGLCKQGDSIKAYG 344 / Match 11.3%; Score 213.5; DB 20; Length 452; Local Similarity 26.6%; Pred. No. 1.1e-12; les 62; Conservative 44; Mismatches 100; Indels 27; Gaps 276 AVLISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPOETLFSIRHFDELVE 328 Query Match Matches ò ò qq ò В

AAY78593 standard; Protein; 452 AA AAY78593

345 AGLLSSFGELQYCLSEKPKLLPLELEKTAIQNYTVTEFQPLYYVAESFNDAKE 397

05-MAY-2000 (first entry)

Human phenylalanine hydroxylase protein sequence.

Phenylalanine hydroxylase; translocation domain; cell destruction; cell binding domain; genetic deficiency disease; cell targetting; cancer; adipocyte; enzyme delivery; anti-viral; HIV.

US6022950-A

95US-0479510. 07-JUN-1995;

84US-0618199. 91US-0722484. 85US-0726808. 07-JUN-1984; 27-JUN-1991; 25-APR-1985; 

New two-part hybrid protein comprising a translocation domain and a cell-binding domain, for treating genetic deficiency diseases, cancer and HIV infections -85US-0742554. 89US-0456095. 90US-0538276. 93US-0102387. WPI; 2000-160390/14. (SERA-) SERAGEN INC N-PSDB; AAZ90020. 22-DEC-1989; 14-JUN-1990; 04-AUG-1993; Murphy JR; 

This sequence represents the phenylalanine hydroxylase protein sequence.

The encoded protein can be included in the hybrid protein of the included in the hybrid protein of the cinvention and used to destroy or modify the cell that the hybrid protein comprises a first part which is a portion of the binding domain of a cell-binding ligand, effective to cause the hybrid molecule to bind to a cell-binding ligand, effective to partion of a translocation domain of a naturally cocurring protein (e.g. the translocation domain of diphtheria toxin) the second part translocates the third part comprises a chemical of second part translocates the third part comprises a chemical of and into the cytosol of the cell. The third part comprises a chemical entity to be introduced into the cell. The third part comprises a chemical entity to be introduced into the second and third part is non-native with respect to naturally occurring protein, and the phenylalanine hydroxylase protein can form part of the third portion of the translocation domain transfers the hybrid molecule across the cell and the translocation domain transfers the hybrid molecule across the cell consistence of diseases by delivering to affected cells an enzyme supplying the missing function. The hybrid molecules are useful for treating genetic deficiency diseases by delivering to affected cells an enzyme supplying the missing function, to supplement cellular levels of a particular enzyme cells of cuttorion, completed cells infections or other poisons to destroy particular cells (autorion) cancer cells or cells infected cells), and to counteract voiral infections such as HIV by introducing into appropriate cells antibodies to viral proteins. Example 5; Fig 13; 32pp; English.

452 AA; Sequence

104 RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHF 155 184 KKTWGTVFKTLKSLYKTHA---CYEYNHIFPLLEKYCGFHEDNIPQLEDVSQFLQTCTGF 240 156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215 241 RLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFA 300 216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLJAIVRCFWFTVESGLIENHEGRKAYG 275 301 QFSQEIG------LASLGAPDEYIEKLAT-----IYWFTVEFGLCKQGDSIKAYG 344 11.3%; Score 213.5; DB 21; Length 452; 26.6%; Pred. No. 1.1-12; Indels 27; Gaps tive 44; Mismatches 100; Indels 27; Gaps 276 AVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328 345 AGLLSSFGELQYCLSEKPKLLPLELEKTAIQNYTVTEPQPLYYVAESFNDAKE 397 Local Similarity 26.6 Query Match Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is Cod-5 from Caenorhabditis elegans. Cod-5 is the aromatic amino acid hydroxylase that synthesises serotonin from CC precursor L tryptophan. The cod-5 gene was knocked out to produce mutants completely lacking in serotonin. These mutants were found to have defects CC in metabolic control. A number of C. elegans proteins that have mammalian homologues acting in the insulin signalling pathway were also contentified. The C. elegans age-1 gene encodes a homologue of the mammalian protein the C. elegans age-1 gene encodes a homologue of the mammalian receptor. The C. elegans AKT kinase and PKB kinase act downstream CC insulin receptor. The C. elegans AKT kinase and PKB kinase act downstream CC insulin signalling. The C. elegans PTEN lipid phosphatase homologue, CC DAF-18, has been found to act upstream of AKT in the pathway. This conserved DAF motifs can be used to design probes to conclude the conserved DAF motifs can be used to design probes to conclude the conserved DAF motifs can be used to design probes to conclude the conserved DAF motifs can be used to design probes to conclude the conserved DAF motifs can be used to design probes to conclude the conserved DAF motifs can be used to design probes to conclude the conserved DAF motifs can be used to send the secondary and disherers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing and treating obesity and impaired glucose tolerance using modulators of daf-18 expression and/or activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-2000
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                                                                                                                                                                                                                                                                                                    SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
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DB; AAA91624.
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                                                                                                ENGSNHERFKVYGAGLLSSAGELOHAVEGSATIIRFDPDRVVEQECLITTFQSAYFYTRN
                                                                                                                                               ---ENHEGRKAYGAVLISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPOETLFSIRH 322
                                                                                                                                                                                                 QFSQEIG-----LASLGASEEDLKKLATL------YFFSIEFGLSSDDAADSPVK 411
                                                                                                                                                                                                                                                EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLI-------
                                                                                                                                                                                                                                                                                                                                                                                                        RKTWGIIYRKLR---ELHKKHACKQFLDNFELLERHCGYSENNIPQLEDICKFLKAKTGF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.9%; Score 206.5; DB 21; 25.2%; Pred. No. 7.1e-12; tive 47; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                   265
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                                                                                                                                                                                                                                                                                                                               Local
                                                                                                RIRPVAGLISSRDFIGDIAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFA 334
                                                                                                                                               SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                                                                 KKTWGTVFKTLKSLYKTHA---CYEYNHIFPLLEKYCASHEDNIPQLEDVSQFLQTCTGF 274
                                           EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG
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Similarity 28.4 58; Conservative

Indels 27; Length 491;

Gaps

-LASLGAPDESIEKL ---

-APIYWFTVEFGLCKQGDSIKAYG

275

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the mucleic acids encoding the polypeptides and cells genetically cendineered to express them are also useful for producing the proteins. They may be used to the proteins are useful in genetic vaccination, testing and concerned to express them are also useful for producing the proteins. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; to restance the cell proliferation; to regulate haematopoiesis; and in treatment of leukaemias. Adu29510-Adu33304 represent the amino acid concerned to fleukaemias. Adu29510-Adu33304 represent the amino acid concerned to the protein and/or stimular expresent the amino acid concerned to the protein and/or stimular expresent the amino acid concerned to the protein and protein accerned proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy - \,
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26-JAN-2001;
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                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 332; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-2001; 2001WO-US08656
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                                                                                                                                                                                491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0552929.
2001US-0770160.
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10.6%; Score 199.5; DB 22; 28.4%; Pred. No. 3.2e-11; tive 36; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491
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279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
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                                                                                                                                                  ABB71186 standard; Protein; 555 AA.
                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.4%
Best Local Similarity 32.0%
Matches 47; Conservative
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC, Adams M,
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                                                                                                                                                                                                                                                                                                                                 WO200171042-A2.
                                                                                                                                                                                                                                                                            pharmaceutical
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                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                            27-SEP-2001.
                                                                                                                                                                             ABB71186;
                                                                                                                        RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 PVAGLLSSRDFLAGLAFRVFHSTQYIRHPSKPMYTPEPDVCHELMGHVPLFADPAFAQFS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 WYRLLSSRFSLWKSYCPRFFLDYLBAFGLLSD----FLDH-----QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 QEIG-----LASLGAPDDYIEKLST-----IFWFTVEYGVCRQEGELKAYGAGL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 WGIIFRNLTKLYKTHACR---EYNHVFPLLVDNCGFREDNIPQLEDVSNFLRDCTGFTLR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 10.3%; Score 194; DB 22; Length 452; Local Similarity 27.1%; Pred, No. 1e-10; Indels 46; Gaps 73; Conservative 39; Mismatches 11; Indels 46; Gaps
                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 10623; 21pp + Sequence Listing; English.
                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 10623.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Myers EW;
                                                                                                        ABB61277 standard; Protein; 452 AA
            276 AVLISSPQELGHAFIDNVRVLPLE 299
                              379 AGLLSSFGEFQYCLSEKPKLLPLE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                           Li PWD,
                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09231.
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                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                              Drosophila melanogaster.
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interactions -
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347 LSSYGELEYCLTDKPQLKDFE-----PEVTGV---TKYPITQFQPLYYVADSFETAKE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDL 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||| | : ||:|| | : |||||| | 344 LGHMPLLANSSFAQFSQEIG-----LASLGASDADIEKLATL------YFFTVEF 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 QDVSVYLKRKTGFQLRPVAGYLSPRDFLSGLAFRVFHCTQYIRHSSDPFYTPEPDCCHEL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Score 178.5; DB 22; Length 555;
32.0%; Pred. No. Sec. 95; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                  339 QGL--LESIP----LYNQEKYLSGFEVL 360
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                                                                                                                                                                                                                             The invention relates to novel human secreted polypeptides. The copyreptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to abstrant expression or physiological interactions of the polypeptide. Vectors comprising the mucleic acids encoding the polypeptide. Vectors comprising the proteins are useful in genetic vaccination, testing and therapy, and can be used as mutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; to dimune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. Adu29510-Adu33304 represent the amino acid or sequences of novel human secreted proteins of the invention.
                                                                                                                                     Query Match
Best Local S
Matches 37
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 332; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-611725/70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2000; 2000US-0552929
26-JAN-2001; 2001US-0770160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-2001; 2001WO-US08656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human secreted protein #1193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388
                                 257
59
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WFTVEFGLCKQGDSIKAYGAGLLSSFGELQYCLSEKPKLLPLELEK 104
                           WFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQ 302
                                                                  DICHELLGHVPLFSDRSFAQFSQEIG-----LASLGAPDEYIEKLAT-----
                                                                                                DLIHDLIGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCF 256
                                                                                                                                                     Similarity
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                                                                                                                                                                                                      200 AA;
                                                                                                                                     Conservative
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                                                                                                                                 8.1%; Score 153; DB 22;
34.9%; Pred. No. 4.3e-07;
tive 21; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200
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                                                                                                                                     32;
                                                                                                                                                                   Length 200;
                                                                                                                                     16;
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RESULT 22
AAE11092
                                                                                The patent discloses novel cells comprising a nucleic acid encoding cas gene product having phenylalanine hydroxylase (phA) activity such cas phenylalanine hydroxylase (phA), 4a-carbinolamine dehydratase (phB) and aromatic aminotransferase (phC), which are derived from a prokaryotic organism. The patent also relates to fusion proteins comprising a protein enhancing and/or stabilising the patent also repaired as a protein addition to PAH activity. The cells are useful for producing PAH. The sequences of the invention are also useful for producing PAH active food product (animal protein such having reduced content of phenylalanine. The method involves contacting the food product starting material with the cells or fusion proteins cuch that at least part of the phenylalanine content of the starting material with the cells or fusion proteins cuch that at least part of the phenylalanine content of the starting material that do not cause phenylketonuria (PKU) by the enzymatically active product. PAH enzyme is useful for menufacturing a medicament for treating PAH enzyme is useful for methodic disorder resulting in an accumulation in the body of L-phenylalanine and metabolites that can cause impaired brain function. The present sequence is a peptide sequence of phhAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel recombinant cells comprising a nucleic acid encoding a gene product having phenylalanine hydroxylase activity, that is derived a prokaryotic organism, is useful for treating phenylketonuria in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phenylalanine hydroxylase; PAH; phhA; 4a-carbinolamine dehydratase; phhB; aromatic aminotransferase; phhC; milk protein; animal protein; casein; proteinaceous food product; globulin; whey protein, phenylketonuria; PKU; inherited metabolic disorder; impaired brain function; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE11092 standard; peptide; 64 AA.
                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnsen M, Ravn P,
Arnau J, Jensen SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phhAB fusion peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 19; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2000; 2000US-0525116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2001; 2001WO-DK00172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                                                                                                   fusion protein.
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                                                                              64 AA;
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5.8%; Score 109.5;
35.6%; Pred. No. 0.0
tive 15; Mismatches
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Gjetting T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vrang A,
, Nielsen
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B;
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Matches Query Match Best Local

al Similarity 35.6 21; Conservative

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N-PSDB; ABN21920
                          WO200192523-A2.
                       Homo sapiens.
      24 - JUN - 2002
                            06-DEC-2001.
   ABP06168;
ABP06168
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                                                                                                                                                                                                                                                     hyperproliferative disorder, psoriasis; benign tumour; haemorrhage, degenerative disorder, osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                           Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
                                                                                                                                                                       Human ORFX protein sequence SEQ ID NO:12318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID 12318; 1037pp; English.
ABP06168 standard; Protein; 104 AA
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29-AUG-2000; 2000US-228716P.
                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                myasthenia gravis.
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Gaps

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DB 23; Length 104; 44; Indels

/ Match 5.8%; Score 109.5; DB 2 Local Similarity 28.6%; Pred. No. 0.0041; Local Similarity 28.6%; Mismatches 4

Query Match Best Loca Matches

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21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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22.4%; Pred. No. 0.24
ive $8; Mismatches 130; Indels 107; Gaps
126 FLDYLEAFGLLSDFLDH-QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVM 184
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                                          10 PKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHK----CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 10374.
                                                                                                                   185 RTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                          Myers EW;
                                                                                                                                                                                                                                                                                                                                  ABB61194 standard; Protein; 1501 AA
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N-PSDB; ABL05297.
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                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DAN sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1083
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   Sequence
                                                         sequences (ABL01840-ABL16175) and the encoded proteins (ABB5737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 23847; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
N-PSDB; ABL09788.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interactions -
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                                                     ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFHSDVVQQQMKALGVLDTVIARQ---KGFS----SRLPFDEFLRRYQFLAFDFDE--P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting for elucidating cell signalling
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                                                                                          WIPO
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Query Match

5.8

Score

103.5;

밁 22;

Length 1782;

The invention relates to improving the production of a secondary metabolite by a fungus. This involves modulating the expression of at least one ZBC (zinc binuclear cluster protein) gene in a manner to improve the yield of the secondary metabolite. Methods of the invention may be used for improving the production of the secondary metabolite e.g. antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such as lovastin or mevastatin), an immunosuppressant (such as cyclosporin A), an ergot alkaloid (such as ergotamine), an anglogenesis inhibitor (such

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RESULT 2
ABP35686
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                                                                                                                                                                                                                                                                                                                                                                                                                          Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein; antibacterial; beta-lactam; anti-hypercholesterial; lovastin; mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine; angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin; fungal toxin; cell surface receptor; plant growth regulator; pigment;
                                                                                                                                              New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation of the expression of at least one zinc binuclear cluster protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP35686 standard; Protein;
                                                                                                                                                                                                                                                                                        19-SEP-2000;
                                                                                                                                                                                                                                                                                                               19-SEP-2001; 2001WO-US29288
                                                                                                                                                                                                                                                                                                                                                                                        Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fungal ZBC protein sequence
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                                                                                                            Disclosure; SEQ ID 236; 49pp + sequence listing; English.
                                                                                                                                                                                                                                     Holtzman D,
                                                                                                                                                                                                                                                                                                                                      28-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                WO200224865-A2
                                                                                                                                                                                                                                                                                                                                                                                                                insecticide; antineoplastic
                                                                                                                                                                                                                                                               (MICR-) MICROBIA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLSSRFSLWKSYCPRFFLDYLEAFGLLS-----DFLDHQAVIKFFELETH----FSYYP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILEF-----FKNLLFVHLLSLSKNQREGCSTDMAV-----VSTPFFNRNLWYR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --IPSHIGEN----
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)B; ABN79875.
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as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds, a fuggal toxin, a modulator of cell surface receptor signalling; a plant growth regulator, a pigment, an insecticide, or an antineoplastic compound. The method results in a decrease in fermentor run-time, a decrease in the size of the fermentor required for the production of equivalent amounts of the secondary metabolite, or a decrease in the biomass required for the production, which translates into decrease in the records ABP35575-ABP3722 represent ZBC processing. The sequences given in records ABP3575-ABP3722 represent ZBC proceins.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 TLLPIIAATIQLSDLPDVILNFYNSAGI-----TPLESSRLINLKLNEISEQEYKHLCLP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 ILEFFKNILFFVHLLSLSKNQREGCSTDM-----AVVSTPFFNRNLWYRLLSSRFSLWKS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 ---LRCFFNDDISYN---FHLLLGR---LLDCGVSIYKSVHSLTVSKFIDKLESYESQLS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 LILVDIEAKFYDPSNEDIQFRYİFLKMVFWTARVNLYQCFITLDSGILEDEE-----T 429
                                                                                                                                                                                                                                                                                                                                 Query Match
5.4%; Score 102; DB 23; Length 563;
Best Local Similarity 21.1%; Pred. No. 0.27;
Matches 80; Conservative 56; Mismatches 142; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 DKEIIQMLLLRAYATKFRTRIRGVNTDLCRSIHVSTLVTPLF--QVTEKIGKNTSDLWFA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 RI------QTLQSNLIAIVRCFW------FTVESGLIENHEGRKAYGAV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 LISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWML 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430 IIGN---LGESCIQCVRLL---ISQITIL-----EKRGWLLVALLEIIHALMLAAFCR 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                    7 TLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EIDGL-----ECVLKY---RPPFIQHDTYGRLKP------
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11-JAN-2000; 2000JP-0118776.
02-MAX-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                         563 AA;
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Comprises: (a) an oligo-dT primer sers for synchesising below comprises: (a) an oligo-dT primer sers of comprises: (a) an oligo-dT primer and an oligonucleotide complementary cromprises: (a) an oligo-dT primer and an oligonucleotide complementary for to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence which comprises a 3'-end sequence; where the polynucleotide comprises a 3'-end sequence; where the complementary to a polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence; a settle data those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length of the primers allow obtaining of the full-length cDNAs represent human cDNA sequences; AAB92446 to AAH13632 AAH18633 to AAH18633 to PAH13632 and AAB95893 respensent human amino acid sequences; and AAH13629 to AAH13632 of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 lill-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs -
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23.3%; Pred. No. 0.28; Indels 128; Gaps
ive 41; Mismatches 98; Indels 128; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 LPGLEPALQVDLVWALCVLQQAREAELQAVLHPEF--------HIQFLGGKS 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 QRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 QKDQNTFQKLLHI-----NATALLEYPE---YSGPLLPASAVAPGPSALDR-KVTPLQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 KCISILEFF-KWLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 CPRFFLDYLEAFGLLS------DFLDHQ-------AVIKFFELETH 154
                                                                           Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 ----PLFGAFAQH-VLNRAQDITLPHLCSVLLAFARLNFH--PDQEDQFFSLVHEKLGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 FSYYPVSGFVAPHQYLSLLQDRYFP-IASVMRTLDKDNFSLTPD-----LIHDLLG--
                                                                                                                                                                                                                                                                                                                                                                          present invention describes primer sets for synthesising 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 LDQIIRLPFNTSTPQETLFSIRHFDE--LVELTSKLEWMLD-QGLLES 344
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                                                                        Saito K, Ya
                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID 14279; 2537pp + CD ROM; English.
                                                                     Isogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
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                    (HELI-) HELIX RES INST.
                                                                                                                                              WPI; 2001-318749/34.
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                                                               Ota T, Is
Ishii S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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11-JUL-2000; 2000US-0614150
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                                                                                              1047
                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 5859; 21pp + Sequence Listing; English
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SPQELGHAFID -- NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                         IIHAF--IILLTYSNSNMPESIPILD-----YWFP------PGRPAPVAFLPS
                                                                                                                                                                                                      LSGLKIIFRHSGDF--ENEW--LLKSLQQIPHFYEVKPFIIPQLRAACQVENCPELIMAY
                                                                                                                                                                                                                               STDMAVV---STPFFNRNLWYRLLSS------
                                                                                                                                                                                                                                                           IINEENSRDAEL-----VNFLRNLIFDGNLSHQIVCELLDYIFRRLSSTVKQSRVAA 930
                                                                                                                                                                                                                                                                                      2001-656860/75.
                                                                  MGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLIS
                                                                                                                       VAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLI---HDLLGHVPWLLHPSFSEFFIN
                                                                                                                                                  IQFITAHTLNDPVNEMLDHVIDMAQLIVERSTMFQHIIISQEDYDYVPDENRIQTLKCLF
                                                                                                                                                                            LE---AFGL---LSDFLDH-----QAVIKFFELETH-----FSYYPVSG-----F
                                                                                                VMFNNYIIKLREYHEPY-----EWTEYPDLLMVQPDDGVQLP--LH-----IN
                                                                                                                                                                                                                                                                                                                             Similarity
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Pred. No. 2
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format directly from
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19 KLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFVH 78

Query Match
Best Local Similarity 19.9
Conservative

5.2**%**; 19.9**%**;

Score 99; DB Pred. No. 1.1; 7; Mismatches

DB 19; 122;

Length 924; Indels 164;

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                           The present sequence represents a p102 protein. This protein is present CC the secretion associated 175 (SA-175) complex. Bight proteins form the CSA-175 complex, which binds a syntaxin-containing (SC) complex. The CSA-175 polypeptides and nucleotide sequences encoding them can be used CC for screening for compounds which modulate vesicular release involved in CC enhance binding between the SA-175 and SC complexes may be used to treat CC an affective disorder such as depression, manic-depressive disorders and CC disease or Huntington's disease. Compounds which inhibit binding between the SA-175 and SC complexes may be used to treat CC disease or Huntington's disease. Compounds which inhibit binding between the SA-175 and SC complexes may be used to treat a disorder of thought, CC such as schizophrenia, or for anaesthesia. The compounds can also be used to inhervent in the endocrine system for treatment of hormonal CC imbalances, the immune system for intervention in antigen processing, as erereted immunomodulators, and virial processing, as well as selficking CC during rapid cell division.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p102 protein; secretion associated 17S complex; SA-17S; syntaxin-containing complex; SC complex; screening; modulate; syntaxin-containing complex; SC complex; secretory process; vesicular release; synaptic transmission; secretory process; treatment; affective disorder; depression; manic-depressive disorder; anxiety disorder; neurodegenerative disease; schizophrenia; anaesthesia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1128 MPQEQVQLLPDWLKLKMIRSSVDRLIEAALNDLTPDQIVLFVQNFGTPVNSMSKLLAMLD 1187
                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated vesicule secretion associated poly:peptide(s) - develop products for treating e.g. effective disorder, neurodegenerative disease, hormone imbalances, immune system
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  Sequence
                                                                                                                                                                                                                                                                                                                                                                  Claim 1e; Pages 116-118; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                        disorders or tumours
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)B; AAV42653.
  924 AA;
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Unidentified
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                                                    Sequence
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206
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                                    79 LLSLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSSRF----SLWKSYCPRFFLDYLEAF 133
                                                             287 PLNIKRNIQKG---DYDVVIND-----YEKAKSLFGKTEVQVFKKY-----YAËVE 329
                                                                                                          330 AGIEDL--RELLIKKI-LETPSTLHDQKRYIRYLSDLHAPGDPAWQCIGAQHKWTLKLMQ 386
                                                                                                                                                             DCKEGHMKSLKGNPGPHSPM-----LDLDN-----DARPSVLGHLSQTASLKRGSSFQS 435
                                                                                                                                                                                         -----PSFSEFFINM--GRLFTKVIEK---VQALPSK 238
                                                                                                                                                                                                                                        KOR-----IQTLQSNLIAIVR--CFWFTVESGLIENHEGRKAYGAVLIS---SPQELG 286
                                                                                                                                                                                                                                                               496 RQRQNDFKKMIQEVMHSLVKLIRGALLPFSLREG-----DGRQ-YGGWEVQAELSGQWLA 549
                                                                                                                                                                                                                                                                                         HAFIDNVRV------HPLELDQIIRLPFNTSTPQETLFSIR-------HFDELV 327
                                                                                                                                                                                                                                                                                                                 550 HV-IQTIRLTYESLTALEIPNDMLQII------QDLILDLRIHCIMVTLQHTAEEIK 599
                                                                                      134 GLLSDFLDHQAVIKFFELETHFSYYPVSGFV-------APHQY-LSLLQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated or recombinant immunogenic polypeptides from Mycoplasma genitalium have mol.wt. of 16 kDa (AAM19663) (MG074) and 116 kDa (AAM19604) (MG075). They are homologues of 16 and 116 kDa (see also AAW19601-02) obtd. from Mycoplasma pneumoniae. A genonic Immes that code for the 2 polypeptides. Mycoplasma poen reading proteins, or immunogenic fragments that include a T or B cell epitope, can be used in vaccines for prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma; immunogen; vaccine; diagnosis; pneumonia; inflammation.
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                                                                                                                                       D-----RYFPIASVMRTLDKDNFSLTPDLIHDLLGHV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma genitalium 116 kDa protein MG075 useful in vaccine.
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                                                                                                                                                                                                                                                                                                                                          328 ELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 19; Page 85-89; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Browning GF, Duffy MF, Walker ID,
                                                                                                                                                                                                                                                                                                                                                                                                                                AAW19604 standard; Protein; 1024 AA
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                                                                                                                                                                                       207 ----PWLLH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel recombinant cells comprising a nucleic acid encoding a gene product having phenylalanine hydroxylase activity, that is derived from a prokaryotic organism, is useful for treating phenylketonuria in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              758 VNVNFHIDARLLTAELQNTVFSNPK------PVIKSPVELSKSLFEVWKTIFENSVNQI 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 LQSNLJAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELG-------- 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 QREGCSTDMAVVSTPFFNRNLMYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      614 -----ELLNFFPDTKDITFT 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 IK--FFELETH-----FSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648 IKKVLFESENYKTLRKKYENEGFPGYHWAKFIVPGTFNSAENTFYSAI-----DKT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            699 KSIRDLFADML-FGKSLESVNDSDSFIKINGSFTLITKNDNLNLLPNYHSLITKNVGYQI 757
                                                                                                                                                                                                                                                                                                                                                                                            29 QNSQSLQRAYSTPYSYYRIILQKENKEK---QALARHKCISILEFFKNLLFVHLLSLSKN 85
Mycoplasma infections, partic, in humans. They can also be used diagnostically to detect Mycoplasma, or to raise antibodies useful in immunoasanys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 QQTDSLKNLFSV----IGDILSETNVNKITLHAVKNNELLSLVETASTLKIKHL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 SLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFT-----KVIEKVQALPSKKQRIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Madsen SM, Vrang A, Israelsen H, Bredmose
Gjetting T, Nielsen E;
                                                                                                                                                                                                                            ch 5.2%; Score 98.5; DB 18; Length 1024;
1 Similarity 19.9%; Pred. No. 1.4;
68; Conservative 41; Mismatches 134; Indels 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            811 LKKEYTFKDNLKFFFFKADGSSRLEFDLSKPDQRVIPFAFVD 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 ----HAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFD 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE11093 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2000; 2000US-0525116.
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Arnau J, Jensen SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-590055/66
                                                                                                                                                           1024 AA;
                                                                                                                                                                                                                                                                         Local Similarity
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Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUN-2002
The present invention provides the protein and coding sequences of
                                         Example 2; SEQ ID NO 474; 509pp; English
                                                                                                                                                                                                                                                                                                                     11-SEP-2000; 2000US-0659671
                                                                                                                                                                                                                                                                                                                                                                 10-SEP-2001; 2001WO-US26015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion protein.
                                                                                 An isolated polynucleotide fencoded polypeptide such as
                                                                                                                                                                                                                Xue AJ,
                                                                                                                                                                                                                                  Tang YT,
                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
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                                                                                                                                                   2002-292408/33.
DB; ABN32392.
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15; Conserv
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Wehrman
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                                                                                   for treating diseases associated with s cancer and multiple sclerosis -
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Matches 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. pneumoniae protein involved in metabolism of nucleic acids.
                                                                                                                                                                                                                                     04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia pneumoniae.
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                                                                                                                                                                               (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 KLRQSLSLFFQNS-----QSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 L-LFVHLISLSKNOREGCSTDM-AVVSTPFFNRNLWYRLLSSRFSLW------KSY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKVQALPS-----KKQRIQTLQSNLIA--IVRCFWFTV-----ESGLIENHEGRKAYGA
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Genome sequence of Chlamydia pneumoniae

WPI; 1999-357842/30

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99US-0136021
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                                           AAX34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidonis, sinusitis, purulent citis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                198 SYTQPISSYRSSRVERLEQISLWHQQIYNSLLEIPK----QVFLDQLTAHISGFKKQPFS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 -VMRTLDKDNF----SLTPDLIHDL-LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQAL 235
                                                                                                                                                                                                                                                                                       5.1%; Score 97; DB 20; Length 439;
22.1%; Pred. No. 0.59;
tive 51; Mismatches 117; Indels 104; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 LLSDFLDHQAVIKFFELETH---FSYYPVS-GFVAPHQYLSLLQDRYFPIAS----- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 WVERTLEFCNLDRIFNTLLVDLOEYLKONYTPW-LSPDESVF-----ALEKLLSS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 PSKKORIQILQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGH---AFIDN 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 SEAQPVVQAL--------REQYQLVLIDEPQDTDKQQMSIFSN 390
                                                                                                                                                                                                                                                                                                                                                                                                                              96 ----VVSTPFFNR------FG 134
                                                                                                                                                                                                                                                                                                                                                          46 RIILOKENKEKQALARHKCISIL--EFFKNLLF---VHLLSLSKNOREGCSTDMA---- 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 LFISPKFTGSL----FLIGDPKQSIYEWRSADLPTYLTAKSSFSEDKQL 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 VRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 38084.
               Page 1164; Disclosure; 1912pp; English.
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           AAG31678;
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                                                                                                                                                                                                                                                                                                                                                             62 HKCISILEFFKNILFVHL-------LSLSKNQREGCSTDMAVVSTPFFNRNLWYR 109
|----TIQEWVQSAPDVHLHLPAFNVFIPTDLSL-KDADDKETVFVLLRKTPF--SRLWYK 472
                                                                                                                                                                                                                                                                                                                                                                                                                               9 DPKYILKIALKLRQSLSLFFQNSQSLQRA-----YSTPYSYYRIILQKENKEKQALAR 61
                                                                                                                                                                              RTFIECYIAGNVENNEAESMYKHIEDVLFNDPKPICRPLPPS-----QHLTNRVVKL---
                                                                                                                                                                                                                       PYHQAMYYCSLILQDQTWP------WTEEL--DVLSHLEAEDVAKFVPMLLS
                                                                                                                                                                                             PSFSEFFI-----NMGRLFTKVIEKV------QALPSKKQRIQTLQSNLIAIVRC
                                                                                                                                                                                                                                       P-HQ---YLSL-LQDRYFFIASVMRTLDKDNFSLTFDLIHDLLGH-----VPWLLH
                                                                                                                                                                                                                                                                      LSDNGFELTLLGYNHKLRILLETVVGKIANFEVKPDRFAVIK----ETVTKEYQNYKFRQ
                                                                                                                                                                                                                                                                                                                  -PDTMFSKPKAYVKMDFNCPLAVSSPDAAVLTDIFTKLLMDYLNEYAYYAQVAGLYYGVS
                                                                                                                                                                                                                                                                                                                                       -----GLLSDF---LDHQAVIKFFELETHFSYYPVSGFVA
                                                                                                                                     -----GEGMKYFYHODGSNPSDENSALVHYIQVHRDDFSMNIKLOLFGLVAKO
                                                                                                                                                        FWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLELELDQIIRLE-FNTSTPQ
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l Similarity 21.7%;
97; Conservative 4
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Pred. No. 2.7;
18; Mismatches 128; Indels 174;
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| US-0147260<br>US-01474303<br>US-01474913<br>US-01474913<br>US-0148174<br>US-0148174<br>US-0148665<br>US-01486665<br>US-01486666<br>US-01486666<br>US-01486666<br>US-01486666 | US-0149723<br>US-0149929<br>US-015956<br>US-0150864<br>US-0151065<br>US-0151065<br>US-0151065<br>US-0151065<br>US-0151065<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069<br>US-0151069   | 99US-0157753<br>99US-0157865<br>99US-0158029<br>99US-0158230<br>99US-0159294<br>99US-0159294<br>99US-0159294<br>99US-0159294<br>99US-0159294<br>99US-0159294<br>99US-0159294<br>99US-0159294<br>99US-0159296<br>99US-0159637<br>99US-0159637<br>99US-0160741<br>99US-016076<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091<br>99US-016091 |
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Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSDNGFELTLLGYNHKLRILLETVVGKIANFEVKPDRFÄVIK----ETVTKEYQNYKFRQ 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HKCISTLEFFKNLLFVHL------LSLSKNOREGCSTDMAVVSTPFFNRNLWYR 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------GEGMKYFYHQDGSNPSDENSALVHYIQVHRDDFSMNIKLQLFGLVAKQ
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96US-0625811.
96US-0758731.
96US-0736905.
96US-0738859.
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8; Mismatches 128; Indels 174; Gaps
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CC The protein may be used in a vaccine to prevent or treat H. pylori collinection or to identify H. pylori polypeptide binding compounds, to identify H. pylori pyloripeptide binding compounds.

CC useful as potential H. pylori life cycle activators or inhibitors. The CNA and probes derived from it may be used for the identification of the pylori in a sample and the diagnosis of H. pylori infection. Nucleic cards sequences complementary to the DNA act as antisense sequences and card sequences complementary to the DNA act as antisense sequences and card sequences complement the translation of H. pylori mRNA. Antibodies can be used to prevent the translation of H. pylori mRNA. Antibodies and card as a continuous continuous continuous continuous continuous conferences of the pylori (ATCC 55679) was determined from overlapping contigs generated the pylori (ATCC 55679) was determined from overlapping contigs generated to mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions cardine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by ERC membrane proteins. Having identified and determined the sequences of control of the pylori by ERC mapplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 38
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Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus epidermidis SR1 strain; infection; diagnosis, vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            S. epidermidis open reading frame protein sequence SEQ ID NO:1930.
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                                                                                        09-NOV-1999;
                                                                                                                                            09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG82418 standard; Protein;
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                                   (GLAX ) GLAXO GROUP LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 KAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRL----PFNTSTPQETLFS---IRHFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 PSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 NDFTPYFVRVGDSWSKIDYSLEAKDWMKPLIRGVETNLVEIPANWYLDDLPPMMFIKKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 PIAMTAKQ-EEDVLLKSVELIKDLTGKAPTGYVAPWWEFSNITNELLLKHGFKYDHSLMH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 5.0%; Score 94; DB 1 Similarity 21.0%; Pred. No. 0.67 38; Conservative 38; Mismatches
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N-PSDB; AAH53268

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AAH53304 to AAH53970 represent nucleic acids (1) encoding polypeptides (II), given in AAGG1454 to AAG83120, from Staphylococcus epidermidis. (II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (1) may be used to produce the spidermidis polypeptides (II) wish the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the polynucleotide sequences from the present invention. AH55991 to AH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N. B. The present invention specifically claims all the polynucleotide sequences given in the esquence listing of the present specification, however the sequence listing only goes up to SRQ ID NO:4454 so even though sequences are given in the disclosure for SRQ ID NO:4455 to 4472, on sequences are given in the disclosure for SRQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 DINNYHFEGIDLLITHDFDTSQ---LLQIPKVIQVSPLFSDEDAKKIEFFVKAMQNPLS 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 KFFELETHFS--YYPVSGFVAPHQYLSLLQDRYFP----IASVMRTLDKD-NFSLTPDL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 LKDNMAVHESRTYLRLMSHVYLNNPLTSQIKRLYPFVFNTLYDSIROLSQDTNIQLSEDE 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 5.0%; Score 94; DB 22; Length 528; Local Similarity 20.5%; Pred No.1.6, No.1.6; Indels 110; Gaps es 91; Conservative 71; Mismatches 172; Indels 110; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 ISKHIDNHQLSTSENKIQQLLVHLILLIKHSQPEEEDWSTDTESLTIAKKCIKDINETLG 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 YOLNNK----TSECFSFFISYHFNKFDLGIQOLFIQSYIDRLIELMEQHIGFPFSQDTI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 IHDLLGHVPWLLHPSFSEF-----FINMGRLFTKVIEKVQALPSKKORIOTLQSNLIA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 LARH---KCISILEFFKNLLFVHLLSLSKN---QREGCSTD-----MAVVSTPFFNRNLW 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 KYILKIALKLRQSLSLFFQNSQSLQRAY-----STPYSYYRIILQK-----ENKEKQA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 KPDIYLSIKKKÓGI-MIDASTTŚISNÁVLHINQLTDDDFKVENLÍLÓELPQAHTRKÍKÓI 93
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                                                                                                                                                                                                             Claim 18; Page 528; 2188pp; English.
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Novel yeast SRB (suppressor of RNA polymerase B) proteins SRB4, SRB5, SRB9, SRB9, SRB10 and SRB11 (AAW18321-28) are transcription regulatory factors that act as positive and negative regulators of RNA polymerase II activity, and are components of the RNA polymerase II nolonezyme. They were identified using methods designed to identify transcription factors involved in RNA polymerase II c-terminal domain (CTD) function. SRBs and SRB9 appear to repress CTD activity. Genomic clones (AAT59904-11) for the SRBs are been obtd. SRBs can be used to treat diseases resulting from alteration or deletion of the SRB gene, pref. by gene transfer technology. They can also be used in in vitro transcription of DNA and to identify endeds. that modify gene transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 DFQLTIVTCKQFPKLSCIQLNCIDTQFTKLLDDNPTBLDMPTYVDQNPLTWHKIIQLILM 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YCPRFF------LDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 HQYLSLLQDRYFPIASVM------RTLDKDNFSL------TPDLIHDLLGHVPW 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 YYIVSSSKSKINDENYIINHIKKNNKIKLNILKILSSLILKIFQEQSLEVFIFPTSNWEI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purified RNA polymerase II holo:enzyme - comprises RNA polymerase II and one or more regulatory proteins, pref. suppressor of RNA polymerase B proteins or SWI/SNP proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 YILE---KLIFDMTNHYNDSQQL-RTWKRQISYFLKLLGNCYSLRLINKE---IFHHWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 YKPLLFEIVSNADTNQNSHMKKKLELISYRNESLKNNSSIR------NVIMSASNAN
                                                                                                                             Transcription regulatory factor; suppressor of RNA polymerase B; SRBB; RNA polymerase II; holoenzyme; SWI/SNF.
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5.0%; Score 94; DB 18; Length 1226;
Best Local Similarity 18.4%; Pred. No. 5.2;
Matches 96; Conservative 67; Mismatches 156; Indels 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 SILEFFKNILF----VHLLSLSKNOREGCSTDMAVVST-----PFF
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                                                                                            Yeast transcription regulatory factor SRB8
                                                                                                                                                                                                                                                                                                                                                                                                                                    (WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chao DM, Koleske AJ, Thompson CM,
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95US-0540804
                                                     (first entry)
                                                                                                                                                                                            Saccharomyces cerevisiae
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N-PSDB; AAT59908.
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11-OCT-1995;
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                                                                                            Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis
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RESULT 40
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                                                                                                                Query Match
Best Local S
Matches 67
                                                                                                                                                                                                                                                                                    The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB3300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogutt and cheese.

Note: The sequence data for this patent is based on equivalent patent wo200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; SEQ ID No 1759; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleotide sequence useful in the identification or Lactococcus lactis and related species - {\sf}
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KIAL--KLROSL---SLFFQNSQSLQRAYSTFYSYYRIILQKE----NKEKQALARHKC 64
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tive 38; Mismatches 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polyp

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   other traits to assess biodiversity
responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00100-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | : : : : : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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4.9%; Score 93; DB 22; Length 744;
Best Local Similarity 19.2%; Pred. No. 3.2;
Matches 87; Conservative 73; Mismatches 140; Indels 152; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     335 YAPNTGAPRFIKQVLSDLQRDL----DSHTLIMGDFNTPLSTLDRSMRQKVNKDTQELNS 390
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The invention relates to an isolated or recombinant homologue of US28 protein which binds a chemokine (encoded by an open reading frame in the unique short (US) region in human cytomegalovirus (CWM) genome), having at least 75* identity to a rheasum smokey RhUS28.1-RhUS28.5, Rh78 and RhUS33 (encoded by an open reading frame 78 in the unique long (UI) and CRM state of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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                                                                                                                                                                                                                                                            Isolated or recombinant homologues of US28 proteins and nucleic acids encoding the proteins, for use in vaccine compositions for treating an animal infected with, or at risk of infection by, cytomegalovirus -
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Schall TJ, Penfold M;
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N-PSDB; ABK68823.
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                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel human secreted polypeptides. The projectides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; in treatment of leukaemias. AAU33510-AAU33304 represent the amino acid of sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
             AAY31237 standard; Protein; 3923
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 750; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding a range of human vaccination, testing and therapy -
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26-JAN-2001; 2001US-0770160
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                                                                           NFTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIABLSATAQEI--IKSQAIA 839
                                                                                                     ---HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                                 NIKQLKEMKFTYLINYIQDEINTIFNDYIPY---VFKLLKENLCLNLHKFNEFIQNELQEA
                                                                                                                                                                                                        RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP----
                                                                                                                                                                                                                                   RKHKLIDVISMYREL----LKDLSKEAQEVFKAIQSLKTTEVL-RNLQDLLQFIFQLIED
                                                                                                                                                                                                                                                             ARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                                                                                                                                                                                                                                                                                      YTREELCTMFIREVGTVLSQVYSKVHNGSEIL-----FSYFQDLVITLPFE-----L
                                                                                                                                                                                                                                                                                                              YCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYR---IILQKENKEKQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
                                                                                                                              SQELQQIHQYIMALREEYFDPSIVGWTVKYYELEEKIVSLIKNLLVALKDFHSEYIVSAS
                                                                                                                                                       -----HQYLSLLQDRYFPIASVMRT-----LDKDNFSLTPDLI--------
                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                        919 AA;
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT
                                                                                                                                                                                                                                                                                                                                                 4.9%;
                                                                                                                                                                                                                                                                                                                                     ; Score 92; DB
; Pred. No. 5.5;
48; Mismatches
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                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 919;
5.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides, useful in genetic
                                                                                                                                                                                                                                                                                                                                       118;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                       68;
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                   899
                                                                                                                                                                                                                                                                                      613
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Matches
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                                                    3618
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  3673 NIKQLKEMKFTYLINYIQDEINTIFNDYIPY--VFKLLKENLCLNLHKFNEFIQNELQEA 3730
                          114 RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP---- 166
                                                                           60 ARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                                                                                                                                                                   Local
                                                                                                                              3 YCERTLDPKYILKIALKLROSLSLFFQNSQSLQRAYSTPYSYYR---IILQKENKEKQAL
                                                                                                      YTREELCTMF IREVGTVLSQVYSKVHNGSEIL-----FSYFQDLVITLPFE-----L
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61;

Conservative

Similarity

4.9%; Score 92; DB 20.7%; Pred. No. 44; tive 48; Mismatches

DB 20; Length 3923; 44;

118;

Indels

68;

Gaps

12;

3617 59

-LKDLSKEAQEVFKAIQSLKTTEVL-RNLQDLLQFIFQLIED

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This invention describes a novel method for the genetic treatment of hyperlipidemia by altering genes, in hepatcoyres, for apoprotein (apo) B, E or Al. Low density lipoprotein (LDL) levels in the blood are reduced by altering an apo B gene (I) in a hepatcoyre. The invention describes a method for the therapeutic and/or prophylactic method involving altering an apo B gene in hepatcoytes by introducing the mutations Argilacys, Argisacys or Cysisakry and a method for ameliorating atherosals by altering the apo Al gene in a hepatcoyte so that the altered protein can dimerize. Altering expression of apo genes regulates levels of high and low density lipoprotein cholesterol. Altering expression of apo B, E and Al genes is used to treat or prevent atherosclerosis, coronary heart disease, Alzheimer's disease, hypobetalipoproteinemia. This sequence represents a fragment of the human Apo B protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apo E; Apo B; hyperlipidemia; human; treatment; hepatcoyte; apoprotein; Apo A; low density lipoprotein; LDI; blood; therapy; atherosclerosis; high density lipoprotein; HDI; cholesterol; coronary heart disease;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutating apolipoprotein genes in hepatocytes to control cholesterol levels, e.g. for treating or preventing hyperlipidemia, particularly atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-527333/44.
N-PSDB; AAZ09525.
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12-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 75-83; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bandyopadhyay PT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09940789-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY31237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-1998;
3923 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease; hypobetalipoproteinemia; dysbetalipoproteinemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
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98US-0074497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Apo B
/note= "Partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kren BT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
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This sequence represents the human apoliporptoein B-100 (apoB-100).

Fragments of this sequence can be used in the peptide of the invention, which has the formula (I), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolloporoein B-100 (apoB-100).

Z1 - KAQ-XI-KKNKHRHS-X2-T-Z2 (I), X1 = 5 or Y; X2 = T or I;
Z1 = the N terminus of the peptide, or 1-47 amino acids (as);
Z2 = the C terminus of the peptide, a terminal amide group or 1-77 as.
CC 22 = the C terminus of the peptide are used for simultaneous, separate or sequential treatment of cencer, particularly to prevent metastatic pread. They are also used to inhibit thromboplastin-mediated processes, specifically to prevent or reduce blood coagulation (e.g. during or after ungery or in cases of hear attack, stroke etc.) and to inhibit a critic as such or as part of a 98-as apptide, inhibits activation of the surface of thromboplastin and of platelets by thrombin. It binds to the surface of thromboplastin and of platelets by thrombin. It binds to the certains of the periduce S8-66 of thromboplastin. Since (I) are much smaller than
                          3731 SQELQQIHQYIMALREEYFDPSIVGWTVKYYELEEKIVSLIKNLLVALKDFHSEYIVSAS 3790
                                                                                                                                                                                                                                                                                                                                                                                      Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14; prothrombinase complex.
167 -----HQYLSLLQDRYFPIASVMRT-----LDKDNFSLTPDLI------- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity - used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis
                                                                                                                    3791 NFTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIAELSATAQEI--IKSQAIA 3843
                                                                              200 ---HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 42-47; 60pp; English
                                                                                                                                                                                                                      AAW41262 standard; peptide; 4536 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bruckdorfer KR, Ettelaie C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-GB01255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96GB-0009702.
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                Apolipoprotein B-100.
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68; Gaps

4.9%; Score 92; DB 19; Length 4536; 20.7%; Pred. No. 55; tive 48; Mismatches 118; Indels 6E

Conservative

Best Local Similarity Matches 61; Conserva

Query Match

4536 AA;

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Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoprotein (IDL), low density lipoproteins (VLDL), and lipoprotein a. The specification density lipoproteins (LDL), and lipoprotein a. The specification binding and in vivo transport of nucleic acids. Binding domains (see AAW96872-77) and nuclear localisation sequences (see AAW96878-97) for use in the composition can be derived from the present sequence. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis.
                           4184 YTRBELCTMFIREVGTVLSQVYSKVHNGSEIL-----FSYFQDLVITLPFE-----L 4230
                                                                                                                                                                                              4286 NIKQLKEMKFTYLINYIQDEINTIFNDYIPY--VFKLLKENLCLNLHKFNEFIQNELQEA 4343
                                                                                                                     4231 RKHKLIDVISMYREL----LKDLSKEAQEVFKAIQSLKTTEVL-RNLQDLLQFIFQLIED 4285
                                                                                                                                                                                                                                                                                      4344 SQELQQIHQYIMALREEYFDPSIVGWTVKYYELEEKIVSLIKNLLVALKDFHSEYIVSAS 4403
                                                                                  60 ARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                                                                                                                                                                   114 RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP---- 166
                                                                                                                                                                                                                                                        167 -----HOYLSLLQDRYFPIASVMRT-----LDKDNFSLTPDLI------ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition comprising nucleic acid bound to LDL or VLDL lipoprotein used for delivering nucleic acid to cells for gene therapy and
YCERTLDPKYILKIALKIRQSLSLFFQNSQSLQRAYSTPYSYYR---IILQKENKEKQAL
                                                                                                                                                                                                                                                                                                                                                                         4404 NFTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIABLSATAQEI--IKSQAIA 4456
                                                                                                                                                                                                                                                                                                                                             200 ---HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of human apolipoprotein B-100 (apoB-100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1A-C; 293pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW96826 standard; protein; 4536 AA.
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This polypeptide comprises a novel thermostable DNA polymerase of the thermophilic anaerobe Thermoanaerobacter thermophicous Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT90447). Recombinant DNA polymerase can be produced in host cells. The enzyme can be used in claimed methods: (a) for strand displacement amplification (SDA) when used with a thermostable restriction enzyme; (b) for production of cDNA when used in conjunction with polymerase and decoxyribonucleotides; and (c) to provide reverse transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4344
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                                                                                                                                                                                                                                                      Example 1; Page 49-52; 92pp; English.
                                                                                                                                                                                                                                                                                                                                     New DNA polymerase from Thermoanaerobacter thermohydrosulfuricus - useful for strand displacement amplification, reverse transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davis M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9721821-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermoanaerobacter thermohydrosulfuricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA polymerase; exonuclease; strand displacement amplification; Thermoanaerobacter thermohydrosulfuricans; reverse transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoanaerobacter thermohydrosulfuricus DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW26605 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4286 NIKQLKEMKFTYLINYIQDEINTIFNDYIPY--VFKLLKENLCLNLHKFNEFIQNELQEA 4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4231 RKHKLÍDVISMYREĹ----ĹKDĹŚKEAQĖVFKAIQSLKTTEVL-KNĹQDLLQFIFQĹIED 4285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4184 YTREELCTMFİREVGTVLSQVYSKVHNGSEIL------FSYFQDLVITLPFE-----L 4230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMSH ) AMERSHAM LIFE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP---- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
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                                                                                                                                                                                                                                                                                                                                                                                                                 1997-332792/30.
DB; AAT90447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQELQQIHQYIMALREEYFDPSIVGWTVKYYELEEKIVSLIKNLLVALKDFHSEYIVSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----HQYLSLLQDRYFPIASVMRT-----LDKDNFSLTPDLI--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 20.7 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mamone JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0008688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US20225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          872
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     RESULT 48
AAY31812
ID AAY31
XX
AAY31812
AC AAY31
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Therm
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Therm
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DA PCR;
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PT Regio
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PD 23-SE
PD 17-MA
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                     Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity in RT-PCR. Mutagenic methods have been used to generate exonuclease-deficient DNA polymerases (see AAW26606-07) suited for sequencing, SDA and cDNA preparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
        Mamone JA, Davis M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY31812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY31812 standard; Protein;
                                                                                                                                                           17-MAR-1999;
                                                                                                                                                                                                             23-SEP-1999.
                                                                                                                                                                                                                                                              WO9947539-A1
                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoanaerobacter thermohydrosulfuricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA polymerase; thermostable enzyme; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermoanaerobacter thermohydrosulfuricus DNA polymerase
                                                                                                            18-MAR-1998;
                                                       (AMSH ) AMERSHAM PHARMACIA BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 LSGF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             525 VNSPKQLSEFLFEKLNLPVIKKTKTGYSTDSEVLEQLVPYNDIVSDIIEYRQLTKLKSTY 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 KKLLLEIEMPĹVEVLKSMEVSĠFTĽDKEVLKELSQKIDDRIGEI---LDKÍYKEAGYQFN 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 KEIFEKEDFEFTTHEÍKDFÍVRLSYKGIECKSKYIDTAVMAYÍLNPŚEŚNY--DLDRVLK 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 IKENIENNKELAIMSKRLATIKRDIPIEIDFEEYKVKKFNEEK------LLELFNK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 LLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 LKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSTPQE-TLFSIRHFDELVELTSKLEWMLDQGLLESIPLYN------QEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----FTVESGLIENHEGRKAYGAVLISSP-QELGHAFIDNVRVLPLELDQIIR----LPFN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KYL-KVD-VPSYEGIFGKGRDKKKIEEIDENILADYICSRCVYLFDLKEKLMNFIEEMDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRTLDKDNFSLTPDLIHDLL-------GHVPWLLHPSFSEFFINMGRLFT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLLQD------NRNIAFYPLIYEGEIKKIAFSFGKDTVYIDVFQTE-----DL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reverse transcription; exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDGF 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVIEKVQALPS-----KKQRIQTLQSNLIA---IVRCFW--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEFFSLIDNIKKE----SSIEIVD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 872 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                            98US-0044106
                                                                                                                                                           99WO-US05612
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
           Sha D;
                                                                                                                                                                                                                                                                                                                "motif B or O-helix region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    872 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --NHKVEKWSK----VDIKELV 309
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Misc-difference
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                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                 This sequence represents the DNA polymerase of Thermoanaerobacter thermohydrosulturious (Tt), deduced from PCR amplified genomic DNA (see AAZ19659). Claimed DNA polymerases (see AAX18131, AAX1815 and AAX31816) have the exonuclease activity of this enzyme removed by having 540-582 amino acids removed from the N-terminus or having an amino acid substitution at position 8 or 706 of the sequence. A novel method for PCR uses an enzymatically active DNA polymerase that has at least 80% identity in its amino acid sequence to the Tt DNA polymerase and has an exonuclease activity removed. Kits for and reverse transcription-PCR are claimed that utilise such Exonand reverse. The Tt DNA polymerase is stable at elevated bNA polymerases. The Tt DNA polymerase is stable at elevated temperatures, e.g. 70+ deg C. Removal of its exonuclease activity does not affect its ability to replicate DNA or its thermostability.
                                                  polymerase from Thermoanaerobacter thermohydrosulfuricus, used amplification, sequencing, polymerase chain reaction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : || :|| KYL-KVD-VPSYEGIFGKGRDKKKIEEIDENILADYICSRCVYLFDLKEKLANFIEEMDM 467
                                                                                                                                                                                                                                                                                                                                                                              4.8%; Score 91.5; DB 20; Length 872;
17.5%; Pred. No. 5.7;
Live 70; Mismatches 141; Indels 139; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 LEFFSLIDNIKKE----SSIEIVD-----NHKVEKWSK-----VDIKELV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 MRTLDKDNFSLTPDLIHDLL-------GHVPWLLHPSFSEFFINMGRLFT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVIEKVQALPS------XKQRIQTLQSNLIA---IVRCFW-------257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----FTVESGLIENHEGRKAYGAVLISSP-QELGHAFIDNVRVLPLELDQIIR---LPFN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468 KKLILEIEMPLVEVLKSMEVSGFTLDKEVLKELSQKIDDRIGEI---LDKIYKEAGYQFN 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 IKENIENNKELAIMSKRLATIKRDIPIEIDFEBYKVKKFNEEK------LLELFNK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 LLFVHLLSLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 GLLSDFLDHQAVIKFFELETHFSYYPV-----SGFVAPHQYLSLLQDRYFPIASV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 TLLQD------DRNIAFYPLIYEGEIKKIAFSFGKDTVYIDVFQTE-----DL 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                       14 LKIALKLROSLSEFFONSOSLORAYSTPYSYYRIILOKENKEKOALARHKCISILEFFKN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoanaerobacter thermohydrosulfuricus DNA polymerase D8A mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY31815 standard; Protein; 872 AA
                                                                                                            Example 6; Fig 2; 71pp; English.
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es 74; Conservative
                                                                                reverse transcription
           WPI; 1999-562049/47.
N-PSDB; AAZ19859.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA polymerase from Thermoanaerobacter thermohydrosulfuricus, used for DNA amplification, sequencing, polymerase chain reaction and
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Local Similarity 17.5%; Pred. No. 5.7;
Les 74; Conservative 70; Mismatches 141; Indels 139; Gaps
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DNA polymerase, thermostable enzyme, amplification; sequencing; PCR; reverse transcription; exonuclease; mutant.
                                                                                                                                                                                                                                                                                                                                           /note= "wild-type Asp is substituted by Ala"
                                                                                                                             Thermoanaerobacter thermohydrosulfuricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMSH ) AMERSHAM PHARMACIA BIOTECH INC.
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ARAY31816
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AXX Therm
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                                                  This sequence represents a claimed mutant DNA polymerase of Thermoanaerobacter thermohydrosulfurious (Tt) in which the Phe-706 residue of the native enzyme is replaced by Tyr. This amino acid substitution removes the exonuclease activity of the DNA polymerase. Claimed DNA polymerases have their exonuclease activity removed by N-terminal deletion or amino acid substitution. A novel method for PCR uses an enzymatically active DNA polymerase that has at least 80% identity in its amino acid sequence to the Tt CDNA polymerase and has an exonuclease activity removed. Kits for PCR, strand displacement amplification of DNA, DNA sequencing, and reverse transcription-PCR are claimed that utilise such Exo-CDNA polymerases. The Tt DNA polymerase is stable at elevated temperatures, e.g. 70+ deg C. Removal of its exonuclease activity does not affect its abbility to replicate DNA or its thermostability. Note: the present sequence is not shown in the specification but is considered from the Tt DNA polymerase sequence given in figure 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA polymerase from Thermoanaerobacter thermohydrosulfuricus, used for DNA amplification, sequencing, polymerase chain reaction and reverse transcription -
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   872 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 IKENIENNKELAIMSKRLATIKRDIPIEIDFEEYKVKKFNEEK------LLELFNK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 LKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKN 73
                                                                                                                                                                                                                                                                                                                                          MRTLDKDNFSLTPDLIHDLL-------GHVPWLLHPSFSEFFINMGRLFT 226
IDGF 588
                                                                        VNSPKQLSEPLFEKLNLPVIKKTKTGYSTDSEVLEQLVPYNDIVSDIIEYRQLTKLKSTY
                                                                                                           TSTPQE-TLFSIRHFDELVELTSKLEWMLDQGLLESIPLYN------QEKY
                                                                                                                                                 KKLLLEIEMPLVEVLKSMEVSGFTLDKEVLKELSQKIDDRIGEI---LDKIYKEAGYQFN
                                                                                                                                                                                                                            KYL-KVD-VPSYEGIFGKGRDKKKIEEIDENILADYICSRCVYLFDLKEKLMNFIEEMDM 467
                                                                                                                                                                                                                                                                                                       KEIFEKEDFEFTTHEIKDFLVRLSYKGIECKSKYIDTAVMAYLLNPSESNY--DLDRVLK 409
                                                                                                                                                                                                                                                                                                                                                                               TLLQD------NRNIAFYPLIYEGEIKKIAFSFGKDTVYIDVFQTE-----DL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEFFSLIDNIKKE-----SSIEIVD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAF 133
                                                                                                                                                                                      ----FTVESGLIENHEGRKAYGAVLISSP-QELGHAFIDNVRVLPLELDQIIR----LPFN
                                                                                                                                                                                                                                                               KVIEKVQALPS-----KKQRIQTLQSNLIA---IVRCFW----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                             --NHKVEKWSK-----VDIKELV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                              353
                                                                          584
                                                                                                                                                   524
                                                                                                                                                                                      309
                                                                                                                                                                                                                                                                 257
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Search completed: January 9, 2003, 15:27:08 Job time: 77 secs